

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 15:33:17 ; Search time 380.684 Seconds

(without alignments)

3996.417 Million cell updates/sec

Title: US-10-692-367-12

Perfect score: 1452

Sequence: 1 SMQNGCQPNVCCSKFGYCG.....GYRYQYRQLGVDFGNMLTC 257

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq l6Dec04:\*

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4: geneseqn2001as:\*  
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6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1452	100.0	774	13 ADS92627	Ads92627 Chitinase
2	1435	98.8	774	13 ADS92645	Ads92645 Chitinase
3	1435	98.8	774	13 ADS92649	Ads92649 Chitinase
4	1405	96.8	774	13 ADS92687	Ads92687 Chitinase
5	1382.5	95.2	771	13 ADS92675	Ads92675 Chitinase

6	1382	95.2	774	13	ADS92661	Ads92661 Chitinase
7	1377	94.8	774	13	ADS92681	Ads92681 Chitinase
8	1373.5	94.6	771	13	ADS92677	Ads92677 Chitinase
9	1366.5	94.1	771	13	ADS92663	Ads92663 Chitinase
10	1363	93.9	774	13	ADS92679	Ads92679 Chitinase
11	1361.5	93.8	771	13	ADS92689	Ads92689 Chitinase
12	1361	93.7	774	13	ADS92639	Ads92639 Chitinase
13	1361	93.7	774	13	ADS92653	Ads92653 Chitinase
14	1356.5	93.4	765	13	ADS92683	Ads92683 Chitinase
15	1353.5	93.2	753	13	ADS92659	Ads92659 Chitinase
16	1351.5	93.1	771	13	ADS92699	Ads92699 Chitinase
17	1342	92.4	780	13	ADS92655	Ads92655 Chitinase
18	1339	92.2	780	13	ADS92691	Ads92691 Chitinase
19	1338.5	92.2	753	13	ADS92697	Ads92697 Chitinase
20	1333.5	91.8	765	13	ADS92641	Ads92641 Chitinase
21	1333	91.8	840	11	ADJ112126	ADJ112126 Maize cDN
22	1332	91.7	774	13	ADS92623	Ads92623 Chitinase
23	1323.5	91.2	753	13	ADS92667	Ads92667 Chitinase
24	1318.5	90.8	753	13	ADS92685	Ads92685 Chitinase
25	1318.5	90.8	771	13	ADS92657	Ads92657 Chitinase
26	1315.5	90.6	753	13	ADS92651	Ads92651 Chitinase
27	1315.5	90.6	777	13	ADS92631	Ads92631 Chitinase
28	1305.5	89.9	753	13	ADS92693	Ads92693 Chitinase
29	1304.5	89.8	753	13	ADS92671	Ads92671 Chitinase
30	1300.5	89.6	777	13	ADS92619	Ads92619 Chitinase
31	1299	89.5	750	13	ADS92695	Ads92695 Chitinase
32	1297.5	89.4	1094	3	AAA96222	AAA96222 cDNA enco
33	1295.5	89.2	753	13	ADS92665	Ads92665 Chitinase
34	1294.5	89.2	753	13	ADS92673	Ads92673 Chitinase
35	1292.5	89.0	753	13	ADS92637	Ads92637 Chitinase
36	1290.5	88.9	753	13	ADS92647	Ads92647 Chitinase
37	1282.5	88.3	753	13	ADS92669	Ads92669 Chitinase
38	1273.5	87.7	753	13	ADS92643	Ads92643 Chitinase
39	1220	84.0	756	13	ADS92629	Ads92629 Chitinase
40	1218	83.9	756	13	ADS92621	Ads92621 Chitinase
41	1212	83.5	756	13	ADS92625	Ads92625 Chitinase
42	1071	73.8	843	8	ADA70140	Ada70140 Rice gene
43	1071	73.8	843	11	ADJ11575	ADJ11575 Rice cDNA
c 44	1071	73.8	906	11	ADJ11773	ADJ11773 Rice cDNA
c 45	1071	73.8	909	11	ADJ11435	ADJ11435 Rice cDNA

#### ALIGNMENTS

RESULT 1  
ADS92627  
ID ADS92627 standard; DNA; 774 BP.  
XX  
XX  
AC ADS92627;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
XX Chitinase variant polynucleotide #5.  
Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
Heterodera.  
XX  
OS Synthetic.  
XX  
XX WO2004037194-A2.  
XX  
XX 06-MAY-2004.  
XX  
XX 22-OCT-2003; 2003WO-US033588.  
XX  
XX 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
XX (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;

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XX WPI; 2004-365417/34.
DR P-PSDB; ADS92628.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
XX Disclosure; SEQ ID NO 11; 197pp; English.
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
XX Sequence 774 BP; 139 A; 251 C; 278 G; 106 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 4,896-114 Length: 774
Score: 1452.00 Matches: 257
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-692-367-12 (1-257) x ADS92627 (1-774)
QY 1 SerMetGlnAnCysGlyCysGlnProAnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTCGCGTGCAGCAACATGATGCTGCAGCAAGTTTGGCTACTGCGGC 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
DB 61 ACGACGACGAGTACTGCGGCGAGCGGTGCCAGTCCGCGCGTCCGCGCGCGGT 120
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ValThrAspAlaPhePheAsnGlyTyrLysAsnGlnAlaGlySerGlyCysGlyCysGly 80
DB 181 GTCACCGACGCGTTCCTCAACGCGATCAAGAACCGAGCGCGGCGCGGCGCGCAAG 240
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaAlaAlaAlaTyrProGlyPheAlaHis 100
DB 241 AACTTCTACACCGAGCGCGTTCCTCGAGCGCATCGCGCGTACCGCGGCTTCGCGCAT 300
QY 101 GlyGlySerGluValGluArgLysArgGluLeuAlaAlaPhePheAlaHisAlaThrHis 120
DB 301 GCGCGCTCCGAGTCCGAGCGAAGCGCGAGATTCGCGCTTCCTTCGCGCACGCCGCGCAC 360
QY 121 GluThrGlyHisPheCysTyrLysSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
DB 361 GAGACCGGCGCATTCCTGTCTACATCGAGCGAGGTCAACAGAGACCGCTACTGCGACCCG 420
QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
DB 421 ACCAAGAGCGAGTGGCGCGCGCGCGCGAGAGTACTACGCGCGCGCGCGCGCGCG 480
QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaAlaGlyPheAspGlyLeuGly 180
DB 481 ATCTCGTGAATACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200
DB 541 GACCCCGGAGGTTGGCGCGGAGCCCGTGTGGTGGCTTCAAGCGCGCGCGCTCTGGTTCGG 600
QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
DB 1 SerMetGlnAnCysGlyCysGlnProAnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTCGCGTGCAGCAACATGATGCTGCAGCAAGTTTGGCTACTGCGGC 60
601 ATGAACAACGTCGACCGTGTGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
221 GlyAlaLeuGluCysAsnGlyAsnAspProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
661 GCGCGCTCCGAGTGCAGCGGAGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
721 AGGCGTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 771
RESULT 2
ADS92645
ID ADS92645 standard; DNA; 774 BP.
XX
AC ADS92645;
XX
DT 02-DEC-2004 (first entry)
XX
DB Chitinase variant polynucleotide #12.
XX
XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX Heterodera.
XX
XX Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
PA
PA (PTON-) PIONEER HI-BRED INT INC.
XX
XX Muller ML, True T, Simmons CR, Yalpani N;
XX
XX WPI; 2004-365417/34.
DR P-PSDB; ADS92646.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 29; 197pp; English.
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
XX Sequence 774 BP; 137 A; 251 C; 279 G; 107 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1,35e-112 Length: 774
Score: 1435.00 Matches: 254
Percent Similarity: 99.22% Conservative: 1
Best Local Similarity: 98.83% Mismatches: 2
Query Match: 98.83% Indels: 0
DB: 13 Gaps: 0
US-10-692-367-12 (1-257) x ADS92645 (1-774)
QY 1 SerMetGlnAnCysGlyCysGlnProAnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTCGCGTGCAGCAACATGATGCTGCAGCAAGTTTGGCTACTGCGGC 60
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QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 DB 61 ACACCGACGAGTACTCGCGGACGGGTGCGAGTGGCGCGCGTCCGCTCGCGGGCGGT 120  
 QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 DB 121 GCG 180  
 QY 61 ValThrAspAlaPhePheAsnGlyIleLeuValAsnGlnAlaGlySerGlyCysGluGly 80  
 DB 181 GTCACCGACGCGTCTTCAACGGCATCAAGAACAGCGCGCGCGCGCGCGCGCG 240  
 QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaTyrProGlyPheAlaHis 100  
 DB 241 AACTTCTACACCGAGCGGTCTCTCGAGGCCATCGCGCGGTACCGCGGCTTCGCGCAT 300  
 QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120  
 DB 301 GCGCGCTCCGAGGTGCGAGCGCAGCGCGAGATTGCGCGCTTCTTCGCGCAGCGCGCAG 360  
 QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
 DB 361 GAGACCGCGCATTTCTGTCTACATCAGCGAGGTCAACAGAGCAACGCTACTCGGACCG 420  
 QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160  
 DB 421 ACCAAGAGCGAGTGGCGTGGCGCGCGCGCGAGAGTACTACGGCGCGCGCGCGCG 480  
 QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 DB 481 ATCTCGTGAACACTACACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
 QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200  
 DB 541 GACCCCGCAGGGTGGCGCGGACCGCGTGGTGGCGTTTCAAGCGCGCGCTCTGGTCTGG 600  
 QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
 DB 601 ATGAACAACGTCACCGGTGATCGCGCAGGGCTTCGCGCGCACCCATCAGGGCGCATCAAC 660  
 QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
 DB 661 GCGCGCTCTGAGTGGCGCGGAGAACACCCCGCCAGATGAACGCGCGCGCTCGGTACTAC 720  
 QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
 DB 721 AAGCAGTACTCGCGCAGCTCGCGGTGCGACCCAGCGCGCCCAACCTTCACTTGC 771

## RESULT 3

ADS92649

ID ADS92649 standard; DNA; 774 BP.

XX AC ADS92649;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #14.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

XX KW Heterodera.

XX OS Synthetic.

XX FN WO2004037194-A2.

XX PD 06-MAY-2004.

XX XX 22-OCT-2003; 2003WO-US033588.

XX XX 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX

(VERD-) VERDIA INC.  
 (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Valpani N;  
 XX DR WPI; 2004-365417/34.

XX DR P-FSDB; ADS92650.

XX PT New chitinase polynucleotides and polypeptides, useful in producing  
 XX PT plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 4; SEQ ID NO 33; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprising introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.

SQ Sequence 774 BP; 138 A; 251 C; 278 G; 107 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.35e-112 Length: 774  
 Score: 1435.00 Matches: 254  
 Percent Similarity: 99.22% Conservative: 1  
 Best Local Similarity: 98.83% Mismatches: 2  
 Query Match: 98.83% Indels: 0  
 DB: 13 Gaps: 0

US-10-692-367-12 (1-257) x ADS92649 (1-774)

QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 DB 1 TCGATGACAGAACTCGCGCTGCCAGCCAAAGATATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
 QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 DB 61 ACAACCGACGAGTACTCGCGCGAGCGGTGCGAGTCCGCGCGCGCTCGCGCGCGGT 120  
 QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 DB 121 GCG 180  
 QY 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
 DB 181 GTACCGACCGGTCTTTCACCGCGCATCAAGAACCGCGCGCGCGCGCGCGCGCG 240  
 QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100  
 DB 241 AACTTCTACACCGAGCGGTCTCTCGAGGCCATCGCGCGGTACCGCGGCTTCGCGCAT 300  
 QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120  
 DB 301 GCGCGCTCCGAGGTGCGAGCGCAGCGCGAGATTGCCGCTTCTTCGCGCAGCGCGCAG 360  
 QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
 DB 361 GAGACCGCGCATTTCTGTCTACATCAGCGAGGTCAACAGAGCAACGCTTACTCGGACCG 420  
 QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
 DB 421 ACCAAGAGCGAGTGGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 DB 481 ATCTCGTGAACACTACACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
 QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200

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Db 541 GACCCCGCAGGCTGGCGCGGAGCGCGTGTGGCTTCAAGGCGCGCTCTGTTCTGG 600
Qy 201 MetAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
Db 601 ATGAACAACGTCACCGCTGTATCGCGCAGGCTTCGGCGCCACCATCAGGGCCATCAAC 660
Qy 221 GlyAlaLeuGluCysAenGlyAenAenProAlaGlnMetAenAlaArgValGlyTyrTyr 240
Db 661 GCGCCCTCTGAGTGGCGGGAACACCCCGCCAGATGAACGCGCGTCTGGCTACTAC 720
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257
Db 721 AAGCAGTACTCCCGCAGCTCGCGTGCAGCCAGGCGCCCACTTGC 771

```

## RESULT 4

ADSS92687  
ID ADS92687 standard; DNA; 774 BP.

XX AC ADSS92687;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #33.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
Heterodera.

XX OS Synthetic.

XX FN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PI (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX DR P-PSDB; ADSS92688.

XX PT New chitinase polynucleotides and polypeptides, useful in producing  
plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 4; SEQ ID NO 71; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
encoding them. A method of enhancing plant resistance to a fungus or  
nematode comprises introducing into a plant a recombinant expression  
cassette comprising a promoter operably linked to a chitinase  
polynucleotide of the invention. The plant is maize or soybean. The  
fungus is from the genus *Fusarium*. The nematode is from the genus  
*Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
plant resistance to a fungus or nematode. This sequence represents a  
chitinase variant polynucleotide of the invention.

XX SQ Sequence 774 BP; 142 A; 249 C; 278 G; 105 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	4.72e-110	Length:	774
Score:	1405.00	Matches:	245
Percent Similarity:	98.44%	Conservative:	8
Best Local Similarity:	95.33%	Mismatches:	4
Query Match:	96.76%	Indels:	0
DB:	13	Gaps:	0

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US-10-692-367-12 (1-257) x ADSS92687 (1-774)
Qy 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAAGAACTCGCGCTGCCAGCCAAAGATATGCTGCAGCAAGTTCCGCTACTCGGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCCAGCAGTACTCGCGCGACGCGGTGCGAGTCCGCGCGCTCGCGCGCGCGGT 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 61 ValThrAspAlaPhePheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTACCCGACGCGTCTTCAACGCGCATCAAGAGCCAGCCGCGGAGCGGTGCGAGGCAAG 240
Qy 81 AenPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIleHis 100
Db 241 AACTTCTACACCGCGAGCGCGTTCCTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCAT 300
Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
Db 301 GCGCGGTCAACAGGTGCGAGGCAAGCGGAGATCGCGCTTCCTTCGCGCGCGCGCGCGC 360
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAenLysSerAenAlaTyrCysAspPro 140
Db 361 GAGACCGCGGCATTCTGCTACATCAGCGAGATCAACAGAGCAACGCTACTCGGACCCG 420
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGGAGTGGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCAG 480
Qy 161 IleSerTyrAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGGAACTACAACACTACGGGCGCGCGGAGGCGCATCGCGCTTCGAGCGGCTCGGG 540
Qy 181 AspProGlyArgValAlaArgAspAlaValAlaAlaPheLysAlaAlaLeuTyrPheTyr 200
Db 541 GACCCCGCAGGTTGGCGCGGAGCGCGTGGTGGCGTTCAAGGCGCGCTCTGGTTCTGG 600
Qy 201 MetAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
Db 601 ATGAACAACGTCACCGCTGTATCGCGCAGGCTTCGGCGCGCCACCATCAGGGCCATCAAC 660
Qy 221 GlyAlaLeuGluCysAenGlyAenAenProAlaGlnMetAenAlaArgValGlyTyrTyr 240
Db 661 GCGCGCTCGAGTGCAGCGGGAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257
Db 721 AAGCAGTACTCCCGCAGCTCGCGTGCAGCCAGGCGCCCACTTGC 771

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## RESULT 5

ADSS92675

ID ADS92675 standard; DNA; 771 BP.

XX AC ADSS92675;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #27.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
Heterodera.

XX OS Synthetic.

XX FN WO2004037194-A2.

XX PD 06-MAY-2004.

XX XX

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PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR P-PSDB; ADS92676.
XX
PT New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 4; SEQ ID NO 59; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 771 BP; 139 A; 247 C; 274 G; 111 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.8e-108 Length: 771
Score: 1382.50 Matches: 244
Percent Similarity: 96.89% Conservative: 5
Best Local Similarity: 94.94% Mismatches: 7
Query Match: 95.21% Indels: 1
DB: 13 Gaps: 1

US-10-692-367-12 (1-257) x ADS92675 (1-771)
QY 1 SerMetGlnAanCysGlyCysGlnProAanValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAAGAACTGCGGCTGCAGGCCAACTTCTCTGCAGCAAGATTGGCTACTCGGCG 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
DB 61 ACGACCGACGCTACTGCGGCGAGCGGTGCGAGTCCGAGTCCGCGCGCTCG---GGCGGC 117
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB 118 GGTGCGCGCGTGGCGCGGAGCGCGCGGCGGAGCGAGTGGCGGTGCGAACTGGCTAATGTG 177
QY 61 ValThrAspAlaPhePheAsnGlyTyrLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
DB 178 GTCAACGACGGCTTCTTCAACGGCATCAAGAACCCAGCGCGGAGCGGTGCGAGCGCAAG 237
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaHis 100
DB 238 AACTTCTACACCCGAGCGGTCTCTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCAT 297
QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaIleAlaPheAlaHisAlaThrHis 120
DB 298 GGCGGGTTCACAGGTGCAGGGAAGCGGAGATTGCGGCTTCTTTCGCGCATGTGCACGCAC 357
QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
DB 358 GAGACCGGGCATTTCTGTACTACGCGAGATCAACAAGACAGCGCTACTGCGACCCG 417
QY 141 ThrLysArgGlnTrrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
DB 418 ACCAAGAGCGAGTGGCGGTGCGCGCGGCGGAGAGTACTACGGGCGGCGGCGCTGCGAG 477

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QY 161 IleserTrpAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
DB 478 ATCTCGTGGAACTACAACTACGGGCGCGGGAGGGCCATCGGCTTCGACGGGCTCGGG 537
QY 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrrPheTrrP 200
DB 538 GACCCCGGACGGGTGGCGGGAGCGCGTGGTGGCGTTCAGAGGGCGGCTCTGGTTCGG 597
QY 201 MetAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
DB 598 ATGAACAACGTCACCGTGTATCGCGAGGGCTTCGCGCGCACCATCAGGGCCATCAAC 657
QY 221 GlyAlaLeuGluCysAsnGlyAsnProAlaGlnMetAenAlaArgValGlyTyrTyr 240
DB 658 GCGCGCTTCGAGTGCAGCGGAAACACCCCGCCAGATGAACGCGCGGCTCGGCTACTAC 717
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAsnLeuThrCys 257
DB 718 AGCAGTACTGCCCGCAGCTCGGCTCGACCCAGGCGCCCACTCCTTGC 768

RESULT 6
ADS92661
ID ADS92661 standard; DNA; 774 BP.
XX
AC ADS92661;
XX
DT 02-DEC-2004 (first entry)
XX
DB Chitinase variant polynucleotide #20.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR P-PSDB; ADS92662.
XX
PT New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 4; SEQ ID NO 45; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 774 BP; 139 A; 249 C; 282 G; 104 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.21e-108 Length: 774
Score: 1382.00 Matches: 241

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Percent Similarity: 97.28%      Conservative: 9
Best Local Similarity: 93.77%    Mismatches: 7
Query Match: 95.18%             Indels: 0
DB: 13                          Gaps: 0

US-10-692-367-12 (1-257) x ADS92661 (1-774)

Qy 1 SerMetGlnAnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGTGCAGCAACGATATGCTGCAGCCGTTTCGGCTACTGCGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlySerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGAGTACTCGCGGACGCGGTTCGGCTGCAGCCGTTTCGGCTACTGCGGC 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGAGCGGCGGAGGCGAGCGGCGGCGGCGGCGGCGGCGGCAAG 180
Qy 61 ValThrAspAlaPhePheAsnGlyLysGlyGlyGlyGlyGlyGlyGlyGlyGly 80
Db 181 GTCAACCGACGCGTTCCTTCAACCGGATCAAGAACCGAGCGGCGGCGGCGGCGGCAAG 240
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaAlaAlaTyrProGlyPheAlaHis 100
Db 241 AACTTCTACACCGGAGCGGCTTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCAT 300
Qy 101 GlyGlySerGluValGluArgLysArgLysArgLysArgLysArgLysArgLys 120
Db 301 GCGCGGTTCGACGAGTGCAGGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 360
Qy 121 GluThrGlyHisPheCysGlyTyrLysSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGGCGATTTCTGCTACATCAGCGAGATCAACAGGAGCAACGCTTCTGCGACCCG 420
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGGAGTGGCGGTGCGCGCGGCGGCGGAGTACTAGCGGCGGCGGCGGCGGCG 480
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaLysGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGGAACTACAATACGCGCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 540
Qy 181 AspProGlyArgValAlaArgAspAlaValAlaAlaPheLysAlaAlaLeuTyrPheTrp 200
Db 541 GACCCCAACAGGTTGGCGGAGCGGCGGAGCGGCGGAGTTCAGGCGGCGGCGGCGGCGG 600
Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaLys 220
Db 601 ATGAACAGCGTGCAGCGGTTGTTGCGCGGCGGCGGAGTTCGCGCGGCGGCGGCGGCGG 660
Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240
Db 661 GCGCGCTTCGAGTGCACGGGAACAACCCCGCCAGATGAACGCGCGGCGGCGGCGGCTACTAC 720
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 721 AAGCAGTACTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 771

RESULT 7
ADS92681
ID ADS92681 standard; DNA; 774 BP.
XX
AC ADS92681;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polynucleotide #30.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX Heterodera.
OS Synthetic.

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XX WO2004037194-A2.
PN
XX
XX 06-MAY-2004.
PD
XX
XX 22-OCT-2003; 2003WO-US033588.
PF
XX
XX 22-OCT-2002; 2002US-0420666P.
PR
XX 06-NOV-2002; 2002US-00290086.
PR
XX 14-MAR-2003; 2003US-00389432.
PR
XX
XX (VERD-) VERDIA INC.
PA
XX (PION-) PIONEER HI-BRED INT INC.
PA
XX
XX Muller ML, True T, Simmons CR, Valpani N;
PI
XX
XX WPI; 2004-365417/34.
DR
XX P-PSDB; ADS92682.
DR
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
PT
XX
XX Claim 4; SEQ ID NO 65; 197pp; English.
PS
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 774 BP; 142 A; 250 C; 272 G; 110 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.12e-107      Length: 774
Score: 1377.00           Matches: 240
Percent Similarity: 96.50%      Conservative: 8
Best Local Similarity: 93.39%    Mismatches: 9
Query Match: 94.83%             Indels: 0
DB: 13                      Gaps: 0

US-10-692-367-12 (1-257) x ADS92681 (1-774)

Qy 1 SerMetGlnAnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGTGCAGCAACGATATGCTGCAGCAAGTTCGGCTACTGCGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlySerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGAGTACTCGCGGACGCGGTTCGGCTGCAGCCGTTTCGGCTACTGCGGC 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGAGCGGCGGAGGCGAGCGGCGGCGGCGGCGGCGGCGGCAAG 180
Qy 61 ValThrAspAlaPhePheAsnGlyLysGlyGlyGlyGlyGlyGlyGlyGlyGly 80
Db 181 GTCAACCGACGCGTTCCTTCAACCGGATCAAGAACCGAGCGGCGGCGGCGGCGGCAAG 240
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaAlaAlaTyrProGlyPheAlaHis 100
Db 241 AACTTCTACACCGGAGCGGCTTCCTGAGCGCCGTCAAGGCGTACCCAGGCTTCGCCCAT 300
Qy 101 GlyGlySerGluValGluArgLysArgLysArgLysArgLysArgLysArgLys 120
Db 301 GCGCGGTTCGACGAGTGCAGGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 360
Qy 121 GluThrGlyHisPheCysGlyTyrLysSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGGCGATTTCTGCTACATCAGCGAGATCAACAGGAGCAACGCTTCTGCGACCCG 420

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QY 141 ThrLysArgGlnTTPProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
 DB |||||  
 QY 421 ACCAAGAGCGAGTGGCGTGGCGCGGAGAGTACTACGGCGGTGGCGCGTGCAG 480  
 DB |||||  
 QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 DB |||||  
 QY 481 ATCTGTGGAACTACACTACGGCGCGCGGAGGCGCATCGGCTTCAGCGGCTGCC 540  
 DB |||||  
 QY 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
 DB |||||  
 QY 541 GACCCCAACAGGTGGCGCAGACGCCGTGGTGGCTTCAAGCGCGGCTCTGGTCTCG 600  
 DB |||||  
 QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
 DB |||||  
 QY 601 ATGAACAACAGTGCACCGGTGTATCCCGCAGGCTTCGGCGCCACCATCAGGGCCATCAAC 660  
 DB |||||  
 QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
 DB |||||  
 QY 661 GGCGCCCTCGAGTGGCGGCGGGAACACCCCGCCAGATGAACGGCGGCTCGGCTACTAC 720  
 DB |||||  
 QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
 DB |||||  
 QY 721 AAGCAGTACTGCCGCCAGCTCGCGCTCGACCCAGGCGCCAACTCACTTGC 771  
 DB |||||

## RESULT 8

ADS92677  
 ID ADS92677 standard; DNA; 771 BP.

XX AC ADS92677;

XX DT 02-DEC-2004 (first entry)

XX CC Chitinase variant polynucleotide #28.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 KW Heterodera.

XX OS Synthetic.

XX FN WO2004037194-A2.

XX PD 06-MAY-2004.

XX XX 22-OCT-2003; 2003WO-US033588.

XX PF 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX XX (VERD-) VERDIA INC.

XX PA (PTON-) PIONEER HI-BRED INT INC.

XX XX Muller ML, True T, Simmons CR, Yalpani N;

XX XX WPI; 2004-365417/34.

XX DR P-PSDB; ADS92678.

XX XX New chitinase polynucleotides and polypeptides, useful in producing

XX PT plants with enhanced resistance against a fungus or a nematode.

XX XX Claim 4; SEQ ID NO 61; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus Fusarium. The nematode is from the genus  
 CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.

XX

SQ Sequence 771 BP; 139 A; 255 C; 272 G; 105 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2.2e-107 Length: 771  
 Score: 1373.50 Matches: 242  
 Percent Similarity: 97.28% Conservative: 8  
 Best Local Similarity: 94.16% Mismatch: 6  
 Query Match: 94.59% Indels: 1  
 DB: 13 Gaps: 1

US-10-692-367-12 (1-257) x ADS92677 (1-771)

QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 DB 1 TCGATGCAGAACTCGCGCTGCCAGCCAAAGTATGTCTGCAGCAAGTTTCGGCTACTCGGCG 60  
 QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 DB 61 ACGACCGACGAGTACTCGCGGACCGGTGCAGTTCGGGCCGCTGCCGCCG---GGCGGC 117  
 QY 41 Gly 60  
 DB 118 GCGCGCGTGGCGCGCGCGAGCGCGGAGCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 177  
 QY 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
 DB 178 GTCACCGGCTCTCTTCAACCGGCATCAAGAGCCAGCGCGAGCGGCTGCAGGGCGAAG 237  
 QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100  
 DB 238 AACTTCTACACCGGAGCGGCTTCTGAGCGCGCTCAAGGGGTACCCAGGGCTTCGCCCAT 297  
 QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120  
 DB 298 GCGCGCTCCGAGTTCGAGCGCAAGCGGAGATTGCCGCTTCTTCGCGCAGCGCACGCGCAC 357  
 QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
 DB 358 GAGACCGGGCATTTCTGTCTACATCAACGAGATCAACAGAGCAACGCGCTACTGCGAGCCG 417  
 QY 141 ThrLysArgGlnTTPProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
 DB 418 ACCAAGAGCGAGTGGCGTGGCGCGCGGCGGAGGAGTACTACGGGCGCGGCGCGCTGCAG 477  
 QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 DB 478 ATCTGTGGAACTACAACTAGCGCGCGCGGAGGCGCATCGCTTCGACGGGCTCGCC 537  
 QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200  
 DB 538 GACCCCGCAGGTGGCGCGGAGCGCGTGGTGGCTTCAAGCGCGGCGCTCTGGTTCGCG 597  
 QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
 DB 598 ATGAACAACGTGCACCGGTGTATCCCGCAGGCTTCGGCGCCACCATCAGGGCCATCAAC 657  
 QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
 DB 658 GCGCGCTCGAGTGCAGCGGAGCAACACCCCGCCAGATGAACGCGCGGCTCGGCTACTAC 717  
 QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
 DB 718 AAGCAGTACTGCCGCCAGCTCGCGCTCGACCCAGGCGCCAACTCACTTGC 768

## RESULT 9

ADS92663

ID ADS92663 standard; DNA; 771 BP.

XX AC ADS92663;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #21.



CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.

SQ Sequence 774 BP; 144 A; 256 C; 269 G; 105 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.72e-106 Length: 774  
 Score: 1363.00 Matches: 237  
 Percent Similarity: 96.11% Conservativeness: 10  
 Best Local Similarity: 92.22% Mismatches: 10  
 Query Match: 93.87% Indels: 0  
 DB: 13 Gaps: 0

US-10-692-367-12 (1-257) x ADS92679 (1-774)

Qy 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20  
 Db 1 TCGATGCAGAACTGGCGTGCAGCCAACTTCCTGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
 Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40  
 Db 61 ACAACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCGCTGCGCGCGCGGC 120  
 Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 Db 121 GCG 180  
 Qy 61 ValThrAspAlaPhePheAsnGlyLysGlnAlaGlySerGlyCysGluGlyLys 80  
 Db 181 GTCACCGACGGCTTCCTCAGCGGATCAGAACCGCGCGCGCGCGCGCGCGCGCGCG 240  
 Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaAlaTyrProGlyPheAlaHis 100  
 Db 241 AACTTCTACACCGCGAGCGCTTCCTGAGCGCGCTCAAGGCGTACCCAGGCTTCGCCAT 300  
 Qy 101 GlyGlySerGluValGluArgGlyArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
 Db 301 GCGCGGTGCAGAGTGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
 Qy 121 GluThrGlyHisPheCysTyrLysSerGluValAlaLysSerAlaTyrCysAspPro 140  
 Db 361 GAGACCGCGCATTTCTGCTACTCAGCGAGATCAACAGACGACCGCTCTCGCGACCG 420  
 Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
 Db 421 ACCAAGAGGCGAGTGGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
 Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaLysGlyPheAspGlyLeuGly 180  
 Db 481 CTGTCGTGGAACTCAACTAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
 Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTyrPheTyr 200  
 Db 541 GACCCCAACAGGGTGGCGCGGAGACCCCGTGTGGCGTTCAAGGCGCGCGCTCTGGTCTGG 600  
 Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaAlaAsn 220  
 Db 601 ATGAACAACGTGCACCGCTGTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
 Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
 Db 661 GCGCGCTTCAAGTGGCGGGAACAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
 Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
 Db 721 AAGCAGTACTGCCCGCAGCTCGCGCTGACCCAGCGCGCGCGCGCGCGCGCGCGCG 771

RESULT 11

ID ADS92689

XX ADS92689 standard; DNA; 771 BP.

AC ADS92689;  
 DT 02-DEC-2004 (first entry)  
 XX Chitinase variant polynucleotide #34.  
 DB Chitinase; gene; ds; plant resistance; fungus; nematode; *Fusarium*;  
 KW *Heterodera*.  
 XX Synthetic.  
 XX WO2004037194-A2.  
 PD 06-MAY-2004.  
 XX 22-OCT-2003; 2003WO-US033588.  
 XX 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX Muller ML, True T, Simmons CR, Valpani N;  
 XX WPI; 2004-365417/34.  
 DR P-PSDB; ADS92690.  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX Claim 4; SEQ ID NO 73; 197pp; English.  
 PS The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.  
 XX SQ Sequence 771 BP; 140 A; 249 C; 275 G; 107 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 2.29e-106 Length: 771  
 Score: 1361.50 Matches: 237  
 Percent Similarity: 96.89% Conservativeness: 12  
 Best Local Similarity: 92.22% Mismatches: 7  
 Query Match: 93.77% Indels: 1  
 DB: 13 Gaps: 1

US-10-692-367-12 (1-257) x ADS92689 (1-771)

Qy 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20  
 Db 1 TCGATGCAGAACTGGCGTGCAGCCAACTTCCTGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
 Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
 Db 61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCGCTGCGCGCGCGCG 117  
 Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 Db 118 GCGCGCGGTGGCG 177  
 Qy 61 ValThrAspAlaPhePheAsnGlyLysGlnAlaGlySerGlyCysGluGlyLys 80  
 Db 178 GTCACCGACTCTCTTCAACGGCATCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCA 237  
 Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaAlaTyrProGlyPheAlaHis 100



Db 238 AACTTCTACACCCGAGCGCTTCTGAGCGCGCTCAAGGGTACTACCCAGGCTTCGCCCAT 297  
Qy 101 GlyGlySerGluValGluArgGlyArgGluLeuAlaPheAlaHisAlaThrHis 120  
Db 298 GCGCGGTCCGAGGTGCGAGGCAAGCGGAGATCCGCGCTTCTTCGGCGCATGTCAACGCAC 357  
Qy 121 GluThrGlyHisPheCysThrIleSerGluValAlaPheAlaHisAlaThrHis 140  
Db 358 GAGACCGGGCATTTCTGTACTACACGAGATCAACAGAGCAACGCCCTACTCGGACCCG 417  
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
Db 418 ACCAAGAGCGAGTGGCGGTGGCGCGGGCAGAGGTACTACGGCGGTGGCGCGCTGCAG 477  
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
Db 478 ATCTCGTGGAACTACAACTACGCGGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGG 537  
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 538 GACCCCGCAGGGTGGCGGGAGCGCGGTGGTGGGGTTCAAGGGCGCGCTCTGGTTCTGG 597  
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
Db 598 ATGAACAACGTGCACCGTGTGTCGCGCAGCGGCTTCGGCGCCACCATCAGGGCCCAAC 657  
Qy 221 GlyAlaLeuGluCysAsnGlyAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
Db 658 GCGCGCTTCGAGTGCAGCGGAACAACCCCGCCAGATGAACGCGCGCATCGGCTACTAC 717  
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257  
Db 718 AAGCAGTACTGCGCGCAGCTCGCGTGCACCGCGGCCCAACCTCCTTC 768  
RESULT 12  
ADS92639  
ID ADS92639 standard; DNA; 774 BP.  
AC ADS92639;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #9.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
FN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
DR WPI; 2004-365417/34.  
DR P-PSDB; ADS92640.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 4; SEQ ID NO 23; 197pp; English.  
XX

CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX

SQ Sequence 774 BP; 146 A; 246 C; 271 G; 111 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 2,54e-106 Length: 774  
Score: 1361.00 Matches: 237  
Percent Similarity: 95.72% Conservative: 9  
Best Local Similarity: 92.22% Mismatches: 11  
Query Match: 93.73% Indels: 0  
DB: 13 Gaps: 0

US-10-692-367-12 (1-257) x ADS92639 (1-774)

Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
Db 1 TCGATGCAGAACTCGCGCTGCCAGCAACGATATGCTGCAGCAAGTTTGGCTACTCGGC 60  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACGACCCAGCAGTACTCGCGGCGAGGTCAGTTCGGCGCGCTCGCGCTCGCGCGCGGC 120  
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
Db 121 GGCAGCAGTGGCGCGCGCGGAGCGCGGAGGCGAGTGGCGTGCAGAACTGGCTAAATGTG 180  
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGlyGlyGly 80  
Db 181 GTCAACCGCGCTTCTTCAACGGCATCAAGAACAGCGCGCGAGCTGGTCGAGGGGCAAG 240  
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleTyrProGlyPheAlaHis 100  
Db 241 AACTTCTACACCCGAGCGCGTTCCTGAGCGCGCTCAAGGCTACCCAGGCTTTCGCCAT 300  
Qy 101 GlyGlySerGluValGluArgLysArgGluLeuAlaAlaPheAlaHisAlaThrHis 120  
Db 301 GCGCGGTCCGAGGTGCAGGGCAAGCGGAGATCGCGCTTCTTCGCGCATGTCAACGCAC 360  
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAlaPheLysSerAsnAlaTyrCysAspPro 140  
Db 361 GAGACCGGGCATTTTGTGTACTACATCAACGAGGTCAACAGAGCAACGCCCTACTCGGACCCG 420  
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
Db 421 ACCAAGAGCGAGTGGCGGTGGCGCGGGGCGAGGATCTACGGCGCGCGCGCGCTGCAG 480  
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
Db 481 ATCTCGTGGAACTACAACTACGCGCGCGCGGAGGCGCATCGGCTTCGACGGGTGGGA 540  
Qy 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 541 GACCCGACAGACTGGCGCGAGGACCCCGTGTGTTCGTTCAAGTCCGCGCTCGGTTCTGG 600  
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
Db 601 ATGAACAACGTGCACCGTGTGATGTCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 660  
Qy 221 GlyAlaLeuGluCysAsnGlyAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240  
Db 661 GCGCGCTTCGAGTGCAGCGGCAACAACCCCGCCAGATGAACGCGCGCGCTCGGCTACTAC 720  
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257  
Db 721 AAGCAGTACTGCGCGCAGCTCGCGTGCACCGCGGCCCAACCTCCTTC 771

RESULT 13
ADSN92653 standard; DNA; 774 BP.
ID AC ADS92653;
XX DT 02-DEC-2004 (first entry)
XX DE Chitinase variant polynucleotide #16.
XX XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX OS Synthetic.
XX PN W02004037194-A2.
XX PD 06-MAY-2004.
XX XX 22-OCT-2003; 2003WO-US033588.
XX PF 22-OCT-2002; 2002US-0420666P.
PR PR 06-NOV-2002; 2002US-00290086.
PR PR 14-MAR-2003; 2003US-00389432.
XX XX (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX PI Muller ML, True T, Simmons CR, Yalpani N;
XX DR WPI; 2004-365417/34.
DR DR P-PSDB; ADS92654.
XX PT New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX PS Claim 4; SEQ ID NO 37; 197bp; English.
CC CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
SQ Sequence 774 BP; 145 A; 251 C; 276 G; 102 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,54e-106 Length: 774
Score: 1361.00 Matches: 238
Percent Similarity: 95.72% Conservative: 8
Best Local Similarity: 92.61% Mismatches: 11
Query Match: 93.73% Indels: 0
DB: 13 Gaps: 0
US-10-692-367-12 (1-257) x ADS92653 (1-774)
Qy 1 SerMetGlnAsnCysGlyCysGlnProAnValCysCysSerIysPheGlyTyrCysGly 20
Dd 1 TCAGTCAGAACTGGCGGTGCCAGCAACATATGCTGCAGCAAGTTTGCTACTCGCGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Dd 61 ACGACCAGACGAGTACTGCGCGGACGGGTGCCAGTCCGGCCCCGTGCCCCGGCGCGC 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyAlaAenVal 60
Dd 121 GGCG 180
TGTAATGTTGCTGGAACGTCGGTGGCAACGTCGGTGAATGTTGCTGTAATGTTGCTG 180

```
PT New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
PS
PS
XX
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 765 BP; 144 A; 248 C; 267 G; 106 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.04e-106 Length: 765
Score: 1356.50 Matches: 239
Percent Similarity: 96.50% Conservativity: 9
Best Local Similarity: 93.00% Mismatches: 6
Query Match: 93.42% Indels: 3
DB: 13 Gaps: 1

US-10-692-367-12 (1-257) x ADS92683 (1-765)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGACAGAACTCGCGTGCAGCCAAACGATATGTCAGCAAGTTTCGGCTACTGGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAsnGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db 61 ACAACCGACGAGTACTGCGGCGAGCGGTGCGAGTGGCGGCGCGTGGCGTGGC----- 111

Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 112 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 171

Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 172 GTACCGCGCTCTTCTTCAACGGCATCAAGAACAGCGCGCGAGCGGTGCGAGCGCAAG 231

Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaTyrProGlyPheAlaHis 100
Db 232 AACTTCTACACCGAGCGCGTCTGAGCGCGCTCAAGGCGTACCCAGGCTTCGCCCAT 291

Qy 101 GlyGlySerGluValGluArgGlyArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
Db 292 GCGGGTTCACAGTGCAGGCAAGCGCGAGATTGCGGCTTCTTCGCGCACGCCCGCAC 351

Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 352 GAGACCGGGCATTTCTGTACATCAGCGAGATCAACAGAGCAAGCGCTACTGCGACCG 411

Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 412 ACCAAGAGCGAGTGGCGCGTGGCGCGCGCGCGAGAGTACTACGGCGCGCGCGCTGGAG 471

Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 472 ATCTCGTGAACCTACCACTACGGCGCGCGCGCGAGGCGCATCGGCTTCGACGGGCTCGG 531

Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 532 GACCCCAACAGGTGGCGCAGCAGCGCGTGGTGGCGTTTCAAGGGCGCGCTCTGGTTTCGG 591

Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 592 ATGAACAACGTGACCGTGTATGCCGCGAGGGCTTCGGCGCGCACCATCAGGGCCATCAAC 651

Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
Db 61 ACACCGACGAGTACTGCGGCGAGCGGTGCGAGTGGCGCGCGCTCGGCGCGCGCGCG 120

Db 652 GCGCGCGTTCGAGTGCAGCGGGAACAACCGCCGCCAGATGAACGCGCGTGGCTACTTAC 711

Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 712 AAGCAGTACTGCGCGCGAGTTCGCGGTGACCCAGGCGCCCAACCTCACTTGC 762

RESULT 15
ADS92659
ID ADS92659 standard; DNA; 753 BP.
XX
AC ADS92659;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polynucleotide #19.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Valpani N;
XX
WPI; 2004-365417/34.
DR P-PSDB; ADS92660.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 43; 197pp; English.
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
XX encoding them. A method of enhancing plant resistance to a fungus or
XX nematode comprises introducing into a plant a recombinant expression
XX cassette comprising a promoter operably linked to a chitinase
XX polynucleotide of the invention. The plant is maize or soybean. The
XX fungus is from the genus Fusarium. The nematode is from the genus
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX plant resistance to a fungus or nematode. This sequence represents a
XX chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 139 A; 243 C; 262 G; 109 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.06e-105 Length: 753
Score: 1353.50 Matches: 240
Percent Similarity: 94.55% Conservativity: 3
Best Local Similarity: 93.39% Mismatches: 7
Query Match: 93.22% Indels: 7
DB: 13 Gaps: 1

US-10-692-367-12 (1-257) x ADS92659 (1-753)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGACAGAACTCGCGTGCAGCCAAACGATATGTCAGCAAGTTTCGGCTACTTGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAsnGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db 61 ACACCGACGAGTACTGCGGCGAGCGGTGCGAGTGGCGCGCGCTCGGCGCGCGCGCG 120
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 15:37:22 ; Search time 3056.63 Seconds

(without alignments)  
4074.095 Million cell updates/sec

Title: US-10-692-367-12

Perfect score: 1452

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Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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3: gb.in:\*  
4: gb.on:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pt:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.py:\*  
13: gb.un:\*  
14: gb.vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1320	90.9	843	8 MZECHITA	M84164 Zea mays ch
2	1297.5	89.4	1094	6 AR321624	AR321624 Sequence
3	1291	88.9	1128	8 AV532740	AV532740 Zea diplo
4	1287	88.6	810	8 MZECHITB	M84165 Zea mays ch

5	1274	87.7	1094	8 AV532775	Zea mays
6	1273	87.7	1123	8 AV532726	Zea mays
7	1273	87.7	1131	8 AV532780	Zea mays
8	1270.5	87.5	1115	8 AV532768	Zea mays
9	1270	87.5	1127	8 AV532733	Zea mays
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13	1269	87.4	1110	8 AV532785	Zea diplo
14	1269	87.4	1110	8 AV532786	Zea diplo
15	1269	87.4	1110	8 AV532787	Zea diplo
16	1269	87.4	1110	8 AV532788	Zea diplo
17	1267.5	87.3	1101	8 AV532770	Zea mays
18	1267	87.3	1133	8 AV532727	Zea mays
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21	1262	86.9	1140	8 AV532731	Zea mays
22	1260.5	86.8	1122	8 AV532771	Zea mays
23	1259	86.7	1121	8 AV532735	Zea mays
24	1256.5	86.5	1126	8 AV532732	Zea mays
25	1256	86.5	1104	8 AV532782	Zea diplo
26	1255.5	86.5	1081	8 AV532737	Zea diplo
27	1255.5	86.5	1081	8 AV532738	Zea diplo
28	1255.5	86.5	1081	8 AV532742	Zea diplo
29	1254.5	86.4	1127	8 AV532730	Zea mays
30	1254	86.4	1132	8 AV532774	Zea mays
31	1251.5	86.2	1123	8 AV532729	Zea mays
32	1250.5	86.1	1127	8 AV532776	Zea mays
33	1248	86.0	1094	8 AV532778	Zea mays
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35	1245.5	85.8	1127	8 AV532723	Zea mays
36	1245	85.7	1122	8 AV532736	Zea diplo
37	1244	85.7	1130	8 AV532722	Zea mays
38	1243.5	85.6	1104	8 AV532772	Zea mays
39	1243.5	85.6	1128	8 AV532777	Zea mays
40	1241.5	85.5	1120	8 AV532769	Zea mays
41	1241.5	85.5	1134	8 AV532734	Zea mays
42	1241	85.5	1118	8 AV532773	Zea mays
43	1238	85.3	985	8 AV532721	Tripsacum
44	1236	85.1	1080	8 AV532739	Zea diplo
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#### ALIGNMENTS

RESULT 1	MZECHITA	Zea mays chitinase A	843 bp	DNA	linear	PLN 27-APR-1993
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ACCESSION	M84164	GI:168440				
VERSION	M84164.1	GI:168440				
KEYWORDS	chitinase A.					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	1	(bases 1 to 843)				
AUTHORS	Huynh, Q.K., Hironaka, C.M., Levine, E.B., Smith, C.E., Borgmeyer, J.R. and Shah, D.M.					
TITLE	Antifungal proteins from plants. Purification, molecular cloning, and antifungal properties of chitinases from maize seed					
JOURNAL	J. Biol. Chem. 267 (10), 6635-6640 (1992)					
MEDLINE	92202208					
PUBMED	1551872					
COMMENT	Original source text: Zea mays (library: Lamda GT 10 corn seed (imibed)) seed DNA.					
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/product="chitinase A"
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/db_xref="GI:168441"
/translation="MANAPRILALGLALLCAAAPAAQNCQCPNFCCKFGYCGT
TNYCGDCQSGPCRSGGGGGGGGGGANVANVTDAPFNGLKNQAGSGCBG
KDFVTRSLASVNAVYPGFAGHGTVEGKREIAAFVHVTHTCFVCYSINKSNAY
CDASNRQWPCAGOKYVGRGPLOJLWNYNGPAGRDIGFNLADPNVADDAVAFKT
ALWFMNNVHVMFGFGATIRAINGLLECNENNPQNNRVRGYYKYQYCCQLRVDPEP
NLIC"

ORIGIN
Alignment Scores:
Pred. No.: 1,01e-86 Length: 843
Score: 1320.00 Matches: 230
Percent Similarity: 93.73% Conservatve: 9
Best Local Similarity: 90.20% Mismatches: 16
Query Match: 90.91% Indels: 0
DB: 8 Gaps: 0

US-10-692-367-12 (1-257) x MZECHITA (1-843)

Qy 3 GlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 76 CAGAACTCGCGTCCAGCAAACTTCTGCTGCAGCAAGTTTCGGCTACTCGCGGACGACC 135
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42
Db 136 GACGCCTACTCGCGGACGGGTGCGAGTCCGGCCCGCTCGCGGCGGGCGGGCGGCG 195
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAAsnValAlaAAsnValThr 62
Db 196 GCGCGCGCGCGGAGGGCGGGAGGCGAGTGGCGGTGCAGCGTGGCTTAATGTGTCTACC 255
Qy 63 AspAlaPheAAsnGlyIleLysAAsnGlnAlaGlySerGlyCysGluGlyLysAAsnPhe 82
Db 256 GACGCGTTCTTCAACGGCATCAAGAACCCAGGCGGGAGCGGTGCGAGGCAAGAACTTC 315
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIleHisGly 102
Db 316 TACACCGGAGCGCGTCTCTGAGCGCGTCAACCGGTACCGCGGCTTCGCCCATCGCGGG 375
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 376 ACGGAGGTGGAGGGCAACGGCGAGATCGCGGCTTCTTCGGCGCATCGACGACGAGACC 435
Qy 123 GlyHisPheCysTyrIleSerGluValAsnLysSerAAsnAlaTyrCysAspProThrLys 142
Db 436 GGACATTTCTGTACTACATCAGCGAGATCAACAAGAGCAACGCGCTACTGCGAGCGCGAAC 495
Qy 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGlnIleSer 162
Db 496 AGGAGTGGCGGTGCGCGGGGGGAGAAATACTACGGGGCGGGCGGCGGCTCGCAGATCTCG 555
Qy 163 TrpAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182
Db 556 TGGAACTACACTACGGGCGCGCGGGAGGAGACATCGGCTTCAACGGGCTCGCGACGCC 615
Qy 183 GlyArgValAlaArgAspAlaValAlaPheLysAlaIleLeuTrpThrTrpMetAen 202
Db 616 AACAGGTGGCGAGGACCGCGTATCGGTTCAGAGCGGCGCTCTGGTCTCTGGATGAAC 675
Qy 203 AenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAAsnGlyVala 222
Db 676 AACGTGCACGGTGTATGCGCGGCGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCC 735
Qy 223 LeuGluCysAAsnGlyAAsnAsnProAlaGlnMetAAsnAlaArgValGlyTyrTyrArgGln 242
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Db 736 CTCGAGTGCAACGGGAACAACCCCGCCAGATGAACGGCGGCTACTACAAGCAG 795
Qy 243 TyrCysArgGlnLeuGlyValAspProGlyAAsnAAsnLeuThrCys 257
Db 796 TACTGCCAGCAGCTCCGCTCGACCCAGGGCCCAACCTCATTTGC 840

RESULT 2
AR321624 LOCUS AR321624 1094 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6563020.
ACCESSION AR321624
VERSION AR321624.1 GI:33706864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1094)
AUTHORS Simmons,C.R. and Valpani,N.
TITLE Maize chitinases and their use in enhancing disease resistance in
crop plants
JOURNAL Patent: US 6563020-A 1 13-MAY-2003;
FEATURES Location/Qualifiers
source 1..1094
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 5,61e-85 Length: 1094
Score: 1297.50 Matches: 229
Percent Similarity: 93.33% Conservatve: 9
Best Local Similarity: 89.80% Mismatches: 10
Query Match: 89.36% Indels: 7
DB: 6 Gaps: 1

US-10-692-367-12 (1-257) x AR321624 (1-1094)

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Db 210 GACGAGTACTCGCGGACGGGTGCGAGTCCGGCCCGCTCGCGGCGGGCGGCGGAGC 269
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAAsnValAlaAAsnValThr 62
Db 270 AGTGGCGGC-----GGTGGTGGCAACGTGGCTAGGCTCGTCAAC 308
Qy 63 AspAlaPheAAsnGlyIleLysAAsnGlnAlaGlySerGlyCysGluGlyLysAAsnPhe 82
Db 309 GGCTCTCTTCTTCAACGGCATCAAGAGCCAGGCGGGAGCGGTGCGAGGGGCAAGACTTC 368
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIleHisGly 102
Db 369 TACACCGGAGCGGTCTCTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATCGCGGG 428
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 429 TCGCAGGTGCAAGCAAGCGCGAGATCGCGGCTTCTTCGGCGCACGCCACGACGAGACC 488
Qy 123 GlyHisPheCysTyrIleSerGluValAAsnLysSerAAsnAlaTyrCysAspProThrLys 142
Db 489 GGGCATTTCTGTACTACATCAGCGAGATCAACAAGAGCAACGCGCTACTGCGAGCCGACCAAG 548
Qy 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 162
Db 549 AGGAGTGGCGGTGCGCGGGGGGAGAACTACTACGGGCGGGCGGCTCGCAGATCTCG 608
Qy 163 TrpAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182
Db 609 TGGAACTACACTACGGGCGCGGGAGGAGGCCATCGCGCTTCGACGGGCTCGGGGACCCC 668
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QY 183 GlyArgValAlaArgAspAlaValValAlaPheLysAlaLeuTyrPheTyrMetAen 202  
 Db 669 GGCAGGTCGGCGCGGAGCCGCTGCTGCTTCAAGCGCGGCTCTGCTTCTGGATGAC 728  
 QY 203 AenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAla 222  
 Db 729 ACCTGTACACGGGGTGGTCCGAGCGGGTTCGCGCCACACACAGGGCCATCAACGGCGCC 788  
 QY 223 LeuGluCysAenGlyAenAsnProAlaGlnMetAenAlaArgValGlyTyrTyrArgGln 242  
 Db 789 CTCGAGTCGGCGGAGCAACACCCCGCAGATGACGCGCGCTGCTACTACAGGAG 848  
 QY 243 TyrCysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257  
 Db 849 TACTGCCCGCAGCTCGCGGTGACCCCGGGCCCACTCACCTGC 893

## RESULT 3

AY532740

LOCUS AY532740 1128 bp DNA linear PLN 29-JUL-2004  
 DEFINITION Zea diploperennis isolate d6 chitinase (chiB) gene, complete cds.

ACCESSION AY532740

VERSION AY532740.1 GI:48093261

## KEYWORDS

SOURCE

ORGANISM

Zea diploperennis

Eukaryota; Viridiplantae

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1128)

Comparative evolutionary histories of chitinase genes in the genus

Tiffin, P.

Genetics 167 (3), 1331-1340 (2004)

15280246

2 (bases 1 to 1128)

Tiffin, P.

Direct Submission

Submitted (23-JAN-2004) Plant Biology, University of Minnesota,

1445 Gortner Ave., St. Paul, MN 55108-1095, USA

Location/Qualifiers

1. 1128

/organism="Zea diploperennis"

/mol\_type="genomic DNA"

/cultivar="PI462368"

/isolate="d6"

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## ORIGIN

Alignment Scores:

Pred. No.: 1.71e-84 Length: 1128

Score: 1291.00 Matches: 233

Percent Similarity: 81.76% Conservative: 9

Best Local Similarity: 78.72% Mismatches: 13

Query Match: 88.91% Indels: 41

DB: 8 Gaps: 1

## RESULT 4

MZECHITB

LOCUS

DEFINITION

Zea mays chitinase B (seed chitinase) gene, 3' end.

ACCESSION M84165

VERSION M84165.1 GI:168442

KEYWORDS chitinase B.

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

US-10-692-367-12 (1-257) x AY532740 (1-1128)

QY 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThrThr 22

Db 107 CAGAACTCGCGCTCCAGCCAAACGTCTGCTGAGCAAGTTCCGCTACTCGGCGACGACC 166

QY 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGly 42

Db 167 GACGAGTACTCGCGCGCAGCGGTGCGTCCGCGCCGCTGCGCTCGGGCGGGCGGCGGC 226

QY 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62

Db 227 GGCAGCGCGCGCGCGCGAGCAGCGTGGCGCGCGTGGTGCAGACGCTGAGCGTGTCTACC 286

QY 63 AspAlaPheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPhe 82

Db 287 GGCTCCTCTTCAACGGCATCAGAACCGCGCGGAGCGGTGCGAGGCGCAGACTTC 346

QY 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 102

Db 347 TACACCGCGAGTGGCTCTCTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGGCGG 406

QY 103 SerGluValGluArgLysArgGluIleAlaIleAlaIleAlaIleAlaIleAlaIleAla 121

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QY 121 ----- 121

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QY 122 -----Thr 122

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QY 123 GlyHis-PheCysTyrIleSerGluValAenLysSerAenAlaTyrCysAspProThrLy 142

Db 587 GGCAGATTCTGCTACATCAGCGAGATCAACAGAGCAACGCCCTACTGCGACCCGAGCAA 646

QY 142 sArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSe 162

Db 647 GAGCAGTGGCGCTGCGCGCGGCGAGAGTACTAGCGGCGCGCGCTGCGAGATCTC 706

QY 162 rTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPr 182

Db 707 GTGGAATACAACTACCGGCGCGCGGAGGCCATCGGCTTCGACGCGCTCGGGGACCC 766

QY 182 oGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTyrMetAs 202

Db 767 CGCAGCGGTGGCGCGGACCGCGTGGTGGCGGTTCAGGCGCGCTCTGGTTCTGGATGAA 826

QY 202 nAenValHisArgValMetProGlnGlyPheGlyValaThrIleArgAlaIleAenGlyAl 222

Db 827 CAGCGTCACGGGGTGGTGGCGAGGGGTTTCGGCGCCACCAACAGGGCCATCAACGGCGC 886

QY 222 aLeuGluCysAenGlyAenAenProAlaGlnMetAenAlaAargValGlyTyrTyrArgGl 242

Db 887 CCTCGAATGGCGGGGAAACACCCCGCCAGATCAACGCGCGCTCGGCTACTACAGCA 946

QY 242 nTyrCysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257

Db 947 GTACTGCCCGCAGCTCGCGCTCGAGCCCGCGGCCCACTCACCTGC 992



## ORIGIN

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 Pred. No.: 2,8e-83 Length: 1094  
 Score: 1274.00 Matches: 229  
 Percent Similarity: 83.92% Conservative: 11  
 Best Local Similarity: 80.07% Mismatches: 15  
 Query Match: 87.74% Indels: 32  
 DB: 8 Gaps: 1

US-10-692-367-12 (1-257) x AY532775 (1-1094)

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Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysAtrGserGlyGlyGlyGly 42
Db 159 GACGCTACTGCGCGCAGCGGTGCCAGTCGGCCCGCTCGCGTCCGGCGCGCGCGCGC 218

Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62
Db 219 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 278

Qy 63 AspAlaPheAenGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 82
Db 279 GACGCTTCTTCAACCGCATCAAGAACACAGCGCGCGCGCGCGCGCGCGCGCGCGCG 338

Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
Db 339 TACACCGGAGCGCGTCTCTGAGCGCGCTCAACGGGTACCGCGGCTTCCCGCATCGCGG 398

Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 399 ACGGAGGTGGAGGCGAGCGCGAGATCGCGCGCTTCTTCCGCGCATCGTCACGACGAGC 458

Qy 123 GlyHis----- 124
Db 459 GGACG- TAAATTAATTAACACCTAACTAGCTAGCATGCGAGGACCTTTTGATCTGAGCGCG 517

Qy 125 -----PheCysTyrIleSerGluVal 131
Db 518 ATCATCGTCGTATGCTGACCATGCAATTTTCGATCAGATTTCTGCTATCATCGCGAGATC 577

Qy 132 AenLysSerAenAlaTyrCysAaspProThrLysArgGlnTrpProCysAlaAlaGlyGln 151
Db 578 AACAGAAACAACCGCTACTGCGACCGGAGCAACAGCGAGTGGCGCGCGCGCGCGCG 637

Qy 152 LysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAenTyrAenTyrGlyProAlaGly 171
Db 638 AAATACTACGGCGCGCGCGCGCGCTGCGATCTGCGAATCTGCGAATCAACTACGGCGCGCG 697

Qy 172 ArgAlaIleGlyPheAaspGlyLeuGlyAspProGlyArgValAlaAtrGAspAlaVal 191
Db 698 AGGGACATCGGCTTCAACGGGCTCGCCGACCCCAACAGGGTGGCGCGAGCGCGCTGATC 757

Qy 192 AlaPheLysAlaAlaLeuTrpPheTrpMetAenAenValHisArgValMetProGlnGly 211
Db 758 GCGTTCAAGACGGCGCTCGTCTTCTGGATGAACACGTCGACCGCGCTGATCGCGCGCG 817

Qy 212 PheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAenGlyAenAenProAla 231
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Qy 252 GlyAenAenLeuThrCys 257
Db 938 GGGCCCAACCTCACTTGC 955
  
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## RESULT 6

AY532726

LOCUS

DEFINITION Zea mays subsp. parviglumis isolate p4 chitinase (chib) gene, complete cds.

ACCESSION AY532726

VERSION AY532726.1

KEYWORDS

SOURCE

ORGANISM

Zea mays subsp. parviglumis  
 Zea mays subsp. parviglumis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

Tiffin, P.

TITLE

Direct Submission

JOURNAL

Submitted (23-JAN-2004)

1445 Gortner Ave., St. Paul, MN 55108-1095, USA

Plant Biology, University of Minnesota,

Location/Qualifiers

1. .1123

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ORIGIN

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Score: 1273.00

Percent Similarity: 80.47%

Best Local Similarity: 77.44%

Query Match: 87.67%

DB: 8

Length: 1123

Matches: 230

Conservative: 9

Mismatches: 10

Indels: 48

Gaps: 2

US-10-692-367-12 (1-257) x AY532726 (1-1123)

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Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysAtrGserGlyGlyGlyGly 42

Db 167 GACGAGTACTGTGCGCGAGCGGTGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCG 226

Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62

Db 227 GGCAGTGTGGC-----GGTGGTGGCAACGTCGTCGCTAGCGTCGTCAACC 268

Qy 63 AspAlaPheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPhe 82



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Db 870 AACGGGAACAACCCCGCCAGATGAACGGCGCGCTACTACAAGCAGTACTGCCAG 929  
QY 246 GlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
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RESULT 8  
AY532768  
LOCUS  
DEFINITION Zea mays subsp. parviglumis isolate p1 chitinase (chia) gene,  
AY532768 1115 bp DNA linear PLN 29-JUL-2004  
complete cds.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays subsp. parviglumis  
Zea mays subsp. parviglumis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 1115)  
AUTHORS Tiffin,P.  
TITLE Comparative evolutionary histories of chitinase genes in the genus  
zea and family poaceae  
JOURNAL Genetics 167 (3), 1331-1340 (2004)  
PUBMED 15280246  
REFERENCE 2 (bases 1 to 1115)  
AUTHORS Tiffin,P.  
TITLE Direct Submission  
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
FEATURES  
Location/Qualifiers  
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ORIGIN

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Percent Similarity: 82.87% Conservative: 9  
Best Local Similarity: 79.72% Mismatches: 16  
Query Match: 87.50% Indels: 33  
DB: 8 Gaps: 2  
US-10-692-367-12 (1-257) x AY532768 (1-1115)  
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QY 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
Db 213 GCGCGCGCAGTGGCGCGGAGCGCGAGTGGCGGTGCGAACGTGGCTTAAACGTGGTCA 272  
QY 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
Db 273 GACGCGTCTTCAACGGCATCAAGAACCGACCGCGGAGCGGTGCGAGGCGCAAGACTTC 332  
QY 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 102  
Db 333 TACACCGGAGCGGCTTCTGAGCGCGCTCAACGCTACCGCGGCTTCCGCCATCGCGGG 392  
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Db 453 GGACGTAAGTTATTAAACACCTAATTAAGTAGTAGCATGACGAGACCTTTGATCTGAC 512  
QY 125 -----PheCysTyrIleSerGluVal 131  
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QY 132 AsnLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAlaGlyGln 151  
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QY 152 LysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGlyProAlaGly 171  
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QY 172 ArgAlaIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaIleArgAspAlaVal 191  
Db 693 AGGACATCGGCTTCAACGGGCTCGCGACCCCAACAGGCGTGGCGAGCAGCGCGTGATC 752  
QY 192 AlaPheLysAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgValMetProGlnGly 211  
Db 753 GCGTTCAGAGCGCGCTCTGGTTCTGGATGAACAACGTCACCGTGTGATCCGCGAGGC 812  
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QY 252 GlyAsnAsnLeuThrCys 257  
Db 933 GGGCCCCAACCTCACTTGC 950  
RESULT 9  
AY532733  
LOCUS  
DEFINITION Zea mays subsp. parviglumis isolate p1 chitinase (chia) gene,  
AY532733 1127 bp DNA linear PLN 29-JUL-2004  
complete cds.

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DEFINITION			
ACCESSION			
VERSION			
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Zea diploperennis			
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD			
Clade; Panicoideae; Andropogoneae; Zea.			
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Tiffin, P.			
Comparative evolutionary histories of chitinase genes in the genus			
zeae and family poaceae			
Genetics 167 (3), 1331-1340 (2004)			
15280246			
2. (bases 1 to 1107)			
Tiffin, P.			
Direct Submission			
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,			
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VERSION    AY532784.1  GI:48093349
KEYWORDS
SOURCE      Zea diploperennis
ORGANISM    Zea diploperennis

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JOURNAL
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mRNA
CDS
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Qy   43  GlyGlyGlyGlyGlyGlyGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62
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VERSION AY532786.1 GI:48093353
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REFERENCE 1 (bases 1 to 1110)
AUTHORS Tiffin,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
JOURNAL ze and family poaceae
PUBMED 15280246
REFERENCE 2 (bases 1 to 1110)
AUTHORS Tiffin,P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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VERSION AY532787.1 GI:48093355
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           1 (bases 1 to 1110)
           Tiffin,P.
REFERENCE 1 (bases 1 to 1110)
AUTHORS Tiffin,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
JOURNAL Genetics 167 (3), 1331-1340 (2004)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2005, 12:21:21 ; Search time 116.081 Seconds  
(without alignments)  
1133.730 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.			
OX	NCBI_TaxID=4576;			
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RP	SEQUENCE FROM N.A.			
RX	PubMed=15280246; DOI=10.1534/genetics.104.026856;			
RA	Tiffin P.;			
RT	zea and family poaceae.;			
RL	Genetics 167:1331-1340(2004).			
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DR	GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.			
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Db 92 GSFENGIRKQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAFHATHET 151
Qy 123 GHFCYISEVKNAYCDPTKQWPCAAQOKYGRGLOISWNNYGPAGRAIGFDGLGDP 182
Db 152 GHFCYISEVKNAYCDPTKQWPCAAQOKYGRGLOISWNNYGPAGRAIGFDGLGDP 211
Qy 183 GRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALECNNGNPAQNNARVGYRQ 242
Db 212 GRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALECNNGNPAQNNARVGYRQ 271
Qy 243 YCRLGVDPGNLTC 257
Db 272 YCRLGVDPGNLTC 286

RESULT 2
Q6JBK8
ID CHIA MAIZE STANDARD; PRT; 280 AA.
AC P29022;
DT 01-DEC-1992 (Rel. 24, Created)
DT 05-JUL-2004 (TRENDELrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENDELrel. 27, Last sequence update)
DE Chitinase.
GN Name=chiA;
OS Zea mays (subsp. parviglumis) (Baleas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RT zeo and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532775; AAT40044.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChitBD1_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
SQ SEQUENCE 280 AA; 29253 MW; 4FC5AABD08ED6671 CRC64;

Query Match 91.4%; Score 1327; DB 2; Length 280;
Best Local Similarity 90.2%; Pred. No. 4.7e-88;
Matches 230; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

Qy 3 QNCGQPNVCCSKFGVCGTTTDEYCGDQSGPCRSQGGGGGGGGGGGGGGGANNVAVT 62
Db 26 QNCGQPNVCCSKFGVCGTTTDEYCGDQSGPCRSQGGGGGGGGGGGGGGGANNVAVT 85
Qy 63 DAFFNGIRKQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAFHATHET 122
Db 86 DAFFNGIRKQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAFHATHET 145
Qy 123 GHFCYISEVKNAYCDPTKQWPCAAQOKYGRGLOISWNNYGPAGRAIGFDGLGDP 182
Db 146 GHFCYISEVKNAYCDPTKQWPCAAQOKYGRGLOISWNNYGPAGRAIGFDGLGDP 205
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Qy 183 GRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALECNNGNPAQNNARVGYRQ 242
Db 206 NRVAQDAVIAFKTALWFMMNNVHRVMPQGFATIRAINGALECNNGNPAQNNARVGYRQ 265
Qy 243 YCRLGVDPGNLTC 257
Db 266 YCQLRLVDPGNLTC 280

RESULT 3
CHIA MAIZE
ID CHIA MAIZE STANDARD; PRT; 280 AA.
AC P29022;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Endochitinase A precursor (EC 3.2.1.14) (Seed chitinase A).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=92202208; PubMed=1551872;
RA Huynh Q.K., Hironaka C.M., Levine E.B., Smith C.E., Borgmeyer J.R.,
RA Shah D.M.;
RT "Antifungal proteins from plants. Purification, molecular cloning, and
RT antifungal properties of chitinases from maize seed.";
RL J. Biol. Chem. 267:6635-6640(1992).
RN [2]
RP SEQUENCE OF 180-195.
RC TISSUE=Seed;
RX MEDLINE=92156129; PubMed=1740436;
RA Verburg J.G., Smith C.E., Lisek C.A., Huynh Q.K.;
RT "Identification of an essential tyrosine residue in the catalytic site
RT of a chitinase isolated from Zea mays that is selectively modified
RT during inactivation with 1-ethyl-3-(3-dimethylaminopropyl)-
RT carbodiimide.";
RL J. Biol. Chem. 267:3886-3893(1992).
CC -!- FUNCTION: This protein functions as a defense against chitin
CC containing fungal pathogens.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC -!- MISCELLANEOUS: Maize Chitinase B seems to be less active than
CC chitinase A.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 19 family. Chitinase
CC class I subfamily.
CC -!- SIMILARITY: Contains 1 chitin-binding type-1 domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M84164; AAA33444.1; -.
CC HSSP; P02877; 1HEV.
CC -----
CC MaizeDB; 25130; -.
CC InterPro; IPR001002; Chitin binding_1.
CC InterPro; IPR000726; Glyco_hydro_19.
CC Pfam; PF00182; Chitin_bind_1; 1.
CC Pfam; PF00182; Glyco_hydro_19; 1.
CC PRINTS; PR00451; CHITINBINDING.
CC ProDom; PD000609; Chitin binding_1; 1.
CC ProDom; PD354900; Glyco_hydro_19; 1.
CC PROSITE; PS00026; CHIT_BIND_1_1; 1.
CC PROSITE; PS00941; CHIT_BIND_1_2; 1.
CC PROSITE; PS00773; CHITINASE_19_1; 1.
CC PROSITE; PS00774; CHITINASE_19_2; 1.
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QY 123 GHFCYISEVNSKNAYCDPTKRWPCAAGQKYGRGLQISWNYNYPAGRAIGFDGLGDP 182
DB 143 GHFCYISEVNSKNAYCDASNRQWPCAAGQKYGRGLQISWNYNYPAGRIDGFNGLGDP 202
QY 183 GRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALECNNGNPAQNNARVGYRQ 242
DB 203 NRVAQDAVIAFKTALWFWMNNVHRVMPQGFATIRAINGALECNNGNPAQNNARVGYRQ 262
QY 243 YCROLGVDPGNNLTC 257
DB 263 YCQLLRVDPGPNLTC 277

RESULT 10
Q6JBQ0 PRELIMINARY; PRT; 280 AA.
AC Q6JBQ0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chIB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532733; AAT40002.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 280 AA; 28993 MW; 7E6E2DA395C32FDB CRC64;

Query Match 90.2%; Score 1309; DB 2; Length 280;
Best Local Similarity 90.6%; Pred. No. 9.3e-87;
Matches 231; Conservative 8; Mismatches 10; Indels 6; Gaps 1;

QY 3 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANNVAVVT 62
DB 32 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANNVAVVT 85
QY 63 DAFNGIKNQAGSGCGEKNFYTRSAFLAIAAYPGFAHGSSEVERKREIAAFFAHATHET 122
DB 86 GSFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHET 145
QY 123 GHFCYISEVNSKNAYCDPTKRWPCAAGQKYGRGLQISWNYNYPAGRAIGFDGLGDP 182
DB 146 GHFCYISEVNSKNAYCDPTKRWPCAAGQKYGRGLQISWNYNYPAGRAIGFDGLGDP 205

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QY 183 GRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALECNNGNPAQNNARVGYRQ 242
DB 206 GRVARDVAVFAKALWFWMNNSVHGVPQGFATIRAINGALECNNGNPAQNNARVGYRQ 265
QY 243 YCROLGVDPGNNLTC 257
DB 266 YCQLLRVDPGPNLTC 280

RESULT 11
Q6JBQ6 PRELIMINARY; PRT; 282 AA.
AC Q6JBQ6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chIB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532727; AAT39996.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 282 AA; 29133 MW; FBB060F48CA67945 CRC64;

Query Match 89.9%; Score 1306; DB 2; Length 282;
Best Local Similarity 90.2%; Pred. No. 1.5e-86;
Matches 230; Conservative 10; Mismatches 9; Indels 6; Gaps 1;

QY 3 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANNVAVVT 62
DB 34 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANNVAVVT 87
QY 63 DAFNGIKNQAGSGCGEKNFYTRSAFLAIAAYPGFAHGSSEVERKREIAAFFAHATHET 122
DB 88 GSFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHET 147
QY 123 GHFCYISEVNSKNAYCDPTKRWPCAAGQKYGRGLQISWNYNYPAGRAIGFDGLGDP 182
DB 148 GHFCYISEVNSKNAYCDPTKRWPCAAGQKYGRGLQISWNYNYPAGRAIGFDGLGDP 207
QY 183 GRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALECNNGNPAQNNARVGYRQ 242
DB 208 GRVARDVAVFAKALWFWMNNSVHGVPQGFATIRAINGALECNNGNPAQNNARVGYRQ 267

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Qy 243 YCROLGVDPGNNLTC 257
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Db 266 YCQLRVDPGNLTC 280

RESULT 2
B42424
chitinase (EC 3.2.1.14) precursor - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 12-Mar-1993 #sequence_revision 03-Feb-1994 #text_change 10-Jul-1998
C;Accession: B42424
R;Huynh, Q.K.; Hironaka, C.M.; Levine, E.B.; Smith, C.E.; Borgmeyer, J.R.; Shah, D.M.
J. Biol. Chem. 267, 6635-6640, 1992
A;Title: Antifungal proteins from plants. Purification, molecular cloning, and antifungal
A;Reference number: A42424; MUID:92202208; PMID:1551872
A;Accession: B42424
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <HUY>
A;Cross-references: GB:M84165
A;Note: the authors translated the codon AAG for residue 104 as Asn, GGC for residue 105
0 as Ile, CAA for residue 231 as Asn and CGC for residue 232 as Gly
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;20-55/Domain: hevein chitin-binding domain homology <HCB>
F;70-268/Domain: plant chitinase homology <PCH>

Query Match 88.6%; Score 1287; DB 2; Length 268;
Best Local Similarity 89.0%; Pred. No. 1.2e-94;
Matches 227; Conservative 9; Mismatches 13; Indels 6; Gaps 1;

Qy 3 QNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGGGGGANVANVT 62
||:|||||
Db 20 QNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGRGGGGGG-----GGANVASVVT 73

Qy 63 DAFENGINKQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFAFAHATHET 122
||:|||||
Db 74 SSFENGINKQAGSGCEGKNFYTRSAFLSAVKGYPGFAHGGSOVQCKREIAAFAFAHATHET 133

Qy 123 GHFCYISEVNVKSNAYCDPTKQWPCACQKYYGRGPIQISWNYNYPAGRAIGFDGLDP 182
||:|||||
Db 134 GHFCYISEVNVKSNAYCDPTKQWPCACQKYYGRGPIQISWNYNYPAGRAIGFDGLDP 193

Qy 183 GRVARDVAVFAKALWFMMNVHVRVMPQGFATIRAINGALECGNNPQAMNARVGYTRQ 242
||:|||||
Db 194 GRVARDVAVFAKALWFMMNVHVRVMPQGFATIRAINGALECGNNPQAMNARVGYTRQ 253

Qy 243 YCROLGVDPGNNLTC 257
||:|||||
Db 254 YCROLGVDPGNNLTC 268

RESULT 3
S51678
chitinase (EC 3.2.1.14) class I - European elder (fragment)
N;Alternate names: pathogenesis-related protein PR-3 type
C;Species: Sambucus nigra (European elder)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51678
R;Coupe, S.A.; Taylor, J.E.; Roberts, J.A.
submitted to the EMBL Data Library, December 1994
A;Description: Characterisation of mRNAs that encode pathogenesis-related proteins that
A;Reference number: S51645
A;Accession: S51678
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <COU>
A;Cross-references: UNIPROT:Q43150; EMBL:Z46948; NID:G603881; PID:CAA87072.1; PID:G6038
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;16-51/Domain: hevein chitin-binding domain homology <HCB>
F;61-261/Domain: plant chitinase homology <PCH>
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Query Match 60.0%; Score 870.5; DB 2; Length 261;
Best Local Similarity 59.6%; Pred. No. 1e-61;
Matches 155; Conservative 30; Mismatches 60; Indels 15; Gaps 4;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGGGGGANVANV 60
||:|||||
Db 14 SGQNCGCPNLCSSQFGYCGSDAAYCGEGRSGFCY-----GSPNGSSASSAVNI 62

Qy 61 VTDAFFNGINKQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFAFAHATH 120
||:|||||
Db 63 VTNNFFNGLISPNQ-CGAGRGFYTRDPLAASAFYPAFGTTGSDNEDRRREIAAFAHATH 121

Qy 121 ETGHFCYISEVNVKSNAYCDPTKQWPCACQKYYGRGPIQISWNYNYPAGRAIGFDGL 179
||:|||||
Db 122 ETGRFCYREBEINGASRDYCDENNRQYPCRPQGYGFRGPIQLQSWNYNYPAGQSIGFDGL 181

Qy 180 GDPGRVARDVAVFAKALWFMMNVHVR--VMPQGFATIRAINGALECGNNPQAMNARV 237
||:|||||
Db 182 GDPGIVARDPVISFRASLWFMMNCHSRISISGQGFSTIRAINGLECNANPGTVVTRV 241

Qy 238 GYTRQYCRQLGVDPGNNLTC 257
||:|||||
Db 242 NYTQFCNLQSLVPPGGNLRC 261

RESULT 4
S25311
chitinase (EC 3.2.1.14) precursor - rape
C;Species: Brassica napus (rape)
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 09-Jul-2004
C;Accession: S25311
R;Raamussen, U.; Bojseen, K.; Collinge, D.B.
Plant Mol. Biol. 20, 277-287, 1992
A;Title: Cloning and characterization of a pathogen-induced chitinase in Brassica napus.
A;Reference number: S25311; MUID:93004480; PMID:1391771
A;Accession: S25311
A;Molecule type: mRNA
A;Residues: 1-268 <RAS>
A;Cross-references: UNIPROT:Q06209; EMBL:X61488; NID:G17798; PID:CAA43708.1; PID:G17799
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: Glycosidase; hydrolase; polysaccharide degradation
F;1-24/Domain: signal sequence #status predicted <Sig>
F;25-268/Product: chitinase #status predicted <MAT>
F;25-60/Domain: hevein chitin-binding domain homology <HCB>
F;74-268/Domain: plant chitinase homology <PCH>

Query Match 59.4%; Score 862.5; DB 2; Length 268;
Best Local Similarity 60.2%; Pred. No. 4.5e-61;
Matches 154; Conservative 30; Mismatches 59; Indels 13; Gaps 4;

Qy 3 QNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGGGGGGANVANVT 62
||:|||||
Db 25 QNCGCAPNLCSSQFGYCGSDAYCGTCRSGPCRSFGTSPGPGSGVGS-----IVT 77

Qy 63 DAFENGINKQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFAFAHATHET 122
||:|||||
Db 78 QAFENGINKQAGSGCAGKKNFYTRDSFINAANTPFNFANSVT-----RREIATMFAHATHET 133

Qy 123 GHFCYISEVNVKSNAYCDPTKQWPCACQKYYGRGPIQISWNYNYPAGRAIGFDGLGD 181
||:|||||
Db 134 GHFCYIBEINGASRDYCDENNRQYPCAPGKGYGFRGPIQLQSWNYNYPAGCGGSLLNLGQ 193

Qy 182 PGRVARDVAVFAKALWFMMNVHVRVMPQGFATIRAINGALECGNNPQAMNARVGYTR 241
||:|||||
Db 194 PELVSSNPTVAFTGLWFMNVSVPVLNQGFATIRAING-MECNCGNSGAVNARIRYR 252

Qy 242 QYCRQLGVDPGNNLTC 257
||:|||||
Db 253 DYCCQLGVDPGPNLSC 268

RESULT 5
T47601
```

Qy	49	-GGSGGANVANVVTDAFFNGIKNQAGSGGEGKNFTYRSAPLEIAIAYPGFAHGSSVER	107
Dd	78	PGTGGGSSVDIVSOAFDGIIGQAASCPGNKFTYRAAFLSAVD--PKFGNEGSSDDN	135
Qy	108	KREIAAFFAHATHETGHFCYIS--VNKSNAVCDPTK-ROMPCAAQOKYYGRGPLQISWN	164
Dd	136	KREIAAFFAHISHETNLCHIERDGVDGDAYCDQKAAYPCAAKGKYTGRGPLQISWN	195
Qy	165	YNYGPAGRAITGFDGLGDPGRVARDVAVFKAALWFWMNNVHRYMPOFGGATIRAINGALE	224
Dd	196	YNYALAGAIFGDLGNPKEVKATDVNTSPKAAMFWMTNVHSVMNQFGGATIRAINGALE	255
Qy	225	CNGNPPAQMARVGTYRQYCRQLGVDPGNLTC	257
Dd	256	CNGQNODQANDRIQFYKKYCADEFGVAPGDNLTC	288

RESULT 7  
A84868  
probable endochitinase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: A84868  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii,  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; T  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.;  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thalian  
A;Reference number: A84420, MUID:20083487; PMID:10617197  
A;Accession: A84868  
A>Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-264 <STO>  
A;Cross-references: UNIPROT:O24658; GB:A8002093; NID:g228111; PIDN:AAB64047.1;  
C;Genetics:  
A;Gene: At2g43590  
A;Map position: 2  
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain hom

Query Match		56.8%;	Score 824.5;	DB 2;	Length 264;
Best Local Similarity		57.0%;	Pred. No. 4.5e-58;		
Matches 146;		Conservative 32;	Mismatches 61;	Indels 17;	Gaps 4;

Qy	3	QNCGPCPNVCCSKFYGCTTDECYCGDCOSGRCRSGGGGGGGGGGGGGGGANVANVT	62
Dd	25	QNCGCAPNLCCSQFYCGTTDAYCVGVCSRGPCK-----GSPTGSGSVSIVT	73
Qy	63	DAFFNGIKNQAGSGGCKNPYTSAPLEIAIAYPGFAHGSSVERKREIAAFPFAHATHET	122
Dd	74	QGFENNIIINQAGNCACGAKRFYTRDSFVNANTPPFNANSVT----RREIATMFHFTHET	129
Qy	123	GHFCYISEYN-KSNAYCDPTKROMPCAAGOKYYGRGPLQISWNYGPAAGRAITGFDGLG	181
Dd	130	GHFCYLEEINGATRNQCQSNTQYPCAPKGYFGRGPLQISWNYGACQSLGLDLRLQ	189
Qy	182	PGRVARDVAVFKAALWFWMNNVHRYMPOFGGATIRAINGALECNNGNPPAQMARVGTYR	241
Dd	190	PELVGNSPIVAFPTGLFWFMWSVRPVLNQGFGATIRAING-MECNCGNSGAVNARIGYYR	248
Qy	242	QYCRQLGVDPGNLTC	257
Dd	249	DYCGQLGVDPGNLSC	264

RESULT 8  
S16579  
chitinase (EC 3.2.1.14) precursor - kidney bean  
C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S16579  
R;Margis-Pinniero, M.; Metz-Boutigue, M.H.; Awade, A.; de Tapia, M.; le Ret, M.  
Plant Mol. Biol. 17, 243-253, 1991  
A;Title: Isolation of a complementary DNA encoding the bean PR4 chitinase: an

A;Reference number: S16579; MUID:91322521; PMID:1863776

A;Accession: S16579

A;Molecule type: mRNA

A;Residues: 1-270 <MAR>

A;Cross-references: UNIPROT:P27054; EMBL:X57187

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;24-59/Domain: hevein chitin-binding domain homology <HCB>

F;70-270/Domain: plant chitinase homology <PCH>

Query Match 56.2%; Score 816; DB 2; Length 270;  
Best Local Similarity 57.9%; Pred. No. 2.2e-57;  
Matches 150; Conservative 32; Mismatches 65; Indels 12; Gaps 4;

Qy 1 SMQNGCOPNVCCSKFGYCGTDTDEYCGDCGQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60

Db 22 SAQNGCAGELCCSQYCGTGEDYCGTGCQGGPCTT-----ASPPPSNNVN-ADI 71

Qy 61 VTDAFFNGIKNOAGSGCGKGFYTRSAFLAIAAAYPGFAHGSGVEVERKREIAAFAHATH 120

Db 72 LTADFLNGIIDQDSGCGKGFYTRDAFLSALNSYTDGFRVGSDDSKREIAAFAHATH 131

Qy 121 ETGHFCYISEVN-KSNAYCDPTK-RQWPCAAQKYGRGLQISWNNYGPAGRAIGPDG 178

Db 132 ETGHFCYIEEDGASKDYCDESIQAQYPCSSSKGYHGRGPTQLSWNFYGPAGSANNPDG 191

Qy 179 LGDPRVARDVAFAKALWFMNNVHVRVMPQGGATIRANGALECNGNPAQMNARVG 238

Db 192 LGAPETVSNVVVVFKTALWMMQHVVRVINGQFGATIRANGALECNGNPAQMNARVG 251

Qy 239 YYROYCROQLGVDGNLTC 257

Db 252 YYTEYCRQLGVATGDNLTG 270

RESULT 9

S57476

chitinase class 4 - cowpea (fragment)

C;Species: Vigna unguiculata (cowpea)

C;Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S57476

R;Vo, L.T.T.; Broughton, W.; Krause, A.

A;Reference number: S57468

A;Accession: S57476

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-249 <VOL>

A;Cross-references: UNIPROT:Q43686; EMBL:X88803; NID:G871767; PID:CAA61281.1; PID:G8717

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

F;4-39/Domain: hevein chitin-binding domain homology <HCB>

F;70-249/Domain: plant chitinase homology <PCH>

Query Match 56.0%; Score 812.5; DB 2; Length 249;

Best Local Similarity 58.3%; Pred. No. 3.8e-57;

Matches 151; Conservative 30; Mismatches 65; Indels 13; Gaps 4;

Qy 1 SMQNGCOPNVCCSKFGYCGTDTDEYCGDCGQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60

Db 2 SAQNGCAGELCCSQYCGTGEEYCGTGCQGGPCTT-----SSSLNNVNADI 51

Qy 61 VTDAFFNGIKNOAGSGCGKGFYTRSAFLAIAAAYPGFAHGSGVEVERKREIAAFAHATH 120

Db 52 VTDAFFNGIIDQDSGCGKGFYTRDAFLSALDSYTDGFRVGSDDSKREIAAFAHATH 111

Qy 121 ETGHFCYISEVN-KSNAYCDPTK-RQWPCAAQKYGRGLQISWNNYGPAGRAIGPDG 178

Db 112 ETGHFCYIEEDGASKDYCDESIQAQYPCSS-SRGYTVVPIQLSWNFYGPAGSANNPDG 170

Qy 179 LGDPRVARDVAFAKALWFMNNVHVRVMPQGGATIRANGALECNGNPAQMNARVG 238

Db 171 LGPPETVSNVVVVFKTALWMMQHVVRVINGQFGAATIRANGALECNGNPAQMNARVG 230

Qy 239 YYROYCROQLGVDGNLTC 257

Db 231 YYTEYCRQLGVATGDNLTG 249

RESULT 10

T03405

probable chitinase (EC 3.2.1.14) Iib - rice

C;Species: Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004

C;Accession: T03405

R;Tuong, N.; Itoh, Y.

A;Description: Nucleotide sequence of rice class II chitinase cDNA.

A;Reference number: Z14936

A;Accession: T03405

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-229 <TRU>

A;Cross-references: UNIPROT:O04138; EMBL:AB003194

A;Experimental source: cv. Nipponbare

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;30-229/Domain: plant chitinase homology <PCH>

Query Match 55.8%; Score 809.5; DB 2; Length 229;

Best Local Similarity 68.1%; Pred. No. 6.1e-57;

Matches 141; Conservative 26; Mismatches 39; Indels 1; Gaps 1;

Qy 52 SGGANVANVYTDAPFNGIKNOAGSGCGKGFYTRSAFLAIAAAYPGFAHGSGVEVERKREI 111

Db 23 AAGVSVESVVTAEAFNGIKNOAGSGCGKGFYTRSAFLAIAAAYPGFAHGSGVEVERKREI 82

Qy 112 AAPFAHATHETGHFCYISEVKNKA-YCDPTKRWPCAAQKYGRGLQISWNNYGP 170

Db 83 AAPFAHATHETGHFCYISEVKNKA-YCDPTKRWPCAAQKYGRGLQISWNNYGP 142

Qy 171 GRAIGFDGLDGPGRVARDVAFAKALWFMNNVHVRVMPQGGATIRANGALECNGNPP 230

Db 143 GKNGFDGLDGPGRVARDVAFAKALWFMNNVHVRVMPQGGATIRANGALECNGNPP 202

Qy 231 AQMNARVYRYQYCRQLGVDGNLTC 257

Db 203 GAVNARVYRYQYCRQLGVDGNLTC 229

RESULT 11

H84867

probable endochitinase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: H84867

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Mofat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84867

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-265 <STO>

A;Cross-references: UNIPROT:O24598; GB:AB020993; NID:G2281112; PIDN:AA64048.1; GSPDB:GN

C;Genetics:

A;Map position: 2

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

Query Match 54.7%; Score 794; DB 2; Length 265;

Best Local Similarity 55.9%; Pred. No. 1.2e-55;

Matches 143; Conservative 33; Mismatches 64; Indels 16; Gaps 4;

Qy 3 QNCGQPNVCCSKFGYCGTDTDEYCGDCGQSGPCRSGGGGGGGGGGGGGGGGGANVANV 62

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Db 25 QNDCAPNLCSSQFGYCGTTADYCGSTQSGPCRVGPPGTGAG-----LVGNIVT 74
Qy 63 DAPFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATHET 122
Db 75 QIFFNNIINOAGNGCAGKSFYTRDSFINATNTPPSFAN-----TVTRREIATWFAHFTYET 130
Qy 123 GHFCYISEVN-KSNAYCDPTKQWPCAAQOKYGRGPGLOISWNNYNGPAGRAIGPDLG 181
Db 131 GHFCYIEBINGASRVCMQDNNRQYPCAPAKSYHGRGPLLLSWNFNYGACGSLGLDLRQ 190
Qy 182 PGVARDVAFAKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGYR 241
Db 191 PELVSSNFVAFRTALWFMKSVRVINQGGFATIRALSG-PDCGRNLGWNARIGYR 249
Qy 242 QYRCQLGVDPGNNLTC 257
Db 250 DYCGQLGDPGANITC 265

RESULT 12
Ti4345
chitinase (EC 3.2.1.14) EP3-3/ET, class IV - carrot
C;Species: Daucus carota (Carrot)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: Ti4345
R;Kragh, K.; De Vries, S.C.
A;Reference number: 217995
A;Accession: Ti4345
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-266 <KRA>
A;Cross-references: UNIPROT:Q96410; EMBL:U52847; NID:g1549332; PID:g1549333
A;Experimental source: strain sg766 trophy
C;Genetics:
A;Gene: EP3
C;Function:
A;Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami
A;Pathway: polysaccharide degradation
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;21-56/Domain: hevein chitin-binding domain homology <HCB>
F;69-266/Domain: plant chitinase homology <PCH>

Query Match 54.2%; Score 786.5; DB 2; Length 266;
Best Local Similarity 55.8%; Pred. No. 4.6e-55;
Matches 144; Conservative 36; Mismatches 67; Indels 11; Gaps 4;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 19 SAQNCNCAAGLCCSKHGYCGTTSYDYGCGCQAGPCTNAPTGGG-----NGSVADI 70
Qy 61 VTDAFFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 120
Db 71 VTDDFFNGIISQATGDCGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 130
Qy 121 ETGHFCYISEVN-KSNAYCDPTKQWPCAAQOKYGRGPGLOISWNNYNGPAGRAIGPDLG 179
Db 131 ETGYFCHKEETNGRDKSYCE-SKAGYPCNANVKYFGRGPLQLTWNNYVIDAGKSNEDFGL 189
Qy 180 GDPGRVARDVAFAKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGY 239
Db 190 NNPDIVASDAVVSFRTALWYKVKVQSVTQGFATIRAIN-SIECNGSGPDVANSRVSL 248
Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 249 YNSYCSKFGVAPGDNQRC 266

RESULT 13
Ti4348
chitinase (EC 3.2.1.14) EP3B/E6, class IV - carrot
C;Species: Daucus carota (Carrot)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: Ti4348
R;Kragh, K.; De Vries, S.C.
A;Reference number: 217995
A;Accession: Ti4348
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-268 <KRA>
A;Cross-references: UNIPROT:Q96409; EMBL:U52846; NID:g1549330; PID:g1549331
A;Experimental source: strain sg766 trophy
C;Genetics:
A;Gene: EP3
C;Function:
A;Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami
A;Pathway: polysaccharide degradation
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;23-58/Domain: hevein chitin-binding domain homology <HCB>
F;71-268/Domain: plant chitinase homology <PCH>

Query Match 53.5%; Score 777.5; DB 2; Length 268;
Best Local Similarity 55.2%; Pred. No. 4.6e-55;
Matches 144; Conservative 36; Mismatches 67; Indels 11; Gaps 4;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 19 SAQNCNCAAGLCCSKHGYCGTTSYDYGCGCQAGPCTNAPTGGG-----NGSVADI 70
Qy 61 VTDAFFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 120
Db 71 VTDDFFNGIISQATGDCGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 130
Qy 121 ETGHFCYISEVN-KSNAYCDPTKQWPCAAQOKYGRGPGLOISWNNYNGPAGRAIGPDLG 179
Db 131 ETGYFCHKEETNGRDKSYCE-SKAGYPCNANVKYFGRGPLQLTWNNYVIDAGKSNEDFGL 189
Qy 180 GDPGRVARDVAFAKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGY 239
Db 190 NNPDIVASDAVVSFRTALWYKVKVQSVTQGFATIRAIN-SIECNGSGPDVANSRVSL 248
Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 249 YNSYCSKFGVAPGDNQRC 266
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C;Species: Daucus carota (carrot)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: Ti4348
R;Kragh, K.; De Vries, S.C.
A;Reference number: 217995
A;Accession: Ti4348
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-266 <KRA>
A;Cross-references: UNIPROT:Q96411; EMBL:U52848; NID:g1549334; PID:g1549335
A;Experimental source: strain sg766 trophy
C;Genetics:
A;Gene: EP3
C;Function:
A;Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami
A;Pathway: polysaccharide degradation
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;21-56/Domain: hevein chitin-binding domain homology <HCB>
F;69-266/Domain: plant chitinase homology <PCH>

Query Match 54.1%; Score 785.5; DB 2; Length 266;
Best Local Similarity 56.2%; Pred. No. 5.5e-55;
Matches 145; Conservative 33; Mismatches 69; Indels 11; Gaps 4;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 19 SAQNCNCAAGLCCSKHGYCGTTSYDYGCGCQAGPCTNAPTGGG-----NGSVADI 70
Qy 61 VTDAFFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 120
Db 71 VTDDFFNGIISQATGDCGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 130
Qy 121 ETGHFCYISEVN-KSNAYCDPTKQWPCAAQOKYGRGPGLOISWNNYNGPAGRAIGPDLG 179
Db 131 ETGYFCHKEETNGRDKSYCE-SKAGYPCNANVKYFGRGPLQLTWNNYVIDAGKSNEDFGL 189
Qy 180 GDPGRVARDVAFAKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGY 239
Db 190 NNPDIVASDAVVSFRTALWYKVKVQSVTQGFATIRAIN-SIECNGSGPDVANSRVSL 248
Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 249 YNSYCSKFGVAPGDNQRC 266

RESULT 14
Ti4344
chitinase (EC 3.2.1.14) EP3-2/H1, class IV - carrot
C;Species: Daucus carota (carrot)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: Ti4344
R;Kragh, K.; De Vries, S.C.
A;Reference number: 217995
A;Accession: Ti4344
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-268 <KRA>
A;Cross-references: UNIPROT:Q96409; EMBL:U52846; NID:g1549330; PID:g1549331
A;Experimental source: strain sg766 trophy
C;Genetics:
A;Gene: EP3
C;Function:
A;Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami
A;Pathway: polysaccharide degradation
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;23-58/Domain: hevein chitin-binding domain homology <HCB>
F;71-268/Domain: plant chitinase homology <PCH>

Query Match 53.5%; Score 777.5; DB 2; Length 268;
Best Local Similarity 55.2%; Pred. No. 4.6e-55;
Matches 144; Conservative 36; Mismatches 67; Indels 11; Gaps 4;
Qy 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 19 SAQNCNCAAGLCCSKHGYCGTTSYDYGCGCQAGPCTNAPTGGG-----NGSVADI 70
Qy 61 VTDAFFNGIKNOAGSGCEGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 120
Db 71 VTDDFFNGIISQATGDCGKFNFTYRSAPLEAIAAYPGFAHGGSEVERKREIAAFAFHATH 130
Qy 121 ETGHFCYISEVN-KSNAYCDPTKQWPCAAQOKYGRGPGLOISWNNYNGPAGRAIGPDLG 179
Db 131 ETGYFCHKEETNGRDKSYCE-SKAGYPCNANVKYFGRGPLQLTWNNYVIDAGKSNEDFGL 189
Qy 180 GDPGRVARDVAFAKALWFMNNVHRVMPQGFATIRAINGALECGNPNPAQNNARVGY 239
Db 190 NNPDIVASDAVVSFRTALWYKVKVQSVTQGFATIRAIN-SIECNGSGPDVANSRVSL 248
Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 249 YNSYCSKFGVAPGDNQRC 266
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Search completed: May 24, 2005, 12:55:12  
Job time : 26.3452 secs

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Best Local Similarity 55.0%; Pred. No. 2.4e-54;
Matches 142; Conservative 35; Mismatches 70; Indels 11; Gaps 4;

Qy 1 SMQNGCGQPNVCCSKFYCGTTDEYCGDGCGSCGRCRSGGGGGGGGGGGGGGGANVANV 60
Db 21 SAQNCNCAAGLCCSKYGYCGTTSYDYGCGCGCQAGPCTNSAPSGG-----NAVSVADI 72

Qy 61 VTDAFFNGIKNOAGSGCGKGFYTRSAFLEAIAAYPGFAHGGSVERKREIAAFFAHATH 120
Db 73 VTDDFFNGIISQATGDCGKGFYTRSAFLEAIAAYPGFAHGGSVERKREIAAFFAHATH 132

Qy 121 ETGHFCYISEVN-KSNAYCDPTKQWPCAAQKQYGRGFLQISWNYNYGPAGRAIGFDGL 179
Db 133 ETGYFCHKEETNGRDHNYCQST-AEYPCNPVNYFGRGFLQITWNYNYIDAGSKNQFDGL 191

Qy 180 GPGRVARDVAVFAKALWFNNVHRVMPQCGFATIRAINGALECNNGNPAQMNARVGY 239
Db 192 NNPDIVASDAVVSFKTALWYWKVQSVTSQGFATIRAIN-SIECNNGSPDAVNSRVSL 250

Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 251 YNSYCSKFGVAPGDNQGC 268

RESULT 15
TI14341
Probable chitinase (EC 3.2.1.14) EP3-1/H5, class IV - carrot (fragment)
C:Species: Daucus carota (Carrot)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: TI14341
R:Kragh, K.; Toonen, M.A.J.; Bucherna, N.; Lo Schiavo, F.; Hendriks, T.; Meijer, E.A.; K
Plant Mol. Biol. 31, 631-645, 1996
A:Title: Characterization of carrot chitinases able to rescue the temperature-sensitive
A:Reference number: Z17992; MUID:96382431; PMID:8790295
A:Accession: TI14341
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-268 <KRA>
A:Cross-references: UNIPROT:Q96408; EMBL:U52845; NID:g1549328; PIDN:AAC49435.1; PID:g154
A:Experimental source: strain sg766 trophy
C:Genetics:
A:Note: EP3
C:Function:
A:Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami
A:Pathway: polysaccharide degradation
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 53.5%; Score 777.5; DB 2; Length 268;
Best Local Similarity 55.0%; Pred. No. 2.4e-54;
Matches 142; Conservative 35; Mismatches 70; Indels 11; Gaps 4;

Qy 1 SMQNGCGQPNVCCSKFYCGTTDEYCGDGCGSCGRCRSGGGGGGGGGGGGGGGANVANV 60
Db 21 SAQNCNCAAGLCCSKYGYCGTTSYDYGCGCGCQAGPCTNSAPSGG-----NAVSVADI 72

Qy 61 VTDAFFNGIKNOAGSGCGKGFYTRSAFLEAIAAYPGFAHGGSVERKREIAAFFAHATH 120
Db 73 VTDDFFNGIISQATGDCGKGFYTRSAFLEAIAAYPGFAHGGSVERKREIAAFFAHATH 132

Qy 121 ETGHFCYISEVN-KSNAYCDPTKQWPCAAQKQYGRGFLQISWNYNYGPAGRAIGFDGL 179
Db 133 ETGYFCHKEETNGRDHNYCQST-AEYPCNPVNYFGRGFLQITWNYNYIDAGSKNQFDGL 191

Qy 180 GPGRVARDVAVFAKALWFNNVHRVMPQCGFATIRAINGALECNNGNPAQMNARVGY 239
Db 192 NNPDIVASDAVVSFKTALWYWKVQSVTSQGFATIRAIN-SIECNNGSPDAVNSRVSL 250

Qy 240 YRQYCRQLGVDPGNNLTC 257
Db 251 YNSYCSKFGVAPGDNQGC 268
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2005, 12:54:28 ; Search time 91.7495 Seconds  
(without alignments)  
936.991 Million cell updates/sec

Title: US-10-692-367-12  
Perfect score: 1452  
Sequence: 1 SMQNCQCPNVCCSKFGYCG.....GYRQYCRQLGVDPNNILTC 257

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1452	100.0	257	17	US-10-692-367-12
2	1435	98.8	257	17	US-10-692-367-30
3	1435	98.8	257	17	US-10-692-367-34
4	1405	96.8	257	17	US-10-692-367-72
5	1382.5	95.2	256	17	US-10-692-367-60
6	1382	95.2	257	17	US-10-692-367-46
7	1377	94.8	257	17	US-10-692-367-66
8	1373.5	94.6	256	17	US-10-692-367-62
9	1366.5	94.1	256	17	US-10-692-367-48
10	1365.5	94.0	256	17	US-10-692-367-74
11	1361	93.9	257	17	US-10-692-367-64
12	1361	93.7	257	17	US-10-692-367-24
13	1361	93.7	257	17	US-10-692-367-38

14	1356.5	93.4	254	17	US-10-692-367-68
15	1353.5	93.2	250	17	US-10-692-367-44
16	1351.5	93.1	256	17	US-10-692-367-84
17	1342	92.4	259	17	US-10-692-367-40
18	1339	92.2	259	17	US-10-692-367-76
19	1338.5	92.2	254	17	US-10-692-367-82
20	1333.5	91.8	250	17	US-10-692-367-26
21	1333	91.8	255	17	US-10-692-367-1
22	1333	91.8	303	15	US-10-425-114-57156
23	1332	91.7	257	17	US-10-692-367-8
24	1327	91.4	280	17	US-10-692-367-19
25	1323.5	91.2	250	17	US-10-692-367-52
26	1320	90.9	280	17	US-10-692-367-17
27	1318.5	90.8	250	17	US-10-692-367-70
28	1318.5	90.8	256	17	US-10-692-367-42
29	1315.5	90.6	250	17	US-10-692-367-36
30	1315.5	90.6	258	17	US-10-692-367-16
31	1305.5	89.9	250	17	US-10-692-367-78
32	1304.5	89.8	250	17	US-10-692-367-56
33	1300.5	89.6	258	17	US-10-692-367-4
34	1299.5	89.5	301	15	US-10-425-114-63860
35	1299.5	89.5	302	15	US-10-425-114-71741
36	1299	89.5	249	17	US-10-692-367-80
37	1297.5	89.4	248	17	US-10-692-367-2
38	1297.5	89.4	281	14	US-10-304-928-2
39	1295.5	89.2	250	17	US-10-692-367-50
40	1294.5	89.2	250	17	US-10-692-367-58
41	1294.5	89.2	293	15	US-10-425-114-64209
42	1294.5	89.2	298	15	US-10-425-114-52906
43	1292.5	89.0	250	17	US-10-692-367-22
44	1290.5	88.9	250	17	US-10-692-367-32
45	1287	88.6	269	17	US-10-692-367-18

#### ALIGNMENTS

#### RESULT 1

US-10-692-367-12  
; Sequence 12, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-12

Query Match 100.0%; Score 1452; DB 17; Length 257;  
Best Local Similarity 100.0%; Pred. No. 5.2e-112;  
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGG 60
Db 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGGGG 60
Qy 61 VTDAFFNGIKNOAGSGCGEKGNYTRSAFLAIAAYPGFAHGSSEVERKREIAAFAHATH 120
Db 61 VTDAFFNGIKNOAGSGCGEKGNYTRSAFLAIAAYPGFAHGSSEVERKREIAAFAHATH 120
Qy 121 ETGHFCYISEVNKSNAYCDPTKRQWPCAGQKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 121 ETGHFCYISEVNKSNAYCDPTKRQWPCAGQKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Qy 181 DPGVARDAVAFKAALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNAVGY 240
Db 181 DPGVARDAVAFKAALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNAVGY 240
Qy 241 ROYCRQLGVDPGNNLTC 257
Db 241 ROYCRQLGVDPGNNLTC 257
RESULT 2
US-10-692-367-30
; Sequence 30, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-30
Query Match 98.8%; Score 1435; DB 17; Length 257;
Best Local Similarity 98.8%; Pred. No. 1.3e-110;
Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGG 60
Db 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGG 60
Qy 61 VTDAFFNGIKNOAGSGCGEKGNYTRSAFLAIAAYPGFAHGSSEVERKREIAAFAHATH 120
Db 61 VTDAFFNGIKNOAGSGCGEKGNYTRSAFLAIAAYPGFAHGSSEVERKREIAAFAHATH 120
Qy 121 ETGHFCYISEVNKSNAYCDPTKRQWPCAGQKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 121 ETGHFCYISEVNKSNAYCDPTKRQWPCAGQKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Qy 181 DPGVARDAVAFKAALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNAVGY 240
Db 181 DPGVARDAVAFKAALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNAVGY 240
Qy 241 ROYCRQLGVDPGNNLTC 257
Db 241 ROYCRQLGVDPGNNLTC 257
RESULT 3
US-10-692-367-34
; Sequence 34, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-34
Query Match 98.8%; Score 1435; DB 17; Length 257;
Best Local Similarity 98.8%; Pred. No. 1.3e-110;
Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGG 60
Db 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGG 60
Qy 61 VTDAFFNGIKNOAGSGCGEKGNYTRSAFLAIAAYPGFAHGSSEVERKREIAAFAHATH 120
Db 61 VTDAFFNGIKNOAGSGCGEKGNYTRSAFLAIAAYPGFAHGSSEVERKREIAAFAHATH 120
Qy 121 ETGHFCYISEVNKSNAYCDPTKRQWPCAGQKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 121 ETGHFCYISEVNKSNAYCDPTKRQWPCAGQKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Qy 181 DPGVARDAVAFKAALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNAVGY 240
Db 181 DPGVARDAVAFKAALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNAVGY 240
Qy 241 ROYCRQLGVDPGNNLTC 257
Db 241 ROYCRQLGVDPGNNLTC 257
RESULT 4
US-10-692-367-72
; Sequence 72, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-72
Query Match 98.8%; Score 1435; DB 17; Length 257;
Best Local Similarity 98.8%; Pred. No. 1.3e-110;
Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGG 60
Db 1 SMQCGCPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGGGGGGGGGGGG 60
Qy 61 VTDAFFNGIKNOAGSGCGEKGNYTRSAFLAIAAYPGFAHGSSEVERKREIAAFAHATH 120
Db 61 VTDAFFNGIKNOAGSGCGEKGNYTRSAFLAIAAYPGFAHGSSEVERKREIAAFAHATH 120
Qy 121 ETGHFCYISEVNKSNAYCDPTKRQWPCAGQKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Db 121 ETGHFCYISEVNKSNAYCDPTKRQWPCAGQKYYGRGPLQISWNYNYPAGRAIGFDGLG 180
Qy 181 DPGVARDAVAFKAALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNAVGY 240
Db 181 DPGVARDAVAFKAALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNAVGY 240
Qy 241 ROYCRQLGVDPGNNLTC 257
Db 241 ROYCRQLGVDPGNNLTC 257
```





Qy 121 ETGHFCYISEVKNKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLG 180  
Db 121 ETGHFCYISEINKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLG 180  
Qy 181 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Db 181 DPNRVARDAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Qy 241 ROYCRQLGVDPGNLTLC 257  
Db 241 ROYCRQLGVDPGNLTLC 257

## RESULT 7

US-10-692-367-66  
; Sequence 66, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; PRIOR FILING DATE: 2003-10-22  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-66

Query Match 94.8%; Score 1377; DB 17; Length 257;  
Best Local Similarity 93.4%; Pred. No. 8.2e-106;  
Matches 240; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGG 60  
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGG 60  
Qy 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFFAHATH 120  
Db 61 VTDFFNGIKNOAGSGCGEKNFYTRSAFLSAVKAIPGFAHGGSQVQKREIAAFFAHATH 120  
Qy 121 ETGHFCYISEVKNKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLG 180  
Db 121 ETGHFCYISEINKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLA 180  
Qy 181 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Db 181 DPNRVARDAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Qy 241 ROYCRQLGVDPGNLTLC 257  
Db 241 ROYCRQLGVDPGNLTLC 257

## RESULT 8

US-10-692-367-62

; Sequence 62, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; PRIOR FILING DATE: 2003-10-22  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-62

Query Match 94.6%; Score 1373.5; DB 17; Length 256;  
Best Local Similarity 94.2%; Pred. No. 1.6e-105;  
Matches 242; Conservative 8; Mismatches 6; Indels 1; Gaps 1;  
Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGG 60  
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRP-GGGGGGGGGGGGGGGG 59  
Qy 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFFAHATH 120  
Db 60 VTGSFFNGIKNOAGSGCGEKNFYTRSAFLSAVKAIPGFAHGGSEVERKREIAAFFAHATH 119  
Qy 121 ETGHFCYISEVKNKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLG 180  
Db 120 ETGHFCYISEINKSNAYCDPTKRWPCAAQKYYGRGFLQISWNNYNGPAGRAIGFDGLA 179  
Qy 181 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
Db 180 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCNGNPAQMNARVGY 239  
Qy 241 ROYCRQLGVDPGNLTLC 257  
Db 240 ROYCRQLGVDPGNLTLC 256

## RESULT 9

US-10-692-367-48  
; Sequence 48, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR FILING DATE: 2002-11-06

```
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-48

Query Match          94.1%; Score 1366.5; DB 17; Length 256;
Best Local Similarity 94.6%; Pred. No. 6e-105;
Matches 243; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVASV 59

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLEIAAAYPGFAHGSSEVERKREIAAPFAHATH 120
Db 60 VTDSFFNGIKSQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHVTH 119

Qy 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 180
Db 120 ETGHFCYINEINKSNAYCDPTKROWPCAAAGQRYYGRGPLQISWNNYNYGPAGRAIGFDGLG 179

Qy 181 DPGRVARDAVVAFKAALWFNNVHRVMPQGFATIRAINGALCNGNNPQMMNARVGY 240
Db 180 DPGRVARDAVVAFKAALWFNNVHRVMPQGFATIRAINGALCNGNNPQMMNARIGY 239

Qy 241 ROYCRQLGVDPGNLTLC 257
Db 240 ROYCRQLGVDPGNLTLC 256

RESULT 10
US-10-692-367-64
; Sequence 64, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-64

Query Match          93.9%; Score 1363; DB 17; Length 257;
Best Local Similarity 92.2%; Pred. No. 1.2e-104;
Matches 237; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNCGQPNFCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGGGANVANV 60

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLEIAAAYPGFAHGSSEVERKREIAAPFAHATH 120
Db 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATH 120

Qy 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQKYYGRGPLQISWNNYNYGPAGRAIGFDGLG 180
Db 121 ETGHFCYISEINKSNAYCDPTKROWPCAAAGQKYYGRGPLQISWNNYNYGPAGRIDGFLA 180

Qy 181 DPGRVARDAVVAFKAALWFNNVHRVMPQGFATIRAINGALCNGNNPQMMNARVGY 240
Db 180 DPGRVARDAVVAFKAALWFNNVHRVMPQGFATIRAINGALCNGNNPQMMNARVGY 240
```



```
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-68

Query Match          93.4%; Score 1356.5; DB 17; Length 254;
Best Local Similarity 93.0%; Pred. No. 4e-104;
Matches 239; Conservative 9; Mismatches 6; Indels 3; Gaps 1;

Qy 1 SMQNGCGOPNVCCSKFGYCGTTDEYCGDGCGPCRCGGGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNGCGOPNVCCSKFGYCGTTDEYCGDGCGPCRC---GGGGGGGGGGGGGGANVASV 57

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFFAHATH 120
Db 58 VTGSFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQCKREIAAFFAHATH 117

Qy 121 ETGHFCYIISEVKNKNAYCDPTKQWPCAAAGOKYGRGPLQISWNYNYGPAGRAIGFDGLG 180
Db 118 ETGHFCYIISEINKSNAYCDPTKQWPCAAAGOKYGRGPLQISWNYNYGPAGRAIGFDGLG 177

Qy 181 DPGRVARDAVVAFKAALWFMNNVHVRVMPQGFATIRAINGALBECGNNPAQMNARVGY 240
Db 178 DPNRVAQDAVVAFKAALWFMNNVHVRVMPQGFATIRAINGALBECGNNPAQMNARVGY 237

Qy 241 RQYCRQLGVDPGNNLTC 257
Db 238 RQYCRQLGVDPGNNLTC 254
```

```
RESULT 15
US-10-692-367-44
; Sequence 44, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-44

Query Match          93.2%; Score 1353.5; DB 17; Length 250;
Best Local Similarity 93.4%; Pred. No. 7e-104;
Matches 240; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

Qy 1 SMQNGCGOPNVCCSKFGYCGTTDEYCGDGCGPCRCGGGGGGGGGGGGGGANVANV 60
Db 1 SMQNGCGOPNVCCSKFGYCGTTDEYCGDGCGPCRCGGGGGGGGGGGGGGANVASV 53

Qy 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFFAHATH 120
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Db 54 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFFAHATH 113
Qy 121 ETGHFCYIISEVKNKNAYCDPTKQWPCAAAGOKYGRGPLQISWNYNYGPAGRAIGFDGLG 180
Db 114 ETGHFCYIISEINKSNAYCDPTKQWPCAAAGOKYGRGPLQISWNYNYGPAGRAIGFDGLG 173
Qy 181 DPGRVARDAVVAFKAALWFMNNVHVRVMPQGFATIRAINGALBECGNNPAQMNARVGY 240
Db 174 DPGRVARDAVVAFKAALWFMNNVHVRVMPQGFATIRAINGALBECGNNPAQMNARVGY 233
Qy 241 RQYCRQLGVDPGNNLTC 257
Db 234 RQYCRQLGVDPGNNLTC 250

Search completed: May 24, 2005, 13:12:27
Job time : 92.7495 sec8
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2005, 12:41:36 ; Search time 31.428 Seconds  
(without alignments)  
610.437 Million cell updates/sec

Title: US-10-692-367-12

Perfect score: 1452

Sequence: 1 SMQNGCQPNVCCSKFGYCG.....GYRQYRQLGVDPGNLTC 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1297.5	89.4	281	4	US-09-522-714-2
2	861.5	59.3	271	4	US-09-522-714-22
3	715.5	49.3	183	4	US-09-522-714-30
4	643	44.3	328	3	US-07-791-931-5
5	637	43.9	330	1	US-07-704-288C-8
6	637	43.9	330	1	US-08-379-259-8
7	626.5	43.1	329	2	US-08-475-427-13
8	626.5	43.1	329	2	US-08-475-427-13
9	623	42.9	310	1	US-07-704-288C-6
10	623	42.9	310	1	US-08-379-259-6
11	622.5	42.9	310	3	US-07-791-931-6
12	619.5	42.7	324	1	US-08-047-413-11
13	619.5	42.7	324	3	US-08-229-050-11
14	619.5	42.7	324	3	US-08-801-563-11
15	615	42.4	314	1	US-07-704-288C-7
16	615	42.4	314	1	US-08-379-259-7
17	585.5	40.3	302	2	US-08-475-427-6
18	585.5	40.3	302	2	US-07-842-165-6
19	578.5	39.8	319	4	US-09-534-229C-3
20	577.5	39.8	336	1	US-07-704-288C-3
21	577.5	39.8	336	1	US-08-093-372-2
22	577.5	39.8	336	1	US-08-379-259-3
23	576	39.7	323	4	US-09-534-229C-2
24	572.5	39.4	328	3	US-07-791-931-7
25	567	39.0	318	1	US-07-704-288C-9
26	567	39.0	318	1	US-08-379-259-9
27	532	36.6	328	4	US-09-125-891-2

28	532	36.6	328	4	US-09-125-891-4	Sequence 4, Appli
29	511.5	35.2	254	2	US-08-475-427-1	Sequence 1, Appli
30	511.5	35.2	254	2	US-07-842-165-1	Sequence 1, Appli
31	511.5	35.2	254	3	US-08-448-398-3	Sequence 3, Appli
32	506.5	34.9	316	3	US-07-791-931-8	Sequence 8, Appli
33	496	34.2	266	1	US-08-812-025-10	Sequence 10, Appli
34	496	34.2	266	3	US-07-791-931-10	Sequence 10, Appli
35	496	34.2	266	3	US-09-138-873A-10	Sequence 10, Appli
36	494	34.0	284	4	US-09-522-714-24	Sequence 24, Appli
37	486.5	33.5	405	4	US-09-902-540-11954	Sequence 11954, A
38	467.5	32.2	271	4	US-09-266-965-141	Sequence 141, App
39	412.5	28.4	372	3	US-07-791-931-4	Sequence 4, Appli
40	405	27.9	259	4	US-09-522-714-18	Sequence 18, Appli
41	393.5	27.1	252	4	US-09-522-714-20	Sequence 20, Appli
42	386.5	26.6	253	3	US-07-791-931-9	Sequence 9, Appli
43	379.5	26.1	253	1	US-08-162-475A-5	Sequence 5, Appli
44	379.5	26.1	254	1	US-08-047-413-9	Sequence 9, Appli
45	379.5	26.1	254	3	US-08-229-050-9	Sequence 9, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-522-714-2

; Sequence 2, Application US/09522714

; Patent No. 6563020

; GENERAL INFORMATION:

; APPLICANT: Simmons, Carl R.

; APPLICANT: Valpani, Nasser

; TITLE OF INVENTION: Maize Chitinases and Their Use in

; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants

; FILE REFERENCE: 1100

; CURRENT APPLICATION NUMBER: US/09/522.714

; CURRENT FILING DATE: 2000-03-10

; EARLIER APPLICATION NUMBER: 60/125,915

; EARLIER FILING DATE: 1999-03-24

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 281

; TYPE: PRT

; ORGANISM: Zea mays

US-09-522-714-2

Query Match 89.4%; Score 1297.5; DB 4; Length 281;

Best Local Similarity 89.8%; Pred. No. 3.4e-103;

Matches 229; Conservative 9; Mismatches 10; Indels 7; Gaps 1;

Qy 3 QNCCQPNVCCSKFGYCGTTDEYCGDQCGQPCRSQGGGGGGGGGGGGGGGANNVAVVT 62

Db 34 QNCCQPNVCCSKFGYCGTTDEYCGDQCGQPCRSQGGGGGGGGGGGGGGGANNVAVVT 86

Qy 63 DAFNGIKNOAGSCGKGFYTRSAFLAIAAYPGFAHGSSEVERKRIIAAFPAHATHET 122

Db 87 GSFNGIKNOAGSCGKGFYTRSAFLAIAAYPGFAHGSSEVERKRIIAAFPAHATHET 146

Qy 123 GHFCYISEVNKSNAYCDPTKQWPCAAQKQYKYGRLQISWNNYGPAGRAIGFDGLDP 182

Db 147 GHFCYISEVNKSNAYCDPTKQWPCAAQKQYKYGRLQISWNNYGPAGRAIGFDGLDP 206

Qy 183 GRVADAVAFKAAWFMNNVHRVMPQGFATTRAINALECNGNPNQNNARVGYTRQ 242

Db 207 GRVADAVAFKAAWFMNNVHRVMPQGFATTRAINALECNGNPNQNNARVGYTRQ 266

Qy 243 YCROLGVDPGNLTC 257

Db 267 YCROLGVDPGNLTC 281

##### RESULT 2

US-09-522-714-22

; Sequence 22, Application US/09522714





; ZIP: 90071-2921  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/704,288C  
; FILING DATE: 22-MAY-1991  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P31 8899  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 546-4737  
; TELEFAX: (619) 546-9392  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 330 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-07-704-288C-8

Query Match 43.9%; Score 637; DB 1; Length 330;  
Best Local Similarity 43.9%; Pred. No. 1.1e-46;  
Matches 130; Conservative 36; Mismatches 80; Indels 50; Gaps 9;  
  
Qy 3 QNCG-----CQPNVCSKFGYCTTDEYCGDCGQSPCRSGGGGGGGGGGGGGGGA 55  
Db 27 QNCGSQGGKACASGQCCSKFGWCNTNDYCG----SGNCQSQCPGGGPGPGDGLGSA 82  
  
Qy 56 NVANVVTDAFNGIKNOAGSCGKGFVTRSAFLAIAAYPGAHGGSEVERKREIAAFA 115  
Db 83 -ISMSFDM---LKHRENESCQGNFYSAFNAARSFPFGTSGDINARKREIAAFA 138  
  
Qy 116 AHATHET-----GHFCYISEVNKSNAYCDPTTKRQWPCAAGQKYGRGPLOIS 162  
Db 139 AQTSHETGGWASAPDGPYANGYCFLERGNGPDYCPSS--QWPCAPGRKYFGRGPLOIS 197  
  
Qy 163 WNYNYGPAGRAIGDGLDGPGRVADAVAFKALWFMMN-----NVHRVM-----PQ- 210  
Db 198 HNYNYGPCGRAIAVDLLNPNLVDTPVISEKTALWFMMTPQSPKPSCHDVIIGRWNPSS 257  
  
Qy 211 -----GFGATIRANGALECNGNPNQMNARVGYTRYCYROLGVDPCNNLTC 257  
Db 258 ADRAANRLPGFVITNIINGLECGRTDNRVQDRIGFYRRYCSILGVTGPDNLDC 313

RESULT 6  
US-08-379-259-8  
; Sequence 8, Application US/08379259  
; Patent No. 585939  
; GENERAL INFORMATION:  
; APPLICANT: LAMB, CHRISTOPHER J.  
; APPLICANT: ZHU, QUN  
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT  
; TITLE OF INVENTION: DEFENSE REGULATORY  
; TITLE OF INVENTION: ELEMENTS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER, BRUGGEMANN & CLARK  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: United States  
; ZIP: 90071-2921  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/379,259  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/704,288  
; FILING DATE: 22-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P31 8899  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 546-4737  
; TELEFAX: (619) 546-9392  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 330 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-379-259-8

Query Match 43.9%; Score 637; DB 1; Length 330;  
Best Local Similarity 43.9%; Pred. No. 1.1e-46;  
Matches 130; Conservative 36; Mismatches 80; Indels 50; Gaps 9;  
  
Qy 3 QNCG-----CQPNVCSKFGYCTTDEYCGDCGQSPCRSGGGGGGGGGGGGGGGA 55  
Db 27 QNCGSQGGKACASGQCCSKFGWCNTNDYCG----SGNCQSQCPGGGPGPGDGLGSA 82  
  
Qy 56 NVANVVTDAFNGIKNOAGSCGKGFVTRSAFLAIAAYPGAHGGSEVERKREIAAFA 115  
Db 83 -ISMSFDM---LKHRENESCQGNFYSAFNAARSFPFGTSGDINARKREIAAFA 138  
  
Qy 116 AHATHET-----GHFCYISEVNKSNAYCDPTTKRQWPCAAGQKYGRGPLOIS 162  
Db 139 AQTSHETGGWASAPDGPYANGYCFLERGNGPDYCPSS--QWPCAPGRKYFGRGPLOIS 197  
  
Qy 163 WNYNYGPAGRAIGDGLDGPGRVADAVAFKALWFMMN-----NVHRVM-----PQ- 210  
Db 198 HNYNYGPCGRAIAVDLLNPNLVDTPVISEKTALWFMMTPQSPKPSCHDVIIGRWNPSS 257  
  
Qy 211 -----GFGATIRANGALECNGNPNQMNARVGYTRYCYROLGVDPCNNLTC 257  
Db 258 ADRAANRLPGFVITNIINGLECGRTDNRVQDRIGFYRRYCSILGVTGPDNLDC 313

RESULT 7  
US-08-475-427-13  
; Sequence 13, Application US/08475427  
; Patent No. 5859340  
; GENERAL INFORMATION:  
; APPLICANT: DUBOIS, Michel  
; APPLICANT: GRISON, Rene  
; APPLICANT: LEGUAY, Jean-Jacques  
; APPLICANT: PIGNARD, Annie  
; APPLICANT: TOPPAN, Alain  
; TITLE OF INVENTION: Recombinant gene coding for a protein  
; TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/475.427  
 FILING DATE: 07-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/842,165  
 FILING DATE: 01-MAY-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/FR91/00607  
 FILING DATE: 21-JUL-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 90 09460  
 FILING DATE: 24-JUL-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 16781/564/BDL  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEFAX: (202)672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 329 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-475-427-13

Query Match 43.1%; Score 626.5; DB 2; Length 329;  
 Best Local Similarity 44.1%; Pred. No. 8.5e-46;  
 Matches 132; Conservative 38; Mismatches 76; Indels 53; Gaps 12;  
 Qy 3 QNCG-----CQPNVCCSKFGYCGTDTDEYCGDG-CQSGPCRCGGGGGGGGGGGGGGG 54  
 Db 25 QNCGSQGGKVCASQCCSKFGWCNTNDHCGSGNCOS-QCPGGGPGPGVGTGDLGS-- 81  
 Qy 55 ANVANVVTDAFFNG-IKNQAGSGCEGK-NFYTRSAFLAIAAYPGFAHGGSEVERKREIA 112  
 Db 82 -----VISNMFQDLKHNENSCQGNFNYSNAPITAARSFPFGTSGDINARKREIA 136  
 Qy 113 APFAHATHET-----GHP-----CVISEVKNKNAYCDPTKQWPCAAQKTYGRGL 159  
 Db 137 APFAQTSHETTTGGWPSADPGFAMGYCFLRERNGPDYCSFSS-QWPCAPGRKYFGRGPI 195  
 Qy 160 QISWNYNYPAGRAIGFDGLDGRVARDVAVFAKALWFWMN-----NVHRVM----- 208  
 Db 196 QISHNYNYPGCGRAIGVLLNPNLDVATDPVISFKTAIWFMTQSPKPSCHDVIIGRW 255  
 Qy 209 PQ-----GFGATIRANGALECNGNPNQMNARVGYRCQLGVDPGNLTC 257  
 Db 256 PSAGDRSANRLPGFVITNIINGLEGCRGNDNRVQDRIGFYRRYCGILGVSPGDNLD 314

RESULT 8  
 US-08-475-427-13  
 ; Sequence 13, Application US/07842165  
 ; Patent No. 5932698  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DUBOIS, Michel  
 ; APPLICANT: GRISON, Rene  
 ; APPLICANT: LEGUAY, Jean-Jacques  
 ; APPLICANT: PIGNARD, Annie  
 ; APPLICANT: TOPPAN, Alain  
 ; TITLE OF INVENTION: Recombinant gene coding for a protein  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY & LARDNER  
 ; STREET: King Street Station, Suite 500, 1800 Diagonal  
 ; STREET: Road, PO Box 299  
 ; CITY: ALEXANDRIA

STATE: VIRGINIA  
 COUNTRY: USA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/07/842,165  
 APPLICATION NUMBER: US/07/842,165  
 FILING DATE: 19920501  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SAXE, Bernhard D  
 REGISTRATION NUMBER: 28,665  
 REFERENCE/DOCKET NUMBER: 16781/348  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-9300  
 TELEFAX: (703) 683-4109  
 TELEX: 899149  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 329 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-842-165-13

Query Match 43.1%; Score 626.5; DB 2; Length 329;  
 Best Local Similarity 44.1%; Pred. No. 8.5e-46;  
 Matches 132; Conservative 38; Mismatches 76; Indels 53; Gaps 12;  
 Qy 3 QNCG-----CQPNVCCSKFGYCGTDTDEYCGDG-CQSGPCRCGGGGGGGGGGGGGGG 54  
 Db 25 QNCGSQGGKVCASQCCSKFGWCNTNDHCGSGNCOS-QCPGGGPGPGVGTGDLGS-- 81  
 Qy 55 ANVANVVTDAFFNG-IKNQAGSGCEGK-NFYTRSAFLAIAAYPGFAHGGSEVERKREIA 112  
 Db 82 -----VISNMFQDLKHNENSCQGNFNYSNAPITAARSFPFGTSGDINARKREIA 136  
 Qy 113 APFAHATHET-----GHP-----CVISEVKNKNAYCDPTKQWPCAAQKTYGRGL 159  
 Db 137 APFAQTSHETTTGGWPSADPGFAMGYCFLRERNGPDYCSFSS-QWPCAPGRKYFGRGPI 195  
 Qy 160 QISWNYNYPAGRAIGFDGLDGRVARDVAVFAKALWFWMN-----NVHRVM----- 208  
 Db 196 QISHNYNYPGCGRAIGVLLNPNLDVATDPVISFKTAIWFMTQSPKPSCHDVIIGRW 255  
 Qy 209 PQ-----GFGATIRANGALECNGNPNQMNARVGYRCQLGVDPGNLTC 257  
 Db 256 PSAGDRSANRLPGFVITNIINGLEGCRGNDNRVQDRIGFYRRYCGILGVSPGDNLD 314

RESULT 9  
 US-07-704-288C-6  
 ; Sequence 6, Application US/07704288C  
 ; Patent No. 5399680  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LAME, CHRISTOPHER J.  
 ; APPLICANT: ZHU, QUN  
 ; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
 ; STREET: 444 South Flower Street, Suite 2000  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 90071-2921  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/704,288C  
FILING DATE: 22-MAY-1991  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P31 8899  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 546-4737  
TELEFAX: (619) 546-9392  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-07-704-288C-6

Query Match 42.9%; Score 623; DB 1; Length 310;  
Best Local Similarity 41.5%; Pred. No. 1.6e-45;  
Matches 124; Conservative 44; Mismatches 77; Indels 54; Gaps 10;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTDTDEYCGDG-CQSGPCRSRGGGGGGGGGGGGS 52  
DB 9 SAEQCGSQAGGARCASGLCCSKFGWCGNTDYGFGNCQS-QC-----PGGPTPP 57

QY 53 GGANVANVVTDAFNG-INKQAGSGCEGKNFYTRSAFLEATAAYPGFAHGSGSEVERKREI 111  
DB 58 GGGDLGSISSSMFQDLKHRNDNACQCGKGYFYNAFINAAARSPFGTSGDTTARKREI 117

QY 112 AAFAHATHET-----GHFCYISEVKNKNAYCDPTKQWPCAAAGQKYGRGP 158  
DB 118 AAFAQTSHETTGWATAPDGPYAWGYCWLREQSGSPGDYCTPS-GQWPCAPGRKYFGRGP 176

QY 159 LQISWNYNYPGAGRAIGDGLGDPGRVARDVAVAFKAALWFMMN-----NVHRVM----- 208  
DB 177 IQISHNYNYPGCGRAIGVLDLNNPDVATDPVISFKSALWFMMTPQSPKPSCHDVIIGRW 236

QY 209 PQ-----GFGATIRANGALECNGNPAQMNARVGYROYCROLDVDPGNLTC 257  
DB 237 PSSADRAANRLPGFVITNIINGLEGCRGTDTSRVQDRIGFYRRYCSILGVSFGDNLDC 295

RESULT 10  
US-07-379-259-6  
Sequence 6, Application US/08379259  
Patent No. 5695939  
GENERAL INFORMATION:  
APPLICANT: LAMB, CHRISTOPHER J.  
APPLICANT: ZHU, QUN  
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT  
TITLE OF INVENTION: DEFENSE REGULATORY  
TITLE OF INVENTION: ELEMENTS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: United States  
ZIP: 90071-2921  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,259

FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/704,288  
FILING DATE: 22-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P31 8899  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 546-4737  
TELEFAX: (619) 546-9392  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-379-259-6

Query Match 42.9%; Score 623; DB 1; Length 310;  
Best Local Similarity 41.5%; Pred. No. 1.6e-45;  
Matches 124; Conservative 44; Mismatches 77; Indels 54; Gaps 10;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTDTDEYCGDG-CQSGPCRSRGGGGGGGGGGGGS 52  
DB 9 SAEQCGSQAGGARCASGLCCSKFGWCGNTDYGFGNCQS-QC-----PGGPTPP 57

QY 53 GGANVANVVTDAFNG-INKQAGSGCEGKNFYTRSAFLEATAAYPGFAHGSGSEVERKREI 111  
DB 58 GGGDLGSISSSMFQDLKHRNDNACQCGKGYFYNAFINAAARSPFGTSGDTTARKREI 117

QY 112 AAFAHATHET-----GHFCYISEVKNKNAYCDPTKQWPCAAAGQKYGRGP 158  
DB 118 AAFAQTSHETTGWATAPDGPYAWGYCWLREQSGSPGDYCTPS-GQWPCAPGRKYFGRGP 176

QY 159 LQISWNYNYPGAGRAIGDGLGDPGRVARDVAVAFKAALWFMMN-----NVHRVM----- 208  
DB 177 IQISHNYNYPGCGRAIGVLDLNNPDVATDPVISFKSALWFMMTPQSPKPSCHDVIIGRW 236

QY 209 PQ-----GFGATIRANGALECNGNPAQMNARVGYROYCROLDVDPGNLTC 257  
DB 237 PSSADRAANRLPGFVITNIINGLEGCRGTDTSRVQDRIGFYRRYCSILGVSFGDNLDC 295

RESULT 11  
US-07-791-931-6  
Sequence 6, Application US/07791931C  
Patent No. 6133507  
GENERAL INFORMATION:  
APPLICANT: Raikhel, Nataasha V.  
TITLE OF INVENTION: Nettle Lectin cDNA  
FILE REFERENCE: MSU 4.1-114  
CURRENT APPLICATION NUMBER: US/07/791.931C  
CURRENT FILING DATE: 1991-11-12  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 310  
TYPE: PRT  
ORGANISM: Nicotiana tabacum  
US-07-791-931-6

Query Match 42.9%; Score 622.5; DB 3; Length 310;  
Best Local Similarity 41.0%; Pred. No. 1.7e-45;  
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTDTDEYCGDG-CQSGPCRSRGGGGGGGGGGGGS 52  
DB 8 SAEQCGSQAGGARCASGLCCSKFGWCGNTDYGFGNCQS-QC-----PGGPTPP 56

Query Match 42.9%; Score 622.5; DB 3; Length 310;  
Best Local Similarity 41.0%; Pred. No. 1.7e-45;  
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTDTDEYCGDG-CQSGPCRSRGGGGGGGGGGGGS 52  
DB 8 SAEQCGSQAGGARCASGLCCSKFGWCGNTDYGFGNCQS-QC-----PGGPTPP 56

QY 53 GGANVANVVDAPFNG-1KNQAGSGCGKKNFYTRSAFLEAIAAYPGFAHGGSEVERKREI 111  
DB 57 GGGDLGSLISSMFDQMLKHNDRNACQKGFYSYNAFINAARSPFGTSGDITARKREI 116  
QY 112 AAFPAHATHET-----GHFCYISEVKNKSNAYCDPTKRWPCAGQKYYGRGP 158  
DB 117 AAFPAQTSHTTGGWATAPDGPYAWGYCWLREQSGPGDYCTPS-GQWPCAPGRKYFGGRP 175  
QY 159 LQISWNNYYPAGRAIGDGLGDPGRVARDVAFAKALWFMWN-----VHRV 207  
DB 176 IQISHNNYYPGCGRAIGVLLNPNLDVATDPVISFKSALWFMWTPQSPKPSCHDVIIIRW 235  
QY 208 MPQ-----GFGATIRAINGALECNNGNPAQMNARVGYRYOYCRQLGVDPGNLTC 257  
DB 236 QPSSADRAANRLPGFGVITNIINGLECGRTDSRVQDRIGFYRYCSILGVSPGDNLDC 295

RESULT 12  
US-08-047-413-11  
; Sequence 11, Application US/08047413  
; Patent No. 5670706  
; GENERAL INFORMATION:  
; APPLICANT: Cornelissen, Bernardus J.C.  
; APPLICANT: Melchers, Leo S.  
; APPLICANT: Meulenhoff, Elisabeth J.S.  
; APPLICANT: van Roekel, Jeroen S.C.  
; APPLICANT: Sela-Buurlage, Marianne B.  
; APPLICANT: Vioemans, Alexandra A.  
; APPLICANT: Woloshuk, Charles P.  
; APPLICANT: Bol, John F.  
; APPLICANT: Linthorst, Hubertus J.M.  
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS. PROCESS FOR  
; TITLE OF INVENTION: OBTAINING FUNGAL-RESISTANT PLANTS AND RECOMBINANT  
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/047,413  
; FILING DATE: 19-APR-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/647,831  
; FILING DATE: 29-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20022.00  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-047-413-11

Query Match 42.7%; Score 619.5; DB 1; Length 324;  
Best Local Similarity 41.0%; Pred. No. 3.3e-45;  
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9;

QY 1 SMONCG-----CQPNVCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGGS 52  
DB 22 SASQCGSQAGCARCAGLCCSKFGWCGNTNDYCGPNCQS-QC-----PGGTPP 70  
QY 53 GGANVANVVDAPFNG-1KNQAGSGCGKKNFYTRSAFLEAIAAYPGFAHGGSEVERKREI 111  
DB 71 GGGDLGSLISSMFDQMLKHNDRNACQKGFYSYNAFINAARSPFGTSGDITARKREI 130  
QY 112 AAFPAHATHET-----GHFCYISEVKNKSNAYCDPTKRWPCAGQKYYGRGP 158  
DB 131 AAFPAQTSHTTGGWATAPDGPYAWGYCWLREQSGPGDYCTPS-GQWPCAPGRKYFGGRP 189  
QY 159 LQISWNNYYPAGRAIGDGLGDPGRVARDVAFAKALWFMWN-----VHRV 207  
DB 190 IQISHNNYYPGCGRAIGVLLNPNLDVATDPVISFKSALWFMWTPQSPKPSCHDVIIIRW 249  
QY 208 MPQ-----GFGATIRAINGALECNNGNPAQMNARVGYRYOYCRQLGVDPGNLTC 257  
DB 250 QPSSADRAANRLPGFGVITNIINGLECGRTDSRVQDRIGFYRYCSILGVSPGDNLDC 309

RESULT 13  
US-08-229-050-11  
; Sequence 11, Application US/08229050  
; Patent No. 6066491  
; GENERAL INFORMATION:  
; APPLICANT: Cornelissen, Bernardus J.C.  
; APPLICANT: Melchers, Leo S.  
; APPLICANT: Meulenhoff, Elisabeth J.S.  
; APPLICANT: van Roekel, Jeroen S.C.  
; APPLICANT: Sela-Buurlage, Marianne B.  
; APPLICANT: Vloemans, Alexandra A.  
; APPLICANT: Woloshuk, Charles P.  
; APPLICANT: Bol, John F.  
; APPLICANT: Linthorst, Hubertus J.M.  
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR  
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/229,050  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/647,831  
; FILING DATE: 29-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20022.00  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-229-050-11

Query Match 42.7%; Score 619.5; DB 3; Length 324;  
Best Local Similarity 41.0%; Pred. No. 3.3e-45;  
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGGGS 52  
DB 22 SAQCCGQAGGARGCAGLCCSKFGWCGNTNDYCGPGNCQS-QC-----PGGPTPP 70  
QY 53 GGANVANVTDAFFNG-IGNQAGSGCEGKNFYTRSAFLAIAAAYPGFAHGSEVERKREI 111  
DB 71 GGGDLGSISSMFDQMLKRNDAACQKGFYSYNAFINAARSFPFGTSGDTTARKREI 130  
QY 112 AAPFAHATHET-----GHFCYISEVKNKNAYCDPTKQWPCAAQKYYGRGP 158  
DB 131 AAFAAQTSHETGGWATAPDGPYANGYCWLRQCSPGDYCTPS-QQWPCAPGRKYFGRGP 189  
QY 159 LOISWNYNGPAGRAIGFDGLGDPGRVARDVAVFAKALWFWNN-----VHRV 207  
DB 190 IQISHNYNGPCGRAIGVDLLNPNDLVATDPVIFSKALWFWMTQSPKPSCHDVIIGRW 249  
QY 208 MPQ-----GFGATIRANGALECNGNPAQMNARVGYRQYCRQLGVDPGNLTLC 257  
DB 250 QPSSADRAANRLPGFVITNIINGGLECGRTDSRVQDRIGFYRRYCYILGVSFGDNLDC 309

RESULT 14

US-08-801-563-11

Sequence 11, Application US/08801563  
Patent No. 6087560

GENERAL INFORMATION:  
APPLICANT: Cornelissen, Bernardus J.C.  
APPLICANT: Melchers, Leo S.  
APPLICANT: Meulenhoff, Elisabeth J.S.  
APPLICANT: van Roekel, Jeroen S.C.  
APPLICANT: Sela-Buurlage, Marianne B.  
APPLICANT: Vloemans, Alexandra A.  
APPLICANT: Woloshuk, Charles P.  
APPLICANT: Bol, John F.  
APPLICANT: Linthorst, Hubertus J.M.

TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR  
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,563  
FILING DATE: 22-MAY-1991  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/047,413  
FILING DATE: 19-APR-1993  
APPLICATION NUMBER: US 07/647,831  
FILING DATE: 29-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20022.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792

US-08-229-050-11

Query Match 42.7%; Score 619.5; DB 3; Length 324;  
Best Local Similarity 41.0%; Pred. No. 3.3e-45;  
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGGGS 52  
DB 22 SAQCCGQAGGARGCAGLCCSKFGWCGNTNDYCGPGNCQS-QC-----PGGPTPP 70  
QY 53 GGANVANVTDAFFNG-IGNQAGSGCEGKNFYTRSAFLAIAAAYPGFAHGSEVERKREI 111  
DB 71 GGGDLGSISSMFDQMLKRNDAACQKGFYSYNAFINAARSFPFGTSGDTTARKREI 130  
QY 112 AAPFAHATHET-----GHFCYISEVKNKNAYCDPTKQWPCAAQKYYGRGP 158  
DB 131 AAFAAQTSHETGGWATAPDGPYANGYCWLRQCSPGDYCTPS-QQWPCAPGRKYFGRGP 189  
QY 159 LOISWNYNGPAGRAIGFDGLGDPGRVARDVAVFAKALWFWNN-----VHRV 207  
DB 190 IQISHNYNGPCGRAIGVDLLNPNDLVATDPVIFSKALWFWMTQSPKPSCHDVIIGRW 249  
QY 208 MPQ-----GFGATIRANGALECNGNPAQMNARVGYRQYCRQLGVDPGNLTLC 257  
DB 250 QPSSADRAANRLPGFVITNIINGGLECGRTDSRVQDRIGFYRRYCYILGVSFGDNLDC 309

RESULT 14

US-08-801-563-11

Sequence 11, Application US/08801563  
Patent No. 6087560

GENERAL INFORMATION:  
APPLICANT: Cornelissen, Bernardus J.C.  
APPLICANT: Melchers, Leo S.  
APPLICANT: Meulenhoff, Elisabeth J.S.  
APPLICANT: van Roekel, Jeroen S.C.  
APPLICANT: Sela-Buurlage, Marianne B.  
APPLICANT: Vloemans, Alexandra A.  
APPLICANT: Woloshuk, Charles P.  
APPLICANT: Bol, John F.  
APPLICANT: Linthorst, Hubertus J.M.

TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR  
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,563  
FILING DATE: 22-MAY-1991  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/047,413  
FILING DATE: 19-APR-1993  
APPLICATION NUMBER: US 07/647,831  
FILING DATE: 29-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20022.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792

US-08-229-050-11

Query Match 42.7%; Score 619.5; DB 3; Length 324;  
Best Local Similarity 41.0%; Pred. No. 3.3e-45;  
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGGGS 52  
DB 22 SAQCCGQAGGARGCAGLCCSKFGWCGNTNDYCGPGNCQS-QC-----PGGPTPP 70  
QY 53 GGANVANVTDAFFNG-IGNQAGSGCEGKNFYTRSAFLAIAAAYPGFAHGSEVERKREI 111  
DB 71 GGGDLGSISSMFDQMLKRNDAACQKGFYSYNAFINAARSFPFGTSGDTTARKREI 130  
QY 112 AAPFAHATHET-----GHFCYISEVKNKNAYCDPTKQWPCAAQKYYGRGP 158  
DB 131 AAFAAQTSHETGGWATAPDGPYANGYCWLRQCSPGDYCTPS-QQWPCAPGRKYFGRGP 189  
QY 159 LOISWNYNGPAGRAIGFDGLGDPGRVARDVAVFAKALWFWNN-----VHRV 207  
DB 190 IQISHNYNGPCGRAIGVDLLNPNDLVATDPVIFSKALWFWMTQSPKPSCHDVIIGRW 249  
QY 208 MPQ-----GFGATIRANGALECNGNPAQMNARVGYRQYCRQLGVDPGNLTLC 257  
DB 250 QPSSADRAANRLPGFVITNIINGGLECGRTDSRVQDRIGFYRRYCYILGVSFGDNLDC 309

RESULT 14

US-08-801-563-11

Sequence 11, Application US/08801563  
Patent No. 6087560

GENERAL INFORMATION:  
APPLICANT: Cornelissen, Bernardus J.C.  
APPLICANT: Melchers, Leo S.  
APPLICANT: Meulenhoff, Elisabeth J.S.  
APPLICANT: van Roekel, Jeroen S.C.  
APPLICANT: Sela-Buurlage, Marianne B.  
APPLICANT: Vloemans, Alexandra A.  
APPLICANT: Woloshuk, Charles P.  
APPLICANT: Bol, John F.  
APPLICANT: Linthorst, Hubertus J.M.

TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR  
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801,563  
FILING DATE: 22-MAY-1991  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/047,413  
FILING DATE: 19-APR-1993  
APPLICATION NUMBER: US 07/647,831  
FILING DATE: 29-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20022.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-494-0792

US-08-229-050-11

Query Match 42.7%; Score 619.5; DB 3; Length 324;  
Best Local Similarity 41.0%; Pred. No. 3.3e-45;  
Matches 123; Conservative 43; Mismatches 79; Indels 55; Gaps 9;

QY 1 SMQNCG-----CQPNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGGGGGGGGGGGGS 52  
DB 22 SAQCCGQAGGARGCAGLCCSKFGWCGNTNDYCGPGNCQS-QC-----PGGPTPP 70  
QY 53 GGANVANVTDAFFNG-IGNQAGSGCEGKNFYTRSAFLAIAAAYPGFAHGSEVERKREI 111  
DB 71 GGGDLGSISSMFDQMLKRNDAACQKGFYSYNAFINAARSFPFGTSGDTTARKREI 130  
QY 112 AAPFAHATHET-----GHFCYISEVKNKNAYCDPTKQWPCAAQKYYGRGP 158  
DB 131 AAFAAQTSHETGGWATAPDGPYANGYCWLRQCSPGDYCTPS-QQWPCAPGRKYFGRGP 189  
QY 159 LOISWNYNGPAGRAIGFDGLGDPGRVARDVAVFAKALWFWNN-----VHRV 207  
DB 190 IQISHNYNGPCGRAIGVDLLNPNDLVATDPVIFSKALWFWMTQSPKPSCHDVIIGRW 249  
QY 208 MPQ-----GFGATIRANGALECNGNPAQMNARVGYRQYCRQLGVDPGNLTLC 257  
DB 250 QPSSADRAANRLPGFVITNIINGGLECGRTDSRVQDRIGFYRRYCYILGVSFGDNLDC 309

RESULT 14

US-08-801-563-11

Sequence 11, Application US/08801563  
Patent No. 6087560

GENERAL INFORMATION:  
APPLICANT: Cornelissen, Bernardus J.C.  
APPLICANT: Melchers, Leo S.  
APPLICANT: Meulenhoff, Elisabeth J.S.  
APPLICANT: van Roekel, Jeroen S.C.  
APPLICANT: Sela-Buurlage

```

; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-704-288C-7

Query Match      42.4%; Score 615; DB 1; Length 314;
Best Local Similarity 42.5%; Pred. No. 7.7e-45;
Matches 122; Conservative 41; Mismatches 74; Indels 50; Gaps 9;

Qy 7 CQNVCCSKFYCGTDEYCGDG-CQSGPCRSGGGGGGGGGGGGGGGAGNVANVVDAP 65
Db 27 CAPGLCCSKFGWCGNTNDYCGPNCQS-QCPGPGPSGDLGG-----VISNSM 73

Qy 66 FNGIKNOAG-SGCEGK-NFYTRSAFLEAIAAYPGFAHGGSEVERKREIAAPFAHATHET- 122
Db 74 FDQMLNHRNDNACQCKGNFYSYNAFISAGSFPFGTGGDITARKREIAAPLAQTSHETT 133

Qy 123 -----GHFCYISEVYKSNAYCDPTKQMPCAAGQYGRGLQISMNNTYGP 170
Db 134 GWPSPADPGPYAWGYCFLEQSGPQDICTPSS-QWPCAPGRKYPGRGPIQISHNNTYGPC 192

Qy 171 GRAIGFDGLDPRVARDNVAFKAAIWFNN-----NVHRVMP-----Q 210
Db 193 GRAIGVDLLNPNPDLVATDSVISFKSAIWFMTQSPKPSCHDVITGRWPSGADQANRVP 252

Qy 211 GFGATIRAINGALCNGNPNQMARVGYRYQYCRQLGVDPGNLTC 257
Db 253 GFGVITNIINGLECGHGSRSRQDRIGFYRYCGILGVSFGDNLDC 299
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Search completed: May 24, 2005, 12:56:20  
Job time : 33.428 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2005, 12:19:56 ; Search time 117.095 Seconds  
(without alignments)  
848.864 Million cell updates/sec

Title: US-10-692-367-12  
Perfect score: 1452  
Sequence: 1 SMQNGCQPNVCCSKFGYCG.....GYRQYCRQLGVDPGNLTC 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A: Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1435	98.8	257	8	ADS92646 Chitinase
3	1435	98.8	257	8	ADS92650 Chitinase
4	1405	96.8	257	8	ADS92688 Chitinase
5	1382.5	95.2	256	8	ADS92676 Chitinase
6	1382	95.2	257	8	ADS92662 Chitinase
7	1377	94.8	257	8	ADS92682 Chitinase
8	1373.5	94.6	256	8	ADS92678 Chitinase
9	1366.5	94.1	256	8	ADS92664 Chitinase
10	1365.5	94.0	256	8	ADS92690 Chitinase
11	1363	93.9	257	8	ADS92680 Chitinase
12	1361	93.7	257	8	ADS92654 Chitinase
13	1361	93.7	257	8	ADS92640 Chitinase
14	1356.5	93.4	254	8	ADS92684 Chitinase
15	1353.5	93.2	250	8	ADS92660 Chitinase
16	1351.5	93.1	256	8	ADS92700 Chitinase
17	1342	92.4	259	8	ADS92656 Chitinase
18	1339	92.2	259	8	ADS92692 Chitinase
19	1338.5	92.2	250	8	ADS92698 Chitinase
20	1333.5	91.8	254	8	ADS92642 Chitinase
21	1333	91.8	255	8	ADS92617 Chitinase
22	1332	91.7	257	8	ADS92624 Chitinase
23	1327	91.4	280	8	ADS92635 Maize chi
24	1323.5	91.2	250	8	ADS92668 Chitinase
25	1320	90.9	280	8	ADS92633 Maize chi

26	1318.5	90.8	250	8	ADS92686 Chitinase
27	1318.5	90.8	256	8	ADS92658 Chitinase
28	1315.5	90.6	250	8	ADS92652 Chitinase
29	1315.5	90.6	258	8	ADS92632 Chitinase
30	1305.5	89.9	250	8	ADS92694 Chitinase
31	1304.5	89.8	250	8	ADS92672 Chitinase
32	1300.5	89.6	258	8	ADS92620 Chitinase
33	1299	89.5	249	8	ADS92696 Chitinase
34	1297.5	89.4	248	8	ADS92618 Maize chi
35	1297.5	89.4	281	3	RAA18894 A maize c
36	1295.5	89.2	250	8	ADS92666 Chitinase
37	1294.5	89.2	250	8	ADS92674 Chitinase
38	1292.5	89.0	250	8	ADS92638 Chitinase
39	1290.5	88.9	250	8	ADS92648 Chitinase
40	1287	88.6	269	8	ADS92634 Maize chi
41	1282.5	88.3	250	8	ADS92670 Chitinase
42	1275.5	87.8	270	8	ADS92636 Maize chi
43	1273.5	87.7	250	8	ADS92644 Chitinase
44	1220	84.0	251	8	ADS92630 Chitinase
45	1218	83.9	251	8	ADS92622 Chitinase

## ALIGNMENTS

RESULT 1  
ADS92628  
ID ADS92628 standard; protein; 257 AA.  
XX  
AC ADS92628;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polypeptide #5.  
XX  
KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX  
OS Synthetic.  
XX  
FN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
(VERD-) VERDIA INC.  
(PION-) PIONEER HI-BRED INT INC.  
Muller ML, True T, Simmons CR, Yalpani N;  
WPI; 2004-365417/34.  
N-PSDB; ADS92627.  
New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.  
Claim 26; SEQ ID NO 12; 197pp; English.  
The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.  
Sequence 257 AA;

Query Match 100.0%; Score 1452; DB 8; Length 257;  
Best Local Similarity 100.0%; Pred. No. 4.5e-123; Indels 0; Gaps 0;  
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SMQNCGCPNVCCSKFGYCGTTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGANVANV 60  
DB 1 SMQNCGCPNVCCSKFGYCGTTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGANVANV 60

QY 61 VTDAFFNGIKNQAGSCGCKNFYTRSAFLAIAAYPGFAHGSGSEVERKRETAAPFAHATH 120  
DB 61 VTDAFFNGIKNQAGSCGCKNFYTRSAFLAIAAYPGFAHGSGSEVERKRETAAPFAHATH 120

QY 121 ETGHFCYISEVNKSNAVCPTKRWPCAAQKYYGRGPLQISWNNYGPAGRAIGFDGLG 180  
DB 121 ETGHFCYISEVNKSNAVCPTKRWPCAAQKYYGRGPLQISWNNYGPAGRAIGFDGLG 180

QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240  
DB 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240

QY 241 RQYCRQLGVDPGNNLTC 257  
DB 241 RQYCRQLGVDPGNNLTC 257

RESULT 2  
ADS92646  
ID ADS92646 standard; protein; 257 AA.  
XX AC ADS92646;  
XX DT 02-DEC-2004 (first entry)  
XX DE Chitinase variant polypeptide #12.  
XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX OS Synthetic.  
XX PN WO2004037194-A2.  
XX PD 06-MAY-2004.  
XX PF 22-OCT-2003; 2003WO-US033588.  
XX PR 22-OCT-2002; 2002US-0420666P.  
XX PR 06-NOV-2002; 2002US-00290086.  
XX PR 14-MAR-2003; 2003US-00389432.  
XX PA (VERD-) VERDIA INC.  
XX PA (PION-) PIONEER HI-BRED INT INC.  
XX PI Muller ML, True T, Simmons CR, Yalpani N;  
XX DR WPI: 2004-365417/34.  
XX DR N-PSDB; ADS92645.  
XX PT New chitinase polynucleotides and polypeptides, useful in producing  
XX PT plants with enhanced resistance against a fungus or a nematode.  
XX PS Claim 3; SEQ ID NO 30; 197pp; English.  
XX CC The invention relates to chitinase polypeptides and the polynucleotides  
XX CC encoding them. A method of enhancing plant resistance to a fungus or  
XX CC nematode comprises introducing into a plant a recombinant expression  
XX CC cassette comprising a promoter operably linked to a chitinase  
XX CC polynucleotide of the invention. The plant is maize or soybean. The  
XX CC fungus is from the genus Fusarium. The nematode is from the genus  
XX CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
XX CC plant resistance to a fungus or nematode. This sequence represents a  
XX CC chitinase variant polypeptide of the invention.

SEQ Sequence 257 AA;  
Query Match 98.8%; Score 1435; DB 8; Length 257;  
Best Local Similarity 98.8%; Pred. No. 1.5e-121; Indels 0; Gaps 0;  
Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SMQNCGCPNVCCSKFGYCGTTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGANVANV 60  
DB 1 SMQNCGCPNVCCSKFGYCGTTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGANVANV 60

QY 61 VTDAFFNGIKNQAGSCGCKNFYTRSAFLAIAAYPGFAHGSGSEVERKRETAAPFAHATH 120  
DB 61 VTDAFFNGIKNQAGSCGCKNFYTRSAFLAIAAYPGFAHGSGSEVERKRETAAPFAHATH 120

QY 121 ETGHFCYISEVNKSNAVCPTKRWPCAAQKYYGRGPLQISWNNYGPAGRAIGFDGLG 180  
DB 121 ETGHFCYISEVNKSNAVCPTKRWPCAAQKYYGRGPLQISWNNYGPAGRAIGFDGLG 180

QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240  
DB 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNAVGY 240

QY 241 RQYCRQLGVDPGNNLTC 257  
DB 241 RQYCRQLGVDPGNNLTC 257

RESULT 3  
ADS92650  
ID ADS92650 standard; protein; 257 AA.  
XX AC ADS92650;  
XX DT 02-DEC-2004 (first entry)  
XX DE Chitinase variant polypeptide #14.  
XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX OS Synthetic.  
XX PN WO2004037194-A2.  
XX PD 06-MAY-2004.  
XX PF 22-OCT-2003; 2003WO-US033588.  
XX PR 22-OCT-2002; 2002US-0420666P.  
XX PR 06-NOV-2002; 2002US-00290086.  
XX PR 14-MAR-2003; 2003US-00389432.  
XX PA (VERD-) VERDIA INC.  
XX PA (PION-) PIONEER HI-BRED INT INC.  
XX PI Muller ML, True T, Simmons CR, Yalpani N;  
XX DR WPI: 2004-365417/34.  
XX DR N-PSDB; ADS92649.  
XX PT New chitinase polynucleotides and polypeptides, useful in producing  
XX PT plants with enhanced resistance against a fungus or a nematode.  
XX PS Claim 3; SEQ ID NO 34; 197pp; English.  
XX CC The invention relates to chitinase polypeptides and the polynucleotides  
XX CC encoding them. A method of enhancing plant resistance to a fungus or  
XX CC nematode comprises introducing into a plant a recombinant expression  
XX CC cassette comprising a promoter operably linked to a chitinase  
XX CC polynucleotide of the invention. The plant is maize or soybean. The  
XX CC fungus is from the genus Fusarium. The nematode is from the genus  
XX CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
XX CC plant resistance to a fungus or nematode. This sequence represents a  
XX CC chitinase variant polypeptide of the invention.

XX Sequence 257 AA;  
SQ  
Query Match 98.8%; Score 1435; DB 8; Length 257;  
Best Local Similarity 98.8%; Pred. No. 1.5e-121;  
Matches 254; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SMQNGCGPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60  
DB 1 SMQNGCGPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGGANVANV 60  
QY 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAYPGFAHGSGSEVERKREIAAPFAHATH 120  
DB 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAYPGFAHGSGSEVERKREIAAPFAHATH 120  
QY 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQKYGRGPLQISWNNYNYGPAGRAIGFDGLG 180  
DB 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQKYGRGPLQISWNNYNYGPAGRAIGFDGLG 180  
QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNARVGY 240  
DB 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNARVGY 240  
QY 241 ROYCRQLGVDPGNLTLC 257  
DB 241 ROYCRQLGVDPGNLTLC 257

RESULT 4  
ADS92688  
ID ADS92688 standard; protein; 257 AA.  
XX  
AC ADS92688;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polypeptide #33.  
XX  
KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
XX  
PR 06-NOV-2002; 2002US-00290086.  
XX  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
XX  
DR N-PSDB; ADS92687.  
XX  
PT New chitinase polynucleotides and polypeptides, useful in producing  
XX  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 3; SEQ ID NO 72; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing  
XX plant resistance to a fungus or nematode. This sequence represents a

CC chitinase variant polypeptide of the invention.  
XX  
SQ Sequence 257 AA;

Query Match 96.8%; Score 1405; DB 8; Length 257;  
Best Local Similarity 95.3%; Pred. No. 8e-119;  
Matches 245; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
QY 1 SMQNGCGPNVCCSKFGYCGTTDBYCGDGCQSGPCRSGGGGGGGGGGGGGANVANV 60  
DB 1 SMQNGCGPNVCCSKFGYCGTTDBYCGDGCQSGPCRSGGGGGGGGGGGGGANVANV 60  
QY 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAYPGFAHGSGSEVERKREIAAPFAHATH 120  
DB 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAYPGFAHGSGSQVQGRKREIAAPFAHATH 120  
QY 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQKYGRGPLQISWNNYNYGPAGRAIGFDGLG 180  
DB 121 ETGHFCYISEVKNKNAYCDPTKROWPCAAAGQKYGRGPLQISWNNYNYGPAGRAIGFDGLG 180  
QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNARVGY 240  
DB 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALCNGNPPAQMNARVGY 240  
QY 241 ROYCRQLGVDPGNLTLC 257  
DB 241 ROYCRQLGVDPGNLTLC 257

RESULT 5  
ADS92676  
ID ADS92676 standard; protein; 256 AA.  
XX  
AC ADS92676;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polypeptide #27.  
XX  
KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
XX  
PR 06-NOV-2002; 2002US-00290086.  
XX  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
XX  
DR N-PSDB; ADS92675.  
XX  
PT New chitinase polynucleotides and polypeptides, useful in producing  
XX  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 3; SEQ ID NO 60; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing

CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX SQ Sequence 256 AA;

Query Match 95.2%; Score 1382.5; DB 8; Length 256;  
 Best Local Similarity 94.9%; Pred. No. 8.7e-117; Indels 1; Gaps 1;  
 Matches 244; Conservative 5; Mismatches 7;  
 QY 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQNGCGQPNVCCSKFGYCGTTDAYCGDGCQSGPCRS-GGGGGGGGGGGGGGGANVANV 59  
 QY 61 VTDAFFNGIKNOAGSCGCKNFYTRSAFLAIAAYPGFAHGSSEVERKRETAAPFAHATH 120  
 DB 60 VTDAFFNGIKNOAGSCGCKNFYTRSAFLSAVKAIPGFAHGSQVQKRETAAPFAHVTH 119  
 QY 121 ETGHFCYI SEVNKSNAYCDPTKRWPCAAGQKYGRGFLQISWNYNYPAGRAIGFDGLG 180  
 DB 120 ETGHFCYI SEINKSNAYCDPTKRWPCAAGQKYGRGFLQISWNYNYPAGRAIGFDGLG 179  
 QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALECNNGNPAQMNARVGY 240  
 DB 180 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALECNNGNPAQMNARVGY 239  
 QY 241 ROYCRQLGVDPGNLTLC 257  
 DB 240 ROYCRQLGVDPGNLTLC 256

RESULT 6

ADSS2662  
 ID ADSS2662 standard; protein; 257 AA.

XX AC ADSS2662;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polypeptide #20.

XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX OS Synthetic.

XX FN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX DR N-PSDB; ADSS2661.

XX PT New chitinase polynucleotides and polypeptides, useful in producing

XX PT plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 3; SEQ ID NO 46; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus

CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX SQ Sequence 257 AA;

Query Match 95.2%; Score 1382; DB 8; Length 257;  
 Best Local Similarity 93.8%; Pred. No. 9.7e-117; Indels 0; Gaps 0;  
 Matches 241; Conservative 9; Mismatches 7;  
 QY 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGANVANV 60  
 DB 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGANVANV 60  
 QY 61 VTDAFFNGIKNOAGSCGCKNFYTRSAFLAIAAYPGFAHGSSEVERKRETAAPFAHATH 120  
 DB 61 VTDAFFNGIKNOAGSCGCKNFYTRSAFLSAVKAIPGFAHGSQVQKRETAAPFAHATH 120  
 QY 121 ETGHFCYI SEVNKSNAYCDPTKRWPCAAGQKYGRGFLQISWNYNYPAGRAIGFDGLG 180  
 DB 121 ETGHFCYI SEINKSNAYCDPTKRWPCAAGQKYGRGFLQISWNYNYPAGRAIGFDGLG 180  
 QY 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALECNNGNPAQMNARVGY 240  
 DB 181 DPGRVARDVAVFAKALWFMMNNVHRVMPQGFATIRAINGALECNNGNPAQMNARVGY 240  
 QY 241 ROYCRQLGVDPGNLTLC 257  
 DB 241 ROYCRQLGVDPGNLTLC 257

RESULT 7

ADSS2682  
 ID ADSS2682 standard; protein; 257 AA.

XX AC ADSS2682;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polypeptide #30.

XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX OS Synthetic.

XX FN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX DR N-PSDB; ADSS2681.

XX PT New chitinase polynucleotides and polypeptides, useful in producing

XX PT plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 3; SEQ ID NO 66; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC polynucleotide of the invention. The plant is maize or soybean. The

CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX Sequence 257 AA;

Query Match 94.8%; Score 1377; DB 8; Length 257;  
 Best Local Similarity 93.4%; Pred. No. 2.8e-116;  
 Matches 240; Conservative 8; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGANVASV 60  
 QY 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAAYPGFAHGGSEVERKREIAAFAHATH 120  
 DB 61 VTDSFFNGIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVGKREIAAFAHATH 120  
 QY 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKTYGRGPLQISWNYNYGPAGRAIGFDGLG 180  
 DB 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKTYGRGPLQISWNYNYGPAGRAIGFDGLA 180  
 QY 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCEGNNPAQMNAVGY 240  
 DB 181 DENRVAQDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCEGNNPAQMNAVGY 240  
 QY 241 ROYCRQLGVDPGNNLTC 257  
 DB 241 ROYCRQLGVDPGNNLTC 257

RESULT 8  
 ADS92678  
 ID ADS92678 standard; protein; 256 AA.  
 XX  
 AC ADS92678;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DB Chitinase variant polypeptide #28.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 XX  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 XX (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 XX WPI; 2004-365417/34.  
 DR N-PSDB; ADS92677.  
 XX  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 62; 197pp; English.  
 XX  
 XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase

CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX Sequence 256 AA;

Query Match 94.6%; Score 1373.5; DB 8; Length 256;  
 Best Local Similarity 94.2%; Pred. No. 5.7e-116;  
 Matches 242; Conservative 8; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQNGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGGGGGGGGGGGANVASV 59  
 QY 61 VTDAFFNGIKNOAGSGCEGKNFYTRSAFLAIAAAYPGFAHGGSEVERKREIAAFAHATH 120  
 DB 61 VTGSFFNGIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFAHATH 119  
 QY 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKTYGRGPLQISWNYNYGPAGRAIGFDGLG 180  
 DB 120 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKTYGRGPLQISWNYNYGPAGRAIGFDGLA 179  
 QY 181 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCEGNNPAQMNAVGY 240  
 DB 180 DPGVARDAVAFKAALWFNNVHVRVMPQGFATIRAINGALCEGNNPAQMNAVGY 239  
 QY 241 ROYCRQLGVDPGNNLTC 257  
 DB 240 ROYCRQLGVDPGNNLTC 256

RESULT 9  
 ADS92664  
 ID ADS92664 standard; protein; 256 AA.  
 XX  
 AC ADS92664;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DB Chitinase variant polypeptide #21.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 XX (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 XX WPI; 2004-365417/34.  
 DR N-PSDB; ADS92663.  
 XX  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 48; 197pp; English.  
 XX  
 XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase

CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.

XX  
XX  
SQ Sequence 256 AA;

Query Match 94.1%; Score 1366.5; DB 8; Length 256;  
Best Local Similarity 94.6%; Pred. No. 2.4e-115;  
Matches 243; Conservative 5; Mismatches 8; Indels 1; Gaps 1;  
QY 1 SMQNCGCPNVCCKFGYCGTTDDEYCGDGCQSGPCRSGGGGGGGGGGGGANVANV 60  
DB 1 SMQNCGCPNVCCKFGYCGTTDDEYCGDGCQSGPCRS- GGGGGGGGGGGGGANVASV 59  
QY 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFHATH 120  
DB 60 VTGSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFHATH 119  
QY 121 ETGHFCTYISEVKNKNAYCDPTKRWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 180  
DB 120 ETGHFCTYISEVKNKNAYCDPTKRWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 179  
QY 181 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCENGNPAQMNARVGY 240  
DB 180 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCENGNPAQMNARVGY 239  
QY 241 RQYCRQLGVDPGNNLTC 257  
DB 240 RQYCRQLGVDPGNNLTC 256

RESULT 10  
ADS92690  
ID ADS92690 standard; protein; 256 AA.  
XX  
XX ADS92690;  
XX  
XX 02-DEC-2004 (first entry)  
XX Chitinase variant polypeptide #34.  
XX Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
XX Synthetic.  
XX WO2004037194-A2.  
XX  
XX 06-MAY-2004.  
XX  
XX 22-OCT-2003; 2003WO-US033588.  
XX  
XX 22-OCT-2002; 2002US-0420666P.  
XX PR 06-NOV-2002; 2002US-00290086.  
XX PR 14-MAR-2003; 2003US-00389432.  
XX  
XX (VERD-) VERDIA INC.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
XX DR N-PSDB; ADS92689.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
XX PT plants with enhanced resistance against a fungus or a nematode.  
XX  
XX Claim 3; SEQ ID NO 74; 197pp; English.  
XX  
XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or

CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.

XX  
XX  
SQ Sequence 256 AA;

Query Match 94.0%; Score 1365.5; DB 8; Length 256;  
Best Local Similarity 92.6%; Pred. No. 3e-115;  
Matches 238; Conservative 12; Mismatches 6; Indels 1; Gaps 1;  
QY 1 SMQNCGCPNVCCKFGYCGTTDDEYCGDGCQSGPCRSGGGGGGGGGGGGANVANV 60  
DB 1 SMQNCGCPNVCCKFGYCGTTDDEYCGDGCQSGPCRP- GGGGGGGGGGGGGANVASV 59  
QY 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGGSEVERKREIAAFHATH 120  
DB 60 VTDSFFNGIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFHATH 119  
QY 121 ETGHFCTYISEVKNKNAYCDPTKRWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 180  
DB 120 ETGHFCTYISEVKNKNAYCDPTKRWPCAAQKQYGRGPLQISWNYNGPAGRAIGFDGLG 179  
QY 181 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCENGNPAQMNARVGY 240  
DB 180 DPGRVARDVAVFAKALWFWMNNVHRVMPQGFATIRAINGALCENGNPAQMNARVGY 239  
QY 241 RQYCRQLGVDPGNNLTC 257  
DB 240 RQYCRQLGVDPGNNLTC 256

RESULT 11  
ADS92680  
ID ADS92680 standard; protein; 257 AA.  
XX  
XX ADS92680;  
XX  
XX 02-DEC-2004 (first entry)  
XX Chitinase variant polypeptide #29.  
XX Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
XX Synthetic.  
XX WO2004037194-A2.  
XX  
XX 06-MAY-2004.  
XX  
XX 22-OCT-2003; 2003WO-US033588.  
XX  
XX 22-OCT-2002; 2002US-0420666P.  
XX PR 06-NOV-2002; 2002US-00290086.  
XX PR 14-MAR-2003; 2003US-00389432.  
XX  
XX (VERD-) VERDIA INC.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
XX DR N-PSDB; ADS92679.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
XX PT plants with enhanced resistance against a fungus or a nematode.  
XX  
XX Claim 3; SEQ ID NO 64; 197pp; English.  
XX  
XX The invention relates to chitinase polypeptides and the polynucleotides

CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 257 AA;

Query Match 93.9%; Score 1363; DB 8; Length 257;  
 Best Local Similarity 92.2%; Pred. No. 5.1e-115; Indels 0; Gaps 0;  
 Matches 237; Conservative 10; Mismatches 10;  
 QY 1 SMQCGCPNVCCKSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQCGCPNVCCKSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGANVANV 60  
 QY 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAAYPGFAHGSVERKREIAAFAHATH 120  
 DB 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAAYPGFAHGSVERKREIAAFAHATH 120  
 QY 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRAIGFDGLG 180  
 DB 121 ETGHFCYISEINKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRDIGFNGLA 180  
 QY 181 DPGVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNARVGYY 240  
 DB 181 DPNRVARDVLAFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMDARVGYY 240  
 QY 241 QYCRQLGVDPGNNLTC 257  
 DB 241 QYCRQLGVDPGNNLTC 257

RESULT 12  
 ADS92654  
 ID ADS92654 standard; protein; 257 AA.  
 XX  
 AC ADS92654;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #16.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PP 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92653.  
 XX  
 PT New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 38; 197pp; English.

CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 257 AA;

Query Match 93.7%; Score 1361; DB 8; Length 257;  
 Best Local Similarity 92.6%; Pred. No. 7.7e-115;  
 Matches 238; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 SMQCGCPNVCCKSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQCGCPNVCCKSKFGYCGTTDEYCGDGCQSGPCRSQGGGGGGGGGGGGGGANVANV 60  
 QY 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAAYPGFAHGSVERKREIAAFAHATH 120  
 DB 61 VTDAFFNGIKNQAGSGCGEKNFYTRSAFLSAVKAAYPGFAHGSVERKREIAAFAHATH 120  
 QY 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRAIGFDGLG 180  
 DB 121 ETGHFCYISEINKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRDIGFNGLA 180  
 QY 181 DPGVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNARVGYY 240  
 DB 181 DPNRVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNARVGYY 240  
 QY 241 QYCRQLGVDPGNNLTC 257  
 DB 241 QYCRQLGVDPGNNLTC 257

RESULT 13  
 ADS92640  
 ID ADS92640 standard; protein; 257 AA.  
 XX  
 AC ADS92640;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #9.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PP 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92639.  
 XX  
 PT New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 24; 197pp; English.



XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 257 AA;

Query Match 93.7%; Score 1361; DB 8; Length 257;  
 Best Local Similarity 92.2%; Pred. No. 7.7e-115;  
 Matches 237; Conservative 9; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60  
 QY 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGSGSEVERKREIAAPFAHATH 120  
 DB 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGSGSQVQGRKREIAAPFAHATH 120  
 QY 121 ETGHFCYISEVKNKNAYCDPTKQWPCAAQKYYGRGLQISWNYNYGPAGRAIGFDGLG 180  
 DB 121 ETGHLCYINEVKNKNAYCDPTKQWPCAAQKYYGRGLQISWNYNYGPAGRAIGFDGLG 180  
 QY 181 DPGRVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
 DB 181 DPDLAQDPVLSFKSALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
 QY 241 ROYCRQLGVDPGNNLTC 257  
 DB 241 ROYCRQLGVDPGNNLTC 257

RESULT 14  
 ADS92684  
 ID ADS92684 standard; protein; 254 AA.  
 XX  
 AC ADS92684;  
 XX  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #31.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 FI  
 XX WPI; 2004-365417/34.  
 DR N-PSDB; ADS92683.  
 DR  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX

PS Claim 3; SEQ ID NO 68; 197pp; English.  
 XX  
 CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 254 AA;

Query Match 93.4%; Score 1356.5; DB 8; Length 254;  
 Best Local Similarity 93.0%; Pred. No. 1.9e-114;  
 Matches 239; Conservative 9; Mismatches 6; Indels 3; Gaps 1;  
 QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGGGGGGGGGGGGGGGANVANV 60  
 DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGGGGGGGGGGGGGGGANVANV 57  
 QY 61 VTDAFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGSGSEVERKREIAAPFAHATH 120  
 DB 58 VTGSFFNGIKNQAGSGCEGKNFYTRSAFLAIAAYPGFAHGSGSQVQGRKREIAAPFAHATH 117  
 QY 121 ETGHFCYISEVKNKNAYCDPTKQWPCAAQKYYGRGLQISWNYNYGPAGRAIGFDGLG 180  
 DB 118 ETGHFCYISEVKNKNAYCDPTKQWPCAAQKYYGRGLQISWNYNYGPAGRAIGFDGLG 177  
 QY 181 DPGRVARDVAVFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNARVGY 240  
 DB 178 DPNEVADAVAVFAKALFWNNVHVRVMPQGFATIRAINGALCNGNPAQMNARVGY 237  
 QY 241 ROYCRQLGVDPGNNLTC 257  
 DB 238 ROYCRQLGVDPGNNLTC 254

RESULT 15  
 ADS92660  
 ID ADS92660 standard; protein; 250 AA.  
 XX  
 AC ADS92660;  
 XX  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #19.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 FI  
 XX WPI; 2004-365417/34.  
 DR N-PSDB; ADS92659.  
 DR  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX

XX Claim 3; SEQ ID NO 44; 197pp; English.  
PS  
XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
SQ Sequence 250 AA;  
Query Match 93.2%; Score 1353.5; DB 8; Length 250;  
Best Local Similarity 93.4%; Pred. No. 3.6e-114;  
Matches 240; Conservative 3; Mismatches 7; Indels 7; Gaps 1;  
QY 1 SMQNGCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGANVANV 60  
DB 1 SMQNGCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGGGGGGANVANV 53  
QY 61 VTDAFFNGIKNOAGSGCGKGFYTRSAFLAIAAYPGFAHGSEVERKRETAAPFAHATH 120  
DB 54 VTDAFFNGIKNOAGSGCGKGFYTRSAFLSAVKAYPGFAHGSEVERKRETAAPFAHATH 113  
QY 121 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 180  
DB 114 ETGHFCYISEVKNKNAYCDPTKRWPCAAAGQKYYGRGPLQISWNYNYGPAGRAIGFDGLG 173  
QY 181 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNARVGY 240  
DB 174 DPGRVARDVAVFAKALWFNNVHVRVMPQGFATIRAINGALCNGNPPAQMNARVGY 233  
QY 241 ROYCRQLGVDPGNLTTC 257  
DB 234 ROYCRQLGVDPGNLTTC 250

Search completed: May 24, 2005, 12:50:19  
Job time : 118.095 secs

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OM nucleic - nucleic search, using sw model

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Title: US-10-692-367-11  
Perfect score: 774  
Sequence: 1 tcgtgcagactgcggctg.....gcaacaacctcacctgtcta 774

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%  
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Database :	EST:*			
	1: gb_est1:*	2: gb_est2:*	3: gb_hic:*	4: gb_est3:*
	5: gb_est4:*	6: gb_est5:*	7: gb_est6:*	8: gb_gse1:*
	9: gb_gse2:*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	691.8	89.4	1179	3 AY103546	AY103546 Zea mays
2	607.6	78.5	958	4 BG837479	BG837479 Zm10.10h0
3	597.6	77.2	855	4 BG837663	BG837663 Zm10.01e1
4	553.4	71.5	767	7 C0524416	C0524416 3530.1.16
5	543.4	70.2	737	6 CD4335649	CD4335649
6	530.4	68.5	625	5 BM895383	BM895383 952073H05
7	529.2	68.4	716	7 C0520138	C0520138 3530.1.13
8	525.6	67.9	628	4 BM736454	BM736454 952051A06
9	519.4	67.1	837	7 CN133023	CN133023 OX1.9.D11
10	503	65.0	647	6 CA197556	CA197556 SCBFAD106
11	502	64.9	710	6 CD443492	CD443492 EOL1N0427
12	501	64.7	820	6 CD995497	CD995497 QB25f07.
13	498.2	64.4	578	6 CD994454	CD994454 QB15f08.
14	497.2	64.2	741	6 CD994869	CD994869 QB18d07.
15	497.2	64.2	753	6 CD994885	CD994885 QB18e05.
16	497	64.2	578	6 CD994156	CD994156 QB13f07.
17	495.6	64.0	575	6 CD994132	CD994132 QB13e04.
18	485.6	62.7	567	5 BU050046	BU050046 111019B0
19	485	62.7	812	7 CN132942	CN132942 OX1.9.D11
20	483	62.4	754	6 CD995176	CD995176 QB20h11.
21	481.2	62.2	550	6 CF001565	CF001565 QBGAf06.x
22	481.2	62.2	559	6 CD999920	CD999920 QBG10a02.
23	481.2	62.2	562	6 CF000010	CF000010 QBG11a02.
24	481.2	62.2	562	6 CF000028	CF000028 QBG13e12.

25	481.2	62.2	562	6 CF000357	CF000357 QBG15b09.
26	481.2	62.2	562	6 CF000565	CF000565 QBG17b11.
27	481.2	62.2	562	6 CF000643	CF000643 QBG18a05.
28	481.2	62.2	573	6 CF000161	CF000161 QBG12g06.
29	481.2	62.2	573	6 CF000412	CF000412 QBG15q11.
30	481.2	62.2	574	6 CD999947	CD999947 QBG10c07.
31	481.2	62.2	574	6 CF000325	CF000325 QBG4911.
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33	481.2	62.2	587	6 CF002109	CF002109 QBG8h11.x
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35	481.2	62.2	606	6 CF001262	CF001262 QBG2b02.x
36	481.2	62.2	606	6 CF001900	CF001900 QBG7c09.x
37	481.2	62.2	742	6 CF001316	CF001316 QBG2e05.p
c	480.2	62.0	573	6 CF000017	CF000017 QBG11a12.
39	479.6	62.0	603	6 CF001775	CF001775 QBG5c07.x
40	479.6	62.0	627	6 CF001901	CF001901 QBG7c10.x
41	479.6	62.0	641	6 CF011507	CF011507 QBJ8h11.x
c	479.6	62.0	746	6 CF001249	CF001249 QBG2a02.p
43	479.6	62.0	751	6 CF014225	CF014225 QBL14a03.
c	477.6	61.7	688	6 CA281399	CA281399 SCAGSD104
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ALIGNMENTS

RESULT 1	AY103546	1179 bp	mrna	linear	HTC 16-OCT-2002
LOCUS	AY103546				
DEFINITION	Zea mays PC0155066 mRNA sequence.				
ACCESSION	AY103546				
VERSION	AY103546.1	GI:21206624			
KEYWORDS	HTC.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	1 (bases 1 to 1179)				
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
TITLE	Hayney,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.				
JOURNAL	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes				
REFERENCE	2 (bases 1 to 1179)				
AUTHORS	Coe,E.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.				

FEATURES	Location/Qualifiers
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	/db_xref="taxon:4577"
	/clone_lib="Maize Mapping Project/DuPont Consensus Library"
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

Query Match 89.4%; Score 691.8; DB 3; Length 1179;

Best Local Similarity 93.9%; Pred. No. 9.8e-131; Mismatches 0; Indels 0; Gaps 0; Matches 720; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 6 GCAGAACTGCGGCTGCCAGCAAGATGCTGCGCAAGTTTGGCTACTCGGCACGAC 65  
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Qy 66 CGACGAGTACTGCGGCGAGCGGTCAGTCCGGCCCGCTCGGCGGCGGCTGGGG 125  
Db 208 CGACGCTTACTGCGGCGAGCGGTCAGTCCGGCCCGCTCGGCGGCGGCTGGGG 267

Qy 126 CGGCGGCGGCGGAGCGGCGGAGGAGTGGCGGTCGCAACGCTGTAATGTGTCAC 185  
Db 268 CGGCGGCGGCGGAGCGGCGGAGGAGTGGCGGTCGCAACGCTGTAATGTGTCAC 327

Qy 186 CGACGCTTCTTCAACGCGATCAAGAACACAGCGCGGAGCGGTCGAGGCAAGAACTT 245  
Db 328 CGACGCTTCTTCAACGCGATCAAGAACACAGCGCGGAGCGGTCGAGGCAAGAACTT 387

Qy 246 CTACACCGGAGCGGTTCTCGAGGCGATCGCGGTCACCGGCTCGCGCATGGCGG 305  
Db 388 CTACACCGGAGCGGTTCTCGAGGCGGTCACCGGTCACCGGCTCGCGCATGGCGG 447

Qy 306 CTCCGAGTCCAGCGCAAGCGGATGCGGCTTCTTTCGCGCACGCGCACGACGAC 365  
Db 448 GACGAGGTGAGGCGCAAGCGGAGTCCGCGCTTCTTCGCGCACGTCACGCGACGAC 507

Qy 366 CGGCGATTTCTGCTACATCAGCGAGTCAACAGAGCAACGCTACTCGGACCGACAA 425  
Db 508 CGGCAATTTCTGCTACATCAGCGAGTCAACAGAGCAACGCTACTCGGACCGAGCAA 567

Qy 426 GAGCGAGTGGCGGCGCGCGGCGGAGGATGCTACCGGCGCGCGCTCGAGATCTC 485  
Db 568 CAGGCGAGTGGCGGCGCGCGGCGGAGGATGCTACCGGCGCGCGCTCGAGATCTC 627

Qy 486 GTGGAATACAACTACCGGCGCGCGGAGGCGCATCGGCTTTCGACGGGCTCGGGACCC 545  
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Qy 546 CGGCGAGGTGGCGGCGCGCGGCGGAGGCGGCTTTCGAGGCGGCGCTCTGGTTCTGATGAA 605  
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Qy 666 CTTGAGTGCACCGGAGCAACCCCGCGGAGATGAAACGCGGCGGCTGCTACTACGAGCA 725  
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Qy 726 GTACTGCGCGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 772  
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RESULT 2  
BG837479 958 bp mRNA linear EST 25-MAY-2001  
LOCUS Zm10\_10h09 A Zm10\_AAPC\_ECORC\_Fusarium graminearum\_corn\_silk Zea  
DEFINITION Zea mays clone Zm10\_10h09, mRNA sequence.

ACCESSION BG837479

VERSION BG837479.1

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 958)  
Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De  
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A.,  
Sprott,D. and Tinker,N.A.

TITLE Expressed Sequence Tags from Maize Silk Six Hours After Silk  
Channel Inoculation with Fusarium graminearum  
JOURNAL Unpublished (2001)  
COMMENT Contact: Harris, Linda J.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-Food Canada  
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,  
CANADA  
Tel: (613) 759-1314  
Fax: (613) 759-8566  
Email: harris@agr.gc.ca.

FEATURES  
source

1. 958  
/location/Qualifiers  
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/cultivar="CO388"  
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/tissue type="Silk"  
/dev stage="4-5 days post-silk emergence"  
/clone\_lib="Zm10\_AAPC\_ECORC\_Fusarium\_graminearum\_corn\_silk"  
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site\_1: EcoRI;  
Site\_2: XhoI; Field-grown corn was silk channel-inoculated  
in the morning (~10 am) with 1 ml of a macroconidial  
suspension (500,000 spores/ml) of Fusarium graminearum and  
silk channels were collected and immediately frozen in  
liquid nitrogen 6 hours later. RNA was extracted from  
silk tissue between 1 cm below and above the inoculation  
point in the silk channel, RNA from five silk channels was  
pooled."

ORIGIN

Query Match 78.5%; Score 607.6; DB 4; Length 958;  
Best Local Similarity 89.7%; Pred. No. 1.3e-113;  
Matches 681; Conservative 6; Mismatches 61; Indels 11; Gaps 3;

Qy 6 GCAGAACTGCGGCTGCCAGCAAGATGCTGCGCAGC-AAGTTTGGCTACTCGGCACGA 64  
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Qy 65 CCGACGAGTACTCGGCGGAGCGGTCAGTCCGCGCGGCTCGGCGGCGGCTGGCG 124  
Db 91 CCGACGAGTACTCGGCGGAGCGGTCAGTCCGCGCGGCTCGGCGGCGGCTGGCG 141

Qy 125 CCGCGCGGCGGCGGAGCGGTCAGTCCGCGCGGCTCGGCGGCGGCTGGCG 184  
Db 142 CCGCGCGGCGGCGGAGCGGTCAGTCCGCGCGGCTCGGCGGCGGCTGGCG 201

Qy 185 CCGACGCGTCTTCAACGCGCATCAAGAACACAGCGCGGCGGTCGCGGCGGCAAGAACT 244  
Db 202 CCGACGCGTCTTCAACGCGCATCAAGAACACAGCGCGGCGGTCGCGGCGGCAAGAACT 261

Qy 245 TCTACACCGGAGCGGTTCTCGAGGCGCATCGCGCGGTCACCGGCGGTCGCGGCGGTCGCG 304  
Db 262 TCTACACCGGAGCGGTTCTCGAGGCGCGTCAACAAAGTACGCGGCTTTCGCGGCGGTCGCG 320

Qy 305 GCTCGAGGTGAGCGCAAGCGGAGATGCGCGCTTCTTCGCGCAGCGCGCACGACGAGA 364  
Db 321 GCGCGAGGTGAGCGCAAGCGGAGATGCGCGCTTCTTCGCGCAGCGCGCACGAGA 380

Qy 365 CCGCGCATTTCTGCTACATCAGCGAGGTCAACAAAGAGCAACGCTTCTGCGACCGGACCA 424  
Db 381 CCGGACATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCTTCTGCGACCGGACCA 440

Qy 425 AGAGCGAGTGGCGGCGCGCGGCGGAGAGTACTACGCGGCGGCGGCGGCGGCGGCGGATCT 484  
Db 441 ACAGCGAGTGGCGGCGCGGCGGCGGAGAGTACTACGCGGCGGCGGCGGCGGCGGATCT 500

Qy 485 CGTGGAACTACAACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 544  
Db 501 CGTGGAACTACAACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 560

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QY |||
605 ACAAGTGCACCGTGTGATGCGCAGGGCTTCGGCGGCCACCATCAGGCGCATCAACGGCG 664
Db |||
621 ACAAGTGCACCGTGTGATGCGCAGGGCTTCGGCGGCCACCATCAGGCGCATCAACGGCG 680
QY |||
665 CCTCGAGTGCAACGGGAAACACCCGCCAGATGAACGCGCGTCTCGGCTACTACAGC 724
Db |||
681 CCTCGAGTGCAACGGGAAACACCCGCCAGATGAACGCGCGTCTCGGCTACTACAGC 740
QY |||
725 AGTACTGGCGCAGCTCGCGTCTGACCGCGGCAACACC 763
Db |||
741 AGTACTGGCGCAGCTCGCGTCTGACCGCGGCAACACC 779

RESULT 3
BG837663/3
LOCUS BG837663 855 bp mRNA linear EST 25-MAY-2001
DEFINITION Zm10_01e10_A Zm10_AAFc_ECORC_Fusarium graminearum_corn_silk Zea
mays cDNA clone Zm10_01e10, mRNA sequence.
ACCESSION BG837663
VERSION BG837663.1 GI:14203986
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 855)
AUTHORS Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
TITLE Expressed Sequence Tags from Maize Silk Six Hours After Silk
Channel Inoculation with Fusarium graminearum
JOURNAL Unpublished (2001)
COMMENT Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrielj@agr.gc.ca.
FEATURES
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/cultivar="CO388"
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"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
Site 2: XhoI; Field-grown corn was silk channel-inoculated
in the morning (~10 am) with 1 ml of a macroconidial
suspension (500,000 spores/ml) of Fusarium graminearum and
silk channels were collected and immediately frozen in
liquid nitrogen 6 hours later. RNA was extracted from
silk tissue between 1 cm below and above the inoculation
point in the silk channel, RNA from five silk channels was
pooled."

ORIGIN
Query Match 77.2%; Score 597.6; DB 4; Length 855;
Best Local Similarity 90.3%; Pred. No. 1.5e-111;
Matches 670; Conservative 0; Mismatches 49; Indels 23; Gaps 2;

QY 31 GTATGCTGCAGCAAGTTTGGCTACTGCGGCAAGAGTACTGCGGCGAAGCGGTGC 90
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794 CAGTCGGGCGCGT-----CCGCTCGGGGCGGCGGCGGCGGCGAGT 757
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Db |||
756 GGCAGTGGCGGTGGAACGTGGCTAAGCTGTCTACCGGCTCTCTTCTTCAACGGGATCAAG 697
QY |||
211 AACACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 270
Db |||
696 AGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 637
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636 GCCGTCAAGGCGTACCCCGAG--TTCGCCCATGCGCGGTCGCGAGGTGCGAGGCGAAGCGCGAG 578
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331 ATTGCGCGCTTTCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 390
Db |||
577 ATCGCGCGCTTCTTTCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 518
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QY |||
571 GTGCGCTTCAAGCGGCGGCGGCTCTGCTTCTGATGAACAAACGTCGACCGGTGTCATGCCGCGAG 630
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QY |||
751 CCGGCGCAACCACTCCTCCTGCT 772
Db |||
157 CCGGCGCAACCACTCCTCCTGCT 136

RESULT 4
LOCUS CO524416
DEFINITION 3530_1_161_1_E12.y_1 3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION CO524416
VERSION CO524416.1 GI:50329290
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 767)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
```

Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 3530\_1161\_1 row: E column: 12.

# FEATURES

source  
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 /tissue\_type="multitple"  
 /dev\_stage="varies by tissue"  
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 /clone\_lib="3530 - Full length cDNA library created by Invitrogen from multiple tissues"  
 /note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT 6.1; Site 1: EcoRI; Site 2: NotI; Maize Gene Discovery Project contracted with Invitrogen to produce a normalized, full length library in a pSPORT vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Query Match 71.5%; Score 553.4; DB 7; Length 767;  
 Best Local Similarity 91.4%; Pred. No. 1.5e-102;  
 Matches 606; Conservative 0; Mismatches 36; Indels 21; Gaps 1;  
 6 GCAGAACTGCGGCTGCCAGCAACGATATGCTGCAGCAAGTTGGCTACTCGGCACGAC 65  
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 66 GCACAGATCTCGCGGACGGTGCAGTCGGGCCCGTCCGCTCGGGCGGGGTGGCG 125  
 186 GCACAGATCTCGCGGACGGTGCAGTCGGGCCCGTCCGCTCGGGCGGGGTGGCG 245  
 126 CGGCGGCGCGCGGCGGCGGAGCGATGTCGGGTGCAAGCTGGCTAATGTGCTCAC 185  
 246 CAGTGGCGGC-----GGTGTGCAACGCTGGCTAGGCTGCTCAC 284  
 186 CGACGCTTTCTTCAACGGCATCAAGAACGAGCCGGGAGCGGGTCGAGGGCAAGACTT 245  
 285 CGGCTCTTCTTCAACGGCATCAAGAGCCAGCGCGGCTGCAGGGCAAGACTT 344  
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 345 CTACACCGGAGCGGCTTCTCGAGGCCGTCAAGCGGTACCCAGCGCTTCGCCCATGGCGG 404

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 DB 525 GAGGCACTGCGCGTGGCGCGCGGCGAGAGTACTACGGGCGCGCGCTGCGAGATCTC 584  
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 DB 645 CGGCGAGGTGCGCGGAGACGCGGTGGGTTCGAGGCGCGCTCTGGTTCTGGATGAA 704  
 QY 606 CAACTGCACCGTGTGATCGCGAGGCGCTTCGGGCGCGCACCATCAGGCGCATCAACGGCGC 665  
 DB 705 CAGCGTGACGCGGTGGTGGCGAGGCGTTCGGGCGCGCACCATCAGGCGCATCAACGGCGC 764  
 QY 666 CCT 668  
 DB 765 CCT 767

## RESULT 5

CD435649  
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 DEFINITION E01N0364B04.b Endosperm\_3 Zea mays cDNA, mRNA sequence.  
 ACCESSION CD435649  
 VERSION CD435649.1 GI:31351292  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 737)  
 Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Becraft, P. and Messing, J.  
 Characterization of the maize endosperm transcriptome and its comparison to the rice genome  
 Genome Res. 14 (10), 1932-1937 (2004)

## JOURNAL

COMMENT

Contact: Lai, Jinsheng  
 Dr. Joachim Messing's lab  
 Wakeman Institute, Rutgers University  
 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA  
 Tel: 732-445-3801  
 Fax: 732-445-5735  
 Email: jlai@wakeman.rutgers.edu  
 Seq primer: T3.

## FEATURES

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## ORIGIN

Query Match 70.2%; Score 543.4; DB 6; Length 737;  
 Best Local Similarity 89.8%; Pred. No. 1.6e-100;  
 Matches 619; Conservative 0; Mismatches 36; Indels 34; Gaps 2;  
 6 GCAGAACTGCGGCTGCCAGCAACGATATGCTGCAGCAAGTTGGCTACTCGGCACGAC 65



Db 82 GCAGAACTGGCGTCCGACGCAAGCTCTGCTGACGAAAGTTTCGGTACTCGGCGACGAC 141  
Qy 66 CGACAGTACTGCGCGACGAGTGCAGTCCGGCCCGTCCGCTCGGCGCGCGTGGCGG 125  
Db 142 CGACAGTACTGCGCGACGAGTGCAGTCCGGCCCGTCCGCTCGGCGCGCGCGCGC-- 199  
Qy 126 CGGCGCGCGCGCGGAGCGCGGAGGAGTGGCGGTGCGAACGTGGTGAATATGTTGTCAC 185  
Db 200 -----GGTGGTGCBAACGTGGCTAGCGTGGTGCAC 228  
Qy 186 CGACCGCTTCTTCAACGCGCATCAAGAACAGCCCGGAGCGGGTGCAGGGCAAGAACTT 245  
Db 229 CGGCTCTTCTTCAACGCGCATCAAGAACAGCCCGGAGCGGGTGCAGGGCAAGAACTT 288  
Qy 246 CTACACCGCGAGCGGTTCTCGAGGCGCATCGCGCGTACCGGGGCTTCGGCGCATGGCGG 305  
Db 289 CTACACCGCGAGCGGTTCTCGAGGCGCGTCAAGGCGTACCGAGGCTTCGCCCATGGCGG 348  
Qy 306 CTCGAGGTTCGAGCGCAAGCGGAGATGCGCGCTTCTTCGCGCACGCCACGACGAGAC 365  
Db 349 GTCGAGGTTCGAGCGCAAGCGGAGATGCGCGCTTCTTCGCGCACGCCACGACGAGAC 408  
Qy 366 CGGCGATTTCTGTACTACGCGAGTCAACAAAGAACGCGCTACTGCGACCCGACCAA 425  
Db 409 CGGCGATTTCTGTACTACGCGAGATCAACAGAGCAACGCTACTGCGACCCGACCAA 468  
Qy 426 GAGCGAGTGGCGGTGCGCGCGGCGGACAGATCTACCGGGCGCGCCGCTGCGAGATCTC 485  
Db 469 GAGCGAGTGGCGGTGCGCGCGGCGGACAGATCTACCGGGCGCGCCGCTGCGAGATCTC 528  
Qy 486 GTGGAATCTACACTACGCGCGCGGCGGAGGCGCATCGCTTCGACGGGCTTCGGGACCC 545  
Db 529 GTGGAATCTACACTACGCGCGCGGCGGAGGCGCATCGCTTCGACGGGCTTCGGGACCC 588  
Qy 546 CGCAGGCTGGCGGCGCGCGGTGGTGGCGTTCAGAGCGCGCTCTGTTCTGTGATGAA 605  
Db 589 CGCAGGCTGGCGGCGCGCGGTGGTGGCGTTCAGAGCGCGCTCTGTTCTGTGATGAA 648  
Qy 606 CAACGTGCAC-CGTGTGATGCGCAGGCGTTCGGCGCCACCATCAGGCGCATCAACGCGC 664  
Db 649 CAGCGTGCACGGGGTGGTGGCGCAGGCGTTCGGCGCCACCATCAGGCGCATCAACGCGC 708  
Qy 665 CCCTCGAGTGCNACGGGACACCCCGCC 693  
Db 709 CCCTCGAGTGGCGGGAACACCCCGCC 737

## RESULT 6

BM895383  
LOCUS 952073H05.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea  
DEFINITION mays cDNA, mRNA sequence.

ACCESSION BM895383

VERSION BM895383.1 GI:19350851

KEYWORDS EST.

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 625)

REFERENCE Walbot,V.

AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford

TITLE University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 952073 row: H column: 05.

FEATURES  
Source

Location/Qualifiers  
1. 625  
/organism="Zea mays"  
/mol\_type="mRNA"  
/culti\_var="BMS (Black Mexican Sweet)"  
/db\_xref="taxon:4577"  
/tissue\_type="suspension culture"  
/dev\_stage="mixed logarithmic and stationary growth  
phases"  
/lab\_host="DH10B"  
/clone\_lib="952 - BMS tissue from Walbot Lab (reduced  
rRNA)"  
/notes="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and Universal Riboclone cDNA Synthesis System  
(Promega). cDNA was synthesized using both random and  
oligo(dT) primers in separate reactions and equipped with  
EcoRI adaptors. Library was size-fractionated on agarose  
gels (for insert size 400bp) and non-directionally cloned  
into EcoRI-digested pUC19 vector. Blue/white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

## ORIGIN

Query Match 68.5%; Score 530.4; DB 5; Length 625;  
Best Local Similarity 92.4%; Pred. No. 7e-98;  
Matches 569; Conservative 0; Mismatches 46; Indels 1; Gaps 1;  
Qy 146 GCGGAGCAGTGGCGGTGCGAAAGTGGCTAATGTGGTCCACGACGCGTCTTCAACGGCA 205  
Db 11 GCGGAGCAGTGGCGGTGCGAAAGTGGCTAAG--GGTCAGCGACGCGTCTTCAACGGCA 69  
Qy 206 TCAAGAACCAAGCGCGGAGCGGGTGCAGAGGCAAGAACTTCTACACCGGAGCGGTTCC 265  
Db 70 TCAAGAACCAAGCGCGGAGCGGGTGCAGAGGCAAGAACTTCTACACCGGAGCGGTTCC 129  
Qy 266 TCGAGGCGCATCGCGGTACCGGGCTTCGCGCATGGCGCTCCGAGGTTCAGGCGCAAGC 325  
Db 130 TGAGCGCGCTCAACAAGTACCCGGGCTTCGCGCATGGCGGACGGAGGTGAGGGGCAAGC 189  
Qy 326 GCGAGATTGCGCGCTTCTTCGCGCACGCGACGACGACGCGGCATTTCTGTACATCA 385  
Db 190 GCGAGATTGCGCGCTTCTTCGCGCACGCTCAGCGACGAGACCGGACATTTCTGTACATCA 249  
Qy 386 GCGAGGTCAACAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGGTGGCGCGCGCG 445  
Db 250 GCGAGATCAACAGAGCAACGCTTACTGCGACGCAAGCAACAGGCAAGTGGCGCGCGG 309  
Qy 446 CGGCGCAGAGTACTACGGGCGCGCGCTGCGAGATCTCGTGAACCTACAACTACGCGGC 505  
Db 310 CGGCGCAGAGTACTACGGGCGCGCGCTGCGAGATCTCGTGAACCTACAACTACGCGGC 369  
Qy 506 CCGCGCGGAGGGCCATCGGGTTCGACGGGCTTCGCGGACCCCGGAGGTGCGCGGAGCG 565  
Db 370 CCGCGCGGAGGGACATCGGGTTCGACGGGCTTCGCGGACCCCAACAGGCTGGCGAGAG 429  
Qy 566 CCGTGTGGGCTTCAAGCGCGCGCTCTGTGTTCTGTGATGAACAACTGTCACCGTGTATGC 625  
Db 430 CCGTGTGCGGTTCAAGACGCGCGCTCTGTGTTCTGTGATGAACAACTGTCACCGTGTATGC 489  
Qy 626 GCGAGGCGCTTCGGCGCGCCACCATCAGGGCCATCAAGGGCGCCCTCGAGTGAACCGGAC 685  
Db 490 GCGAGGCGCTTCGGCGCGCCACCATCAGGGCCATCAAGGGCGCCCTCGAGTGAACCGGAC 549  
Qy 686 ACCCGCGCCAGATGAACGCGCGCTCGGCTACTACAGCAGTACTGCGCGCAGCTCGCGG 745  
Db 550 ACCCGCGCCAGATGAACGCGCGCTCGGCTACTACAGCAGTACTGCGCGCAGCTCGCGG 609  
Qy 746 TCGACCCCGGCAACAA 761  
Db 610 TCGACCCCGGCGCCAA 625

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RESULT 7
COS20138
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

3530_1_132_1_F10.Y_1_3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.

COS20138
EST.
GI:50325012

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 716)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530_1_132_1 row: F column: 10.

FEATURES
source
location/Qualifiers
1..716
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="multiple"
/dev_stages="varies by tissue"
/lab_host="DH10B"
/clone_lib="3530 - Full length cDNA library created by
Invitrogen from multiple tissues"
/notes="Organ: silks, husks, ears, pollen, shoot tips,
leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
6.1; Site: 1; EcoRV; Site 2: NotI; Maize Gene Discovery
Project contracted with Invitrogen to produce a
normalized, full length library in a pSPORT vector. This
is a Gateway compatible vector, permitting clone movement
to new vector backbones for expression in diverse host
cells using recombination rather than restriction enzymes.
Details of the vector and sequencing primers are available
at ZmDB in the EST library description tables. poly(A)+
mRNA was prepared by Invitrogen, and equimolar amounts of
RNA from each of the 12 tissue samples were mixed together
for selection of mRNA with a 5' cap. After synthesis of
cDNA, a normalization step was conducted against the
mixture of RNA sources. This step effected a 20X to 80X
reduction in common transcript types. Tissues prepared: 1.
just emerging silks; 2. inner husks from ears of sample
#1; 3. 20 dap aleurone; 4. immature tassels, stages from
1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
vegetative shoot tips from 15 day old seedlings; all
leaves with an expanded or partially expanded sheath
were removed; 8. mature leaf tissue; 9. 0.5 cm long root
tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
12 dap endosperm and embryo; 12. 17 dap endosperm and
embryo. All of the sequenced clones in project 3530 will
be archived at the University of Arizona along with the
UniGene clones from the Maize Gene Discovery EST
sequencing projects. Clones can be ordered through the
ZmDB web site or directly from the University of Arizona
(http://www.genome.arizona.edu/orders/). High density
filters containing over 18,000 clones can also be ordered
from the University of Arizona."

ORIGIN
Query Match 68.4%; Score 529.2; DB 7; Length 716;
Best Local Similarity 93.5%; Pred. No. 1.2e-97;

Matches 563; Conservative 0; Mismatches 38; Indels 1; Gaps 1;
Qy 6 GCAGAACTGGCGTGCAGCAACAGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGAC 65
Db 116 GCAGAACTGGCGTGCAGCAACAGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGAC 175
Qy 66 CGACGAGTACTGCGGCGACGGGTGCCAGTGGCGCCCGTGGCGTGGCGCGCGGTGGCGG 125
Db 176 CGACGCTACTGCGGCGACGGGTGCCAGTGGCGCCCGTGGCGTGGCGCGCGGTGGCGG 235
Qy 126 CGGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185
Db 236 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 295
Qy 186 CGACGCGTCTTCAACGCGCATCAAGAACACGAGGCGGCGGCGGCGGCGGCGGCGGCGG 245
Db 296 CGACGCGTCTTCAACGCGCATCAAGAACACGAGGCGGCGGCGGCGGCGGCGGCGGCGG 355
Qy 246 CTACACCGCGGAGCGGTTCTCTCGAGGCGCATCGCGCGTACCCGGGCTTCGCGCATGGCGG 305
Db 356 CTACACCGCGGAGCGGTTCTCTCGAGGCGCGTCAACCGCGTACCCGGGCTTCGCGCATGGCGG 415
Qy 306 CTCCGAGGTGAGCGCGCAAGCGCGGAGATGCGCGCTTCTTGGCGCAGCGCAGCGCAGAC 365
Db 416 GACGAGGTGAGCGCGCAAGCGCGGAGATGCGCGCTTCTTGGCGCAGCGTCAACGCGCAGAC 475
Qy 366 CGGCGATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCTTCTCGGACCGCACCA 425
Db 476 CGGCGATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCTTCTCGGACCGCACCA 535
Qy 426 GAGCGAGTGGCGCGTGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 485
Db 536 CAGCGAGTGGCGCGTGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 595
Qy 486 GTGGAATACAACTACCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 545
Db 596 GTGGAATACAACTACCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 654
Qy 546 CGGCGAGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 605
Db 655 CAACAGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 714
Qy 606 CA 607
Db 715 CA 716

RESULT 8
BM736454
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM736454
952051A06.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.
BM736454
BM736454.1 GI:19057787
EST.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 628)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952051 row: A column: 06.

```



```
186 CGACGCGTCTTCAACGGCATCAAGAACCGAGCGCGGAGCGCGGTGCGAGGCGCAAGAACTT 245
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283 CGACGCACTTCTTCAACAGCATCAAGAACCGAGCGCGGAAACGGGTGCGAGGCGCAAGAACTT 342
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246 CTACACCGGAGCGGTCTCGAGGCGCATCGCGCGTACCGCGGCTTCGGCGCATGCGG 305
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343 CTACACCGGAGCGGTCTCGAGGCGCATCGCGCGTACCGCGGCTTCGGCGCATGCGG 396
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346 |||||
306 CTCGAGGTCTGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGACGCGCCACGCGACGAC 365
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308 |||||
309 |||||
397 CAGGTCTGCGTTCAGGCGCAAGCGCGAGATCGCGCGCTTCTTCGCGCCACATCAACGCGAGAC 456
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366 CGGCGATTCTCTGCTACATCAGCGAGGTCAACAGAGGAAACGCTTACTGCGACCCGACCA 425
367 |||||
368 |||||
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457 CGGCAATTTCTGCTACATCAGCGAGATCAACAGAGAAACGCTTACTGCGACTCGAGCA 516
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459 |||||
459 |||||
426 GAGGCGAGTGGCGGTGCGCGCGCGGCGCAGAGTACTACGCGGCGCGCGCTGCGAGATCTC 485
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517 CAGGCGAGTGGCGGTGCGCGCGGCTCAGAGTACTACGCGGCGCGCGCTGCGAATCTC 576
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577 GTGGAATCTACAACTACGCGCGCGTCCGCGGAGGCAATCGGCTTCGACGCGGTTCGGAACCC 636
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546 CGGAGGCTGCGCGGCGCGGCGGTGCTGCGCTTCAAGCGCGCGCTCTGTTCTCGATGAA 605
547 |||||
548 |||||
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637 GAGCAGGCTGCGCGGCGCGGCGGTGCTGCGCTTCAAGACGCGCGCTCTGTTCTCGACCA 696
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606 CAACCTGCGACCGTGTGATGCGCGAGGCTTCGCGCGCACCATCAAGGCGCATCAACGCGCG 665
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697 CAAGTGCAACGCGGTGATGTCGAGGCGTTCGCGCGCACCATCAAGGCGCATCAACGCGCG 756
698 |||||
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666 CCTCGAGTGCAACGCGGAAACACCGCGCCGATGAAACGCGCGCTGCGCTACTACAGGCA 725
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757 CCTCGAGTGCAACGCGGAAATCTGCGCGAGTGAACGCGCGGTGCGCTACTACAGGCA 816
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726 GTACTGCGCGCGCTCGCGGT 746
727 |||||
727 |||||
817 GTACTGCGCGAGCTCGCGGT 837
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RESULT 10
CAL197556 647 bp mRNA linear EST 25-SEP-2003
LOCUS SCBFAD1067A11.g AD1 Saccharum officinarum cDNA clone SCBFAD1067A11
DEFINITION 5', mRNA sequence.
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```
ACCESSION CAL197556
VERSION CAL197556.1 GI:35227930
```

```
KEYWORDS EST.
```

```
SOURCE Saccharum officinarum
```

```
ORGANISM Saccharum officinarum
```

```
REFERENCE 1 (bases 1 to 647)
AUTHORS Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parrude@unicamp.br
```

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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 067 row: A column: 11
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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## FEATURES

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/organism="Saccharum officinarum"
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/db_xref="taxon:4547"
/clone="SCBFAD1067A11"
/lab_host="DH10B"
/clone_lib="AD1"
/notes="Organ: seedlings inoculated with Gluconacetobacter
diatrophicans; Vector: pSport1; Site_1: SalI; Site_2:
NotI; An unidirectional cDNA library generated from
[seedlings inoculated with Gluconacetobacter
diatrophicans]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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## ORIGIN

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Query Match 65.0%; Score 503; DB 6; Length 647;
Best Local Similarity 86.8%; Pred. No. 2.6e-92;
Matches 567; Conservative 0; Mismatches 80; Indels 6; Gaps 1;
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Qy 104 GCCGCTCGGCGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTG 163
Db 1 GCCAGTCGGGCGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTG 60
Qy 164 CGAACGTGGGTAAATGTGGTCAACGACCGCGTCTTCAACGCGGATCAAGAACGAGCGCGGA 223
Db 61 GGAACGTGGGTAGCGTTGTCAACGACGCAATTTCTCAACGCGCATCAAGAACGAGCGCGGA 120
Qy 224 CGCGGTGCGAGGCGCAAGCAATCTTACACCGCGAGCGGTCTTCTCGAGGCCATCGCGCGT 283
Db 121 ACGGGTGCGAGGCGCAAGCAATTTTACACCGCGAGTGGGTCTTCTGAGCGCGCGCGTCT 180
Qy 284 ACCCGGCTTCGCGCATATGGCGGTCTCGAGGTTCGAGCGCAAGCGCGAGATTGCGCGCTTCT 343
Db 181 ACAAGGCTTC-----GGTGGCGGTCTGGAGGCGCAAGCGCGAGATCGCGCGCTTCT 234
Qy 344 TCGCGCACGCGCAACGCGAGACCGGGCATTTTCTCTACATCAGCGAGGTCAACAGAGCA 403
Db 235 TCGCGCACGCTCACGCAACGAGACCGGACATTTCTCTACATCAGCGGAAATCAACAGAAC 294
Qy 404 ACGCCTACTCGACCCCGACCAAGAGGAGTGGCGGTGCGCGCGCGCGCGCGAGTACTACG 463
Db 295 ACGCCTACTCGCATCTCGAGCAACAGGAGTGGCGGTGCGCGCGCGCGCGAGTACTACG 354
Qy 464 GGCGCGCGCGCTGCAGATCTCTGTGGAATACTACAACTACGGGCGCGCGCGGAGGCGCATCG 523
Db 355 GGCGCGCGCGCTGCAGATCTCTGTGGAATACTACAACTACGGGCGCTGCGGCGAGGACATCG 414
Qy 524 GCTTCGACGCGGTCTCGGGAACCGCGGAGGTGGCGCGCGGAGCGCGGTGGTGGCGTTCAGG 583
Db 415 GCTTCAACGCGGTCTCGGGAACCGCGGAGGTGGCGCGGAGGACGCGGTGATCGCGTTCAGA 474
Qy 584 CGCGCTCTGCTGCTTGGATGAACACCGTGCACCGTGTGTGATGTCGCGCGCGGTCTTCGCGGCA 643
Db 475 CGCGCTCTGCTGCTTGGACGAAACCGTGCACCGGTGTGATGTCGAGGGGTTCGAGGCA 534
Qy 644 CCATCAGGCGCATCAACGCGCGCTTCGAGTGCACCGGAAACAAACCGCGCGCGAGATGAACG 703
Db 535 CCATCAGGCGCTATCAACGCGGCGCTTCGAGTGCACCGGAAACAAACCGCGCGCGAGATGAACG 594
Qy 704 CGCGGTGCGGTACTACAGGAGTACTGCGCGCGAGTCTCGCGCGCGCGCGCGCGCGCGG 756
Db 595 CGCGGTGCGGTACTACAGGAGTACTGTCAGAGCAGTCTGTCAGAGCTCGCGGTGACCGCGCG 647
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## RESULT 11

```
CD443492
```

```
LOCUS
```

```
DEFINITION EL01N0427B11.b Endosperm_4 Zea mays cDNA, mRNA sequence.
```

```
710 bp mRNA linear EST 03-JUN-2003
```

```
CD443492
```

```
LOCUS
```

```
DEFINITION EL01N0427B11.b Endosperm_4 Zea mays cDNA, mRNA sequence.
```

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ACCESSION CD443492
VERSION CD443492.1 GI:31359135
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 710)
Larkin, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
Characterization of the maize endosperm transcriptome and its
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinheng
Dr. Joachim Messing's lab
Wakeman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakeman.rutgers.edu
Seq primer: T3.

FEATURES             Location/Qualifiers
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         /mol_type="mRNA"
         /cultivar="W22"
         /db_xref="taxon:4577"
         /tissue_type="Endosperm of 7-23DAP"
         /clone_lib="Endosperm 4"
         /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match      64.9%; Score 502; DB 6; Length 710;
Best Local Similarity 91.2%; Pred. No. 4.2e-92;
Matches 551; Conservative 0; Mismatches 35; Indels 18; Gaps 1;

QY      6 GCAGAACTGCGGCTCCAGCCAAACGATGTCGACGAGTGTGGCTACTGCGGACGAC 65
DB      125 GCAGAACTGCGGCTCCAGCCAAACGATGTCGACGAGTGTGGCTACTGCGGACGAC 184
QY      66 CGACGAGTACTGCGGCGAGGTCGAGTCGGGCGCGTCCGCTCGGGGGGGTGGCG 125
DB      185 CGACGAGTACTGTCGCGAGCGGTGCAGTCGGGCGCGTCCGCTCGGGCGCGCGCG 244
QY      126 CGGCGCGCGCGCGGCGGCGGAGGCGAGTGGCGGTGCGAACGTGGCTTAATGTGTCAC 185
DB      245 CGGCGAGTGGTGC-----GGTGTGGAACTGGCTAGCTGCTGCTC 286
QY      186 CGACGCGTTCTTCAACGGCATCAAGAACGAGCCGCGGAGCGGGTCGAGGGCAAGAACTT 245
DB      287 CAGCTCCTTCTTCAACGGCATCAAGAACGAGCCGCGGAGCGGGTCGAGGGCAAGAACTT 346
QY      246 CTACACCGGAGCGGTCCTCGAGGCCATCGCCCGCTACCGGCGTTCGGCGCATGGCG 305
DB      347 CTACACCGGAGCGGTTCTTCTGAGCGCGCTCAAGCGCTACCGAGCTTCGCCCAATGGCG 406
QY      306 CTCGCGAGTCGAGCGCAAGCGCGAGATTGCGCGCTTCTTGGCGCAGCGCAGCAGAGAC 365
DB      407 GTCGCGAGTGCAGGGCAAGCGAGATCGCGCTTCTTGGCGCAGCGCAAGCAGAGAC 466
QY      366 CGGGCATTTCTGCTCATCATCGAGGTCAACAAGAGCAACGCTACTCGGACCGGACCAA 425
DB      467 CGGGCATTTCTGCTACATCAGCGAGATCAACAAGAGCAAGCGCTACTCGGACCGGACCAA 526
QY      426 GAGGCACTGGCGCTCGCGCGGGGCGAGAGTACTACGGGCGCGCGCTGCGATCTC 485
DB      527 GAGGCACTGGCGCTCGCGCGGGGCGAGAGTACTACGGGCGCGCGCTGCGATCTC 586
QY      486 GTGGAACTACAACTACGGGCGCGGGGAGGGCCATCGGCTTCGACAGGCTCGGGGACCC 545
DB      587 GTGGAACTACAACTACGGGCGCGGGGAGGGCCATCGGCTTCGACAGGCTCGGGGACCC 646

QY      546 CGGCAAGGTGCGCGGAGACGCCGTGGTGCGCTTCAAGCGCGCGCTCTGGTTCTGATGAA 605
DB      647 CGGCAAGGTGCGCGGAGACGCCGTGGTGCGCTTCAAGCGCGCGCTCTGGTTCTGATGAA 706
QY      606 CAAC 609
DB      707 CAGC 710

RESULT 12
CD995497
LOCUS CD995497 QBB25f07.xg QBB Zea mays cDNA clone QBB25f07, mRNA sequence.
DEFINITION QBB25f07.xg QBB Zea mays cDNA clone QBB25f07, mRNA sequence.
ACCESSION CD995497
VERSION CD995497.1 GI:32855816
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 820)
Genopiante.
Genopiante, a major partnership french program in plant genomes
Unpublished (2003)
Contact: Genopiante
Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genopiante' (http://www.genopiante.com
and http://genopiante-info.infobiogen.fr).

FEATURES             Location/Qualifiers
     source
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Best Local Similarity 93.7%; Pred. No. 6.7e-92;
Matches 522; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY      216 GGCGGAGAGCGGGTGCAGGGCAAGAACTTCTACACCGGAGCGGTTCTCGAGGCCAT 275
DB      45 GGCGGTGAGCGGGTGCAGGGCAAGAACTTCTACACCGGAGCGGTTCTCGAGCGCGT 104
QY      276 GGCGGCTTACCGGGCTTCGGCATGGCGCTCCGAGTCCGAGTCGAGCGCAAGCGGAGATGC 335
DB      105 CAAGGGGTACCGAGGCTTCGCCCTTCGCGGCTCGAGTGCAGGGCAAGCGGAGATGC 164
QY      336 CGCCTTCTTCGCGCAGCGCACGACGACCGGGCATTTCTGCTACATCAGCGAGGTCAA 395
DB      165 CGCCTTCTTCGCGCAGCGCACGACGACCGGGCATTTCTGTTACATCAGCGAGATCAA 224
QY      396 CAAGAGCAACCGCTTACTGCGACCCGACCAAGAGGAGTGGCGGTGCGCGCGGGGCGAG 455
DB      225 CAAGAGCAACCGCTTACTGCGACCCGCGAGCAAGAGGCAAGTGGCGGTGCGCGCGGGGCGAG 284
QY      456 GTACTAGGGGCGCGCGCTGCGAGATCTCGTGGAACTTACAACTACCGGGCCCGGGGAG 515
DB      285 GTACTAGGGGCGCGCGCTGCGAGATCTCGTGGAACTTACAACTACCGGGCCCGGGGAG 344
QY      516 GGCCATCGGCTTCGACGGGCTTCGGGAGCCCGCGGAGGGTGGCGGAGACGCGCTGGTGGC 575
DB      345 GGCCATCGGCTTCGACGGGCTTCGGGAGCCCGCGGAGGGTGGCGGAGACGCGCTGGTGGC 404
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QY 576 GTTCAAGCGCGCTCTGTTCTGGATGAACAACTGCAACCGTGTGATGCGCGAGGGCTT 635
Db 405 GTTCAAGCGCGCGCTCTGTTCTGGATGAACAACTGCAACCGTGTGATGCGCGAGGGTC 464
QY 636 CGGCGCCACCATCAGGCGCATCAACAGCGCGCTCTGAGTGCAACGCGGAACAACCCCGCCCA 695
Db 465 CGGCGCCACCATCAGGCGCATCAACAGCGCGCTCTGAGTGCGCGCGGAACAACAACCCCGCCCA 524
QY 696 GATGAACCGCGCTCGGCTACTACAGCAGTACTGCGCCAGCTCGGCGTTCGACCCGGG 755
Db 525 GATGAACCGCGCTCGGCTACTACAGCAGTACTGCGCCAGCTCGGCGTTCGACCCGGG 584
QY 756 CAACAACCTCACCTGCT 772
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RESULT 13
CD994454
LOCUS QBB15f08.xg QBB Zea mays 578 bp mRNA linear EST 16-JUL-2003
DEFINITION QBB15f08.xg QBB Zea mays cDNA clone QBB15f08, mRNA sequence.
ACCESSION CD994454
VERSION CD994454.1 GI:32854773
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 578)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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/clone_lib="QBB"

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Best Local Similarity 93.8%; Pred. No. 2.5e-91;
Matches 518; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 221 GGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGCTTCTCGAGGCGCATCGCG 280
Db 6 GGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGCTTCTCGAGGCGCGTCAAGG 65
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Db 306 TCGGCTTCGACGGGCTCGGGGACCCCGGCAAGGTGGCGCGGAGCCGCTGCTGCGCTCA 365
QY 581 AGGCGCGCTCTGGTTCGTGATGAACAACTGCAACCGTGTGATGCGCGAGGGCTTCGGCG 640
Db 366 AGGCGCGCTCTGGTTCGTGATGAACAACTGCAACCGTGTGATGCGCGAGGGTTCGGCG 425
QY 641 CCACCATCAGGCGCATCAACGCGCGCTTCGAGTGCAACGCGGAACAACCCCGCCAGATGA 700
Db 426 CCACCATCAGGCGCATCAACGCGCGCTTCGAGTGCGGGGGAACAACCCCGCCAGATGA 485
QY 701 ACGGCGCGCTCGGCTACTACAGGCGTACTGCGCGCAGCTCGGCGTTCGACCCGGGCAACA 760
Db 486 ACGGCGCGCTCGGCTACTACAGGCGTACTGCGCGCAGCTCGGCGTTCGACCCGGGCAACA 545
QY 761 ACCTCACCTGCT 772
Db 546 ACCTCACCTGCT 557

RESULT 14
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LOCUS QBB18d07.xg QBB Zea mays 741 bp mRNA linear EST 16-JUL-2003
DEFINITION QBB18d07.xg QBB Zea mays cDNA clone QBB18d07, mRNA sequence.
ACCESSION CD994869
VERSION CD994869.1 GI:32855188
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 741)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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ORIGIN
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Best Local Similarity 94.0%; Pred. No. 4e-91;
Matches 517; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 223 AGCGGTCGAGGCAAGAACTTCTACACCGGAGCGCTTCTCGAGGCGCATCGCGCG 282
Db 1 AGCGGTCGAGGCAAGAACTTCTACACCGGAGCGCTTCTCGAGGCGCGTCAAGCG 60
QY 283 TACCGGCTTCGCGCATGCGGCTTCGAGGTGCGAGGTGCGAGGTGCGAGGCAAGCGAGATTCGCGCTTC 342
Db 61 TACCGGCTTCGCGCATGCGGCTTCGAGGTGCGAGGTGCGAGGTGCGAGGCAAGCGAGATTCGCGCTTC 120
QY 343 TTGCGGACGCGCAGCAGAGACCGGGCATTTCTGTACATCAGGAGGTCAACAGAGC 402
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Db 181 AACGCTACTGCGACCCGAGCAAGAGGAGTGCGCGTGCGCGCGGGGCGAGAGTACTTAC 240  
Qy 463 GGGCGGGCGCGCTGAGATCTCGTGGAACTACACTACAGGCGCGCGGGGCGAGGCGATC 522  
Db 241 GGGCGGGCGCGCTGAGATCTCGTGGAACTACACTACAGGCGCGCGGGGCGAGGCGATC 300  
Qy 523 GCTTTGCGACGGGCTCGGGGACCCCGGCGAGGTGGCGCGGAGCGCGTGTGGCGTTCAAG 582  
Db 301 GCTTTGCGACGGGCTCGGGGACCCCGGCGAGGTGGCGCGGAGCGCGTGTGGCGTTCAAG 360  
Qy 583 GGGCGGCTCTGCTTCTGATGAACAACGTGCAACGTGTGATGCCGAGGGCTTCGGCGCC 642  
Db 361 GGGCGGCTCTGCTTCTGATGAACAACGTGCAACGTGTGATGCCGAGGGGTTCGGCGCC 420  
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Db 421 ACCATCAGGGCCATCAACGGCGCCTCGAGTGCAGGGGACAAACCCCGCCAGATGAAC 480  
Qy 703 GGGCGGCTCGGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGGTGCACCCGGGCAACAAC 762  
Db 481 GGGCGGCTCGGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGGTGCACCCGGGCAACAAC 540  
Qy 763 CTCACCTGCT 772  
Db 541 CTCACCTGCT 550

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DEFINITION QBB18e05.xg QBB Zea mays cDNA clone QBB18e05, mRNA sequence.  
ACCESSION CD994885  
VERSION CD994885.1 GI:32855204  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 753)  
REFERENCE  
AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).  
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Best Local Similarity 94.0%; Pred. No. 4e-91;  
Matches 517; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
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Db 1 AGCGGGTGGAGGGAAGAACTTCTACACCCGAGCGGCTTCTCGAGGCGCGTCAAGGCG 60

Qy 283 TACCGGGCTTCGCGCATGCGGGCTTCGAGGTTCGAGGCGCAAGCGGAGATTTGCGCGCTTC 342  
Db 61 TACCGAGGCTTCGCGCATGCGGGGTTCGAGGTTCGAGGCGCAAGCGGAGATTCGCGCTTC 120  
Qy 343 TTCGGCAGCGCCAGCGACGAGACCGGGCATTTCTGTACATCAGCGAGGTCAACAAGAGC 402  
Db 121 TTCGGCAGCGCCAGCGACGAGACCGGGCATTTCTGTACTTCAGCGAGATCAACAAGAGC 180  
Qy 403 AACGCTACTGCGACCCCGACCAAGAGGAGTGCGCGTGCGCGGGGCGAGAGTACTTAC 462  
Db 181 AACGCTACTGCGACCCCGAGCAAGGAGTGCGCGTGCGCGGGGCGAGAGTACTTAC 240  
Qy 463 GGGCGGCGCGCTGCGAGATCTCGTGGAACTACAACTACAGGCGCGCGGGGCGAGGCGATC 522  
Db 241 GGGCGGCGCGCTGCGAGATCTCGTGGAACTACAACTACAGGCGCGCGGGGCGAGGCGATC 300  
Qy 523 GCTTTGCGACGGGCTCGGGGACCCCGGCGAGGTGGCGCGGAGCGCGTGTGGCGTTCAAG 582  
Db 301 GCTTTGCGACGGGCTCGGGGACCCCGGCGAGGTGGCGCGGAGCGCGTGTGGCGTTCAAG 360  
Qy 583 GCGGCGCTCTGCTTCTGATGAACAACGTGCAACGTGTGATGCCGCGAGGGCTTCGGCGCC 642  
Db 361 GCGGCGCTCTGCTTCTGATGAACAACGTGCAACGTGTGATGCCGAGGGGTTCGGCGCC 420  
Qy 643 ACCATCAGGGCCATCAACGGCGCCTTCGAGTGCAGGGGACAAACCCCGCCAGATGAAC 702  
Db 421 ACCATCAGGGCCATCAACGGCGCCTTCGAGTGCAGGGGACAAACCCCGCCAGATGAAC 480  
Qy 703 GCGCGGCTCGGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGGTGCACCCGGGCAACAAC 762  
Db 481 GCGCGGCTCGGCTACTACAGGCGAGTACTGCCCGCAGCTCGGGGTGCACCCGGGCAACAAC 540  
Qy 763 CTCACCTGCT 772  
Db 541 CTCACCTGCT 550

Search completed: May 23, 2005, 15:33:07  
Job time : 2221.06 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 14:20:22 ; Search time 397.391 Seconds  
(without alignments)  
11943.947 Million cell up

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Perfect score: 774
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%  
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Listing first 45 s

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query %			DB	ID	Description
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1	774	100.0	774	19	US-10-692-367-11	Sequence 11, Appl	
2	771	99.6	771	18	US-10-389-432B-11	Sequence 11, Appl	
3	761.2	98.3	774	19	US-10-692-367-29	Sequence 29, Appl	
4	759.6	98.1	774	19	US-10-692-367-33	Sequence 33, Appl	
5	758.2	98.0	771	18	US-10-389-432B-29	Sequence 29, Appl	
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7	727.6	94.0	774	19	US-10-692-367-71	Sequence 71, Appl	
8	714.8	92.4	774	19	US-10-692-367-45	Sequence 45, Appl	
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10	711.6	91.9	774	19	US-10-692-367-23	Sequence 23, Appl	
11	710	91.7	771	19	US-10-692-367-59	Sequence 59, Appl	

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28	686.8	88.7	765	19	US-10-692-367-67
29	686	88.6	771	19	US-10-692-367-83
30	682.8	88.2	774	19	US-10-692-367-7
31	680.4	87.9	753	19	US-10-692-367-43
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## ALIGNMENTS

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RESULT 1
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; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffle
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-11

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Best Local Similarity 100.0%; Pred. No. 1.1e-184;  
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QY 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTGCAGTGGGCCCGTGCCTCGCGGCGCGGT 120  
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DB 541 GACCCCGCAGGCG 600

QY 601 ATGAACAACGTCACCGTGTGATGCCGCGAGGCGCTTCGCGCGCGCGCGCGCGCGCGCGCG 660  
DB 601 ATGAACAACGTCACCGTGTGATGCCGCGAGGCGCTTCGCGCGCGCGCGCGCGCGCGCGCG 660

QY 661 GCGCGCTTCGAGTGCACCGGAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
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QY 721 AGGCAGTACTGCG 774  
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## RESULT 2

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; Sequence 11, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 489492000300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029

PRIOR FILING DATE: 2001-11-07  
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; SEQ ID NO 11  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; OTHER INFORMATION: r2c2 nucleic acid  
US-10-389-432B-11

Query Match 99.6%; Score 771; DB 18; Length 771;  
Best Local Similarity 100.0%; Pred. No. 6.2e-184;  
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGATGCAGAACTGCGGTGCGAGCAAACTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
DB 1 TCGATGCAGAACTGCGGTGCGAGCAAACTATGCTGCAGCAAGTTTGGCTACTGCGGC 60

QY 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTGCAGTGGGCCCGTGCCTCGCGGCGCGGT 120  
DB 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTGCAGTGGGCCCGTGCCTCGCGGCGCGGT 120

QY 121 GCG 180  
DB 121 GCG 180

QY 181 GTCAACCGACGCGTCTTCAACCGGATCAAGAACAGCGCGCGGAGCGGTGCGAGGCGCAAG 240  
DB 181 GTCAACCGACGCGTCTTCAACCGGATCAAGAACAGCGCGCGGAGCGGTGCGAGGCGCAAG 240

QY 241 AACTTCTACACCGGAGCGGTTCCTCGAGGCGCGTTCCTCGAGGCGCATCGCGCGTTCGCGCAT 300  
DB 241 AACTTCTACACCGGAGCGGTTCCTCGAGGCGCGTTCCTCGAGGCGCATCGCGCGTTCGCGCAT 300

QY 301 GCGCGCTCCGAGGTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 360  
DB 301 GCGCGCTCCGAGGTGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 360

QY 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCGG 420  
DB 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCGCTACTGCGACCGG 420

QY 421 ACCAAGAGCGAGTGCCTGCG 480  
DB 421 ACCAAGAGCGAGTGCCTGCG 480

QY 481 ATCTCGTGGAATCAACTACG 540  
DB 481 ATCTCGTGGAATCAACTACG 540

QY 541 GACCCCGCAGGCG 600  
DB 541 GACCCCGCAGGCG 600

QY 601 ATGAACAACGTCACCGTGTGATGCCGCGAGGCGCTTCGCGCGCGCGCGCGCGCGCGCGCG 660  
DB 601 ATGAACAACGTCACCGTGTGATGCCGCGAGGCGCTTCGCGCGCGCGCGCGCGCGCGCGCG 660

QY 661 GCGCGCTTCGAGTGCACCGGAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
DB 661 GCGCGCTTCGAGTGCACCGGAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720

QY 721 AGGCAGTACTGCG 771  
DB 721 AGGCAGTACTGCG 771

## RESULT 3

US-10-692-367-29  
; Sequence 29, Application US/10692367  
; Publication No. US20050050595A1

```

; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-29

Query Match 98.3%; Score 761.2; DB 19; Length 774;
Best Local Similarity 99.0%; Pred. No. 1.8e-181;
Matches 766; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TCGATGCAGAACTGGCGTCCAGCAACCTATGCTGCAGCAAGTTTGGCTACTCGGC 60
Db 1 TCGATGCAGAACTGGCGTCCAGCAACCTATGCTGCAGCAAGTTTGGCTACTCGGC 60

Qy 61 ACACCCAGCAGTACTCGCGGACGAGTGCAGTCCGCGCCGCTCGCGTCCGCGCGGT 120
Db 61 ACACCCAGCAGTACTCGCGGACGAGTGCAGTCCGCGCCGCTCGCGTCCGCGCGGT 120

Qy 121 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 121 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Qy 181 GTACCCGACGCGTCTTCAACGGCATCAAGAACCGAGCGCGCGCGCGCGCGCGCG 240
Db 181 GTACCCGACGCGTCTTCAACGGCATCAAGAACCGAGCGCGCGCGCGCGCGCGCG 240

Qy 241 AACTTCTACACCCCGAGCGCGTTCCTCGAGGCCATCCCGCGGCTTCGCGCAT 300
Db 241 AACTTCTACACCCCGAGCGCGTTCCTCGAGGCCATCCCGCGGCTTCGCGCAT 300

; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-33

Query Match 98.1%; Score 759.6; DB 19; Length 774;
Best Local Similarity 98.8%; Pred. No. 4.5e-181;
Matches 765; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TCGATGCAGAACTGGCGTCCAGCAACCTATGCTGCAGCAAGTTTGGCTACTCGGC 60
Db 1 TCGATGCAGAACTGGCGTCCAGCAACCTATGCTGCAGCAAGTTTGGCTACTCGGC 60

Qy 61 ACACCCAGCAGTACTCGCGGACGAGTGCAGTCCGCGCCGCTCGCGTCCGCGCGGT 120
Db 61 ACACCCAGCAGTACTCGCGGACGAGTGCAGTCCGCGCCGCTCGCGTCCGCGCGGT 120

Qy 121 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 121 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Qy 181 GTACCCGACGCGTCTTCAACGGCATCAAGAACCGAGCGCGCGCGCGCGCGCGCG 240
Db 181 GTACCCGACGCGTCTTCAACGGCATCAAGAACCGAGCGCGCGCGCGCGCGCGCG 240

Qy 241 AACTTCTACACCCCGAGCGCGTTCCTCGAGGCCATCCCGCGGCTTCGCGCAT 300
Db 241 AACTTCTACACCCCGAGCGCGTTCCTCGAGGCCATCCCGCGGCTTCGCGCAT 300

; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-37

Query Match 98.0%; Score 758.0; DB 19; Length 774;
Best Local Similarity 98.5%; Pred. No. 1.2e-181;
Matches 764; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TCGATGCAGAACTGGCGTCCAGCAACCTATGCTGCAGCAAGTTTGGCTACTCGGC 60
Db 1 TCGATGCAGAACTGGCGTCCAGCAACCTATGCTGCAGCAAGTTTGGCTACTCGGC 60

Qy 61 ACACCCAGCAGTACTCGCGGACGAGTGCAGTCCGCGCCGCTCGCGTCCGCGCGGT 120
Db 61 ACACCCAGCAGTACTCGCGGACGAGTGCAGTCCGCGCCGCTCGCGTCCGCGCGGT 120

Qy 121 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 121 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Qy 181 GTACCCGACGCGTCTTCAACGGCATCAAGAACCGAGCGCGCGCGCGCGCGCGCG 240
Db 181 GTACCCGACGCGTCTTCAACGGCATCAAGAACCGAGCGCGCGCGCGCGCGCGCG 240

Qy 241 AACTTCTACACCCCGAGCGCGTTCCTCGAGGCCATCCCGCGGCTTCGCGCAT 300
Db 241 AACTTCTACACCCCGAGCGCGTTCCTCGAGGCCATCCCGCGGCTTCGCGCAT 300
```

```
QY 301 GCGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGCAGCGCAC 360
DB 301 GCGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGCAGCGCAC 360
QY 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCTACTGCGACCG 420
DB 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCTACTGCGACCG 420
QY 421 ACCAAGAGCGAGTGGCGGTGCGCGCGCGGCGAGAGTACTACGCGCGCGCGCGCTGCGAG 480
DB 421 ACCAAGAGCGAGTGGCGGTGCGCGCGCGGCGAGAGTACTACGCGCGCGCGCGCTGCGAG 480
QY 481 ATCTGCTGGAACATAACAATGAGCGCGCGCGGCGAGGCGCATCGGCTTCGACGGGCTCGGG 540
DB 481 ATCTGCTGGAACATAACAATGAGCGCGCGCGGCGAGGCGCATCGGCTTCGACGGGCTCGGG 540
QY 541 GACCCCGCAGGTGGCGCGGAGCGCGGTGCGGCTTCAAGGCGGCGCTCTGGTTCTGG 600
DB 541 GACCCCGCAGGTGGCGCGGAGCGCGGTGCGGCTTCAAGGCGGCGCTCTGGTTCTGG 600
QY 601 ATGAACAAAGTGCACCGGTGATGCGCGAGGCTTTCGCGCGCACCATCAGGGGCCATCAAC 660
DB 601 ATGAACAAAGTGCACCGGTGATGCGCGAGGCTTTCGCGCGCACCATCAGGGGCCATCAAC 660
QY 661 GCGCGCTCGAGTGCACCGGAAACACCCCGCGCGAGTGAACGCGCGGCTCGGCTACTAC 720
DB 661 GCGCGCTCGAGTGCACCGGAAACACCCCGCGCGAGTGAACGCGCGGCTCGGCTACTAC 720
QY 721 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGCGGCAACACCTCAGCTGCTGA 774
DB 721 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGCGGCAACACCTCAGCTGCTGA 774
```

## RESULT 5

```
US-10-389-432B-29
; Sequence 29, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 48949200300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-389-432B-29
```

Query Match 98.0%; Score 758.2; DB 18; Length 771;  
Best Local Similarity 99.0%; Pred. No. 1e-180; Indels 0; Gaps 0;  
Matches 763; Conservative 0; Mismatches 8;

```
QY 1 TCAGTCGAGAACTGGCGGTGCGCGCAACAAAGTATGTCGAGCAAGTTGGCTACTGCGGC 60
DB 1 TCAGTCGAGAACTGGCGGTGCGCGCAACAAAGTATGTCGAGCAAGTTGGCTACTGCGGC 60
QY 61 ACGACGCGAGTACTGCGCGCAACGCGGTGCGAGTGGGCGCGCTGCGGCTCGGCGCGGT 120
DB 61 ACGACGCGAGTACTGCGCGCAACGCGGTGCGAGTGGGCGCGCTGCGGCTCGGCGCGGT 120
```

```
QY 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GTCAACCGACCGTCTTTCAAACGCGCATCAAGAAACAGCGCGCGCGCGCGCGCGCGCG 240
DB 181 GTCAACCGACCGTCTTTCAAACGCGCATCAAGAAACAGCGCGCGCGCGCGCGCGCGCG 240
QY 241 AACTTCTACACCGCGAGCGGTCTCTGAGGCGCATCGCGCGGTACCGCGGCTTCGCGCAT 300
DB 241 AACTTCTACACCGCGAGCGGTCTCTGAGGCGCATCGCGCGGTACCGCGGCTTCGCGCAT 300
QY 301 GCGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGCGCGCGCGCAC 360
DB 301 GCGCGCTCCGAGGTCGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGCGCGCGCGCAC 360
QY 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCTACTGCGACCG 420
DB 361 GAGACCGGGCATTTCTGCTACATCAGCGAGGTCAACAGAGCAACGCTACTGCGACCG 420
QY 421 ACCAAGAGCGAGTGGCGGTGCGCGCGGCGAGAGTACTACGCGCGCGCGCGCTGCGAG 480
DB 421 ACCAAGAGCGAGTGGCGGTGCGCGCGGCGAGAGTACTACGCGCGCGCGCGCTGCGAG 480
QY 481 ATCTGCTGGAACATAACAATGAGCGCGCGCGGCGAGGCGCATCGGCTTCGACGGGCTCGGG 540
DB 481 ATCTGCTGGAACATAACAATGAGCGCGCGCGGCGAGGCGCATCGGCTTCGACGGGCTCGGG 540
QY 541 GACCCCGCAGGTGGCGCGGAGCGCGGTGCGGCTTCAAGGCGGCGCTCTGGTTCTGG 600
DB 541 GACCCCGCAGGTGGCGCGGAGCGCGGTGCGGCTTCAAGGCGGCGCTCTGGTTCTGG 600
QY 601 ATGAACAAAGTGCACCGGTGATGCGCGAGGCTTTCGCGCGCACCATCAGGGGCCATCAAC 660
DB 601 ATGAACAAAGTGCACCGGTGATGCGCGAGGCTTTCGCGCGCACCATCAGGGGCCATCAAC 660
QY 661 GCGCGCTCGAGTGCACCGGAAACACCCCGCGCGAGTGAACGCGCGGCTCGGCTACTAC 720
DB 661 GCGCGCTCGAGTGCACCGGAAACACCCCGCGCGAGTGAACGCGCGGCTCGGCTACTAC 720
QY 721 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGCGGCAACACCTCAGCTGCTGC 771
DB 721 AGGCAGTACTGCGCGCAGCTCGGCGTGCACCGCGGCAACACCTCAGCTGCTGC 771
```

## RESULT 6

```
US-10-389-432B-33
; Sequence 33, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 48949200300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-389-432B-33
```

Query Match 97.8%; Score 756.6; DB 18; Length 771;



```
RESULT 8
US-10-692-367-45
; Sequence 45, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-45

Query Match          92.4%; Score 714.8; DB 19; Length 774;
Best Local Similarity 95.2%; Pred. No. 7.9e-137;
Matches 737; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 TCGATGACGAACTGCGGCTGCCAGCCAAACGATATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Db 1 TCGATGACGAACTGCGGCTGCCAGCCAAACGATATGCTGCAGCGGTTCGGCTACTGCGGC 60
Qy 61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTGCCTCGGGCGGCGGT 120
Db 61 ACGACCGACGAGTACTGCGGCGACGGGTGCCGGTCCGGCCCGTGCCTCGGGCGGCGGT 120
Qy 121 GCGGCGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGG 180
Db 121 GCGGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGG 180
Qy 181 GTCACCGACGCGGTTCTTCAACGGCATCAAGAACCAAGCGGCGGAGCGGCGGCGGCGG 240
Db 181 GTCACCGACGCGGTTCTTCAACGGCATCAAGAACCAAGCGGCGGAGCGGCGGCGGCGG 240
Qy 241 AACTTCTACACCGGAGCGGTTCTCTCGAGCGCATTCGCGCGGTACCCCGGGCTTCGCGCAT 300
Db 241 AACTTCTACACCGGAGCGGTTCTCTCGAGCGCATTCGCGCGGTACCCCGGGCTTCGCGCAT 300
Qy 301 GCGGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGG 360
Db 301 GCGGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGG 360
Qy 361 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCGCTACTGCGACCG 420
Db 361 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCGCTACTGCGACCG 420
Qy 421 ACCAAGAGGAGTGGCGGCGGCGGCGGAGGAGTACTAGGCGGCGGCGGCGGCGGCGGCGG 480
Db 421 ACCAAGAGGAGTGGCGGCGGCGGCGGAGGAGTACTAGGCGGCGGCGGCGGCGGCGGCGG 480
```

```
Qy 481 ATCTCGTGGAACTACAACTAGCGGCCCGCGGGAGGGCCATCGGCTTTCGACGGGCTCGGG 540
Db 481 ATCTCGTGGAACTACAACTAGCGGCCCGCGGGAGGGCCATCGGCTTTCGACGGGCTCGGG 540
Qy 541 GACCCCGGCGAGGGTGGCGCGGAGCGCGTGGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGG 600
Db 541 GACCCCAACAGAGGTGGCGCGGAGCGCGTGGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGG 600
Qy 601 ATGAACAACGTGACCGCTGTGATGCGCGACGGCTTCGGCGCCACCATCAGGCCCATCAAC 660
Db 601 ATGAACAACGTGACCGCGGTGGTTCGGCGAGGGTTTCGGCGCCACCATCAGGCCCATCAAC 660
Qy 661 GCGCCCTCTCGAGTGCACACGGGAACAACCCCGCCCGCAGATGAACGCGCGCGTCCGCTACTAC 720
Db 661 GCGCCCTCTCGAGTGCACACGGGAACAACCCCGCCCGCAGATGAACGCGCGCGTCCGCTACTAC 720
Qy 721 AGGCAGTACTGCCGCCAGCTCGCGGTGCGACCCCGGGCAACCAACCTCACCCTGCTGA 774
Db 721 AAGCAGTACTGCCGCCAGCTCGCGGTGCGACCCCGGGCCCAACCTCACCCTGCTGA 774

RESULT 9
US-10-389-432B-45
; Sequence 45, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 489492000300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: 4N1/80_F8 nucleic acid
US-10-389-432B-45

Query Match          92.0%; Score 711.8; DB 18; Length 771;
Best Local Similarity 95.2%; Pred. No. 4.5e-169;
Matches 734; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 TCGATGACGAACTGCGGCTGCCAGCCAAACGATATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Db 1 TCGATGACGAACTGCGGCTGCCAGCCAAACGATATGCTGCAGCCGGTTTCGGCTACTGCGGC 60
Qy 61 ACGACCGACGAGTACTGCGGCGACGGGTGCAGTCCGGCCCGTGCCTCGGGCGGCGGT 120
Db 61 ACGACCGACGAGTACTGCGGCGACGGGTGCAGTCCGGCCCGTGCCTCGGGCGGCGGT 120
Qy 121 GCGGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGTGGCGGTGCGAACGTGGCTAATGTG 180
Db 121 GCGGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGTGGCGGTGCGAACGTGGCTAATGTG 180
Qy 181 GTCACCGACGCGGTTCTTCAACGGCATCAAGAACCAAGCGGCGGAGCGGCGGCGGCGGCAAG 240
Db 181 GTCACCGACGCGGTTCTTCAACGGCATCAAGAACCAAGCGGCGGAGCGGCGGCGGCGGCAAG 240
Qy 241 AACTTCTACACCGGAGCGGTTCTCTCGAGCGCATTCGCGCGGTACCCCGGGCTTCGCGCAT 300
Db 241 AACTTCTACACCGGAGCGGTTCTCTCGAGCGCATTCGCGCGGTACCCCGGGCTTCGCGCAT 300
Qy 301 GCGGCGCTCCGAGGTGAGCGCAAGCGGAGATTGCGGCTTCTTCGCGCGACGCCACGCCAC 360
```



```
Db 301 GCGGGTTCAGGTGAGGCAAGCGGAGATCGCGCTTCTTCGCGCAAGCCACGCGAC 360
Qy 361 GAGACCGGGCATTTCTGTACATCAGCGAGGTCAACAGAGCAACGCCCTACTTGCAGCCG 420
Db 361 GAGACCGGGCATTTCTGTACATCAGCGAGATCAACAGAGCAACGCCCTACTTGCAGCCG 420
Qy 421 ACCAAGAGCAGTGCCTGTCGCGCGGGGCGAGAGTACTAGCGGGCGGCGCGCTGCGAG 480
Db 421 ACCAAGAGCAGTGCCTGTCGCGCGGGGCGAGAGTACTAGCGGGCGGCGCGCTGCGAG 480
Qy 481 ATCTCGTGGAACTACAATACCGGCGCGGAGGCGCATCGGCTTCGAGCGGCTCGGG 540
Db 481 ATCTCGTGGAACTACAATACCGGCGCGGAGGCGCATCGGCTTCGAGCGGCTCGGG 540
Qy 541 GACCCCGCAGGTCGCGCGGACCGCGGTCGAGTGGGTTCAAGCGCGCGCTCTGGTTCTGG 600
Db 541 GACCCCAACAGGTCGCGCGGAGCGCGCTGTTCAAGCGCGCGCTCTGGTTCTGG 600
Qy 601 ATGAACAGTCGACCGTGTGATGTCGCGAGGCTTTCGCGGCGCACCATCAGGGCCATCAAC 660
Db 601 ATGAACAGTCGACCGGTCGTCGCGAGGTCGTCGCGGCTTTCGCGGCGCACCATCAAC 660
Qy 661 GCGCGCTCGAGTGAACAGGAAACCGCGCGAGTGAACGCGCGCGCTCGGCTACTAC 720
Db 661 GCGCGCTCGAGTGAACAGGAAACCGCGCGAGTGAACGCGCGCGCTCGGCTACTAC 720
Qy 721 AGGCAGTACTGCGCGCAGCTCGCGTCGACCCGCGGCAACACCTCACCTGC 771
Db 721 AAGCAGTACTGCGCGCAGCTCGCGTCGACCCGCGGCAACACCTCACCTGC 771
```

## RESULT 10

```
US-10-692-367-23
; Sequence 23, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-23
```

```
Query Match 91.9%; Score 711.6; DB 19; Length 774;
Best Local Similarity 95.0%; Pred. No. 5e-169;
Matches 735; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
Qy 1 TCGATGCAAGAACTCGCGCTGCCAGCAACCTATGCTGACGAAAGTTTGGCTACTTGGCGGC 60
```

```
Db 1 TCGATGCAAGAACTCGCGCTGCCAGCAACCTATGCTGACGAAAGTTTGGCTACTTGGCGGC 60
Qy 61 ACACCCGACAGTACTTGCAGCGAGGTCGAGTGCAGGTCGCGGCGCGCTCTCGCGCGCGGT 120
Db 61 ACACCCGACAGTACTTGCAGCGAGGTCGAGTGCAGGTCGCGGCGCGCTCTCGCGCGCGGC 120
Qy 121 GCGCGCGCGCGCGCGGAGGCGCGGAGGAGTGCAGGTCGCGGTCGAAAGTGGCTTAATGTG 180
Db 121 GCGAGCAGTGCAGCGCGCGGAGGCGCGGAGGAGTGCAGTGCAGTGCAGTGCAGTGCAGT 180
Qy 181 GTCAACCGACGCTTCTTCAACCGCATCAAGAAACAGAGCGCGGAGGTCGAGGCGCAAG 240
Db 181 GTCAACCGACGCTTCTTCAACCGCATCAAGAAACAGAGCGCGGAGGTCGAGGCGCAAG 240
Qy 241 AACTTCTACACCCGAGCGCGTTCTCTGAGGCGCATTCGCGCGCTACCCAGGCTTCGCCCAT 300
Db 241 AACTTCTACACCCGAGCGCGTTCTCTGAGCGCGCTTCTGAGCGCGCTACCCAGGCTTCGCCCAT 300
Qy 301 GCGCGCTCCGAGTTCGAGCGCAAGCGGAGATTCGCGCGCTTCTTTCGCGCAAGCGCGCAC 360
Db 301 GCGCGCTCCGAGTTCGAGCGCAAGCGGAGATTCGCGCGCTTCTTTCGCGCATGTCAAGCAC 360
Qy 361 GAGACCGGGCATTTCTGTACATCAGCGAGGTCAACAGAGCAACGCCCTACTTGCAGACCG 420
Db 361 GAGACCGGGCATTTCTGTGTACTCAACAGAGTCAACAGAGCAACGCCCTACTTGCAGACCG 420
Qy 421 ACCAAGAGGTCGCGCGCTGCGCGCGGCGAGAGTACTACGCGCGCGCGCTCGGCTCGAG 480
Db 421 ACCAAGAGGTCGCGCGCTGCGCGCGGCGAGAGTACTACGCGCGCGCGCTCGGCTCGAG 480
Qy 481 ATCTCGTGGAACTACAACCTACGCGCGCGCGGAGGCGCATCGGCTTTCGAGCGGCTCGGG 540
Db 481 ATCTCGTGGAACTACAACCTACGCGCGCGCGGAGGCGCATCGGCTTTCGAGCGGCTCGGA 540
Qy 541 GACCCCGCAGGTCGCGCGGAGCGCGTGTGTCGCTTCAAGCGCGCGCTCTGTGTTCTGG 600
Db 541 GACCCCGACAGACTGCGCGGAGCAACCGCTGTGTCGTTGTCGTTCAAGTGGCGCTCTGTGTTCTGG 600
Qy 601 ATGAACAAACGTCACCGTGTGATGCCGAGCGGCTTTCGCGCGCACCATCAGGGCCATCAAC 660
Db 601 ATGAACAAACGTCACCGTGTGATGCCGAGCGGCTTTCGCGCGCACCATCAGGGCCATCAAC 660
Qy 661 GCGCGCTCGAGTGAACAGGAAACCGCGCGGAGGCGCATCGGCTTTCGAGCGGCTACTAC 720
Db 661 GCGCGCTCGAGTGAACAGGAAACCGCGCGGAGGCGCATCGGCTTTCGAGCGGCTACTAC 720
Qy 721 AGGCAGTACTGCGCGCAGCTCGCGTCGAGCGCGGCAACCGCGGCAACACCTCACCTGCTGA 774
Db 721 AGGCAGTACTGCGCGCAGCTCGCGTCGAGCGCGGCAACCGCGGCAACACCTCACCTGCTGA 774
```

## RESULT 11

```
US-10-692-367-59
; Sequence 59, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
```

```
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(771)
US-10-692-367-59

Query Match      91.7%; Score 710; DB 19; Length 771;
Best Local Similarity 95.7%; Pred. No. 1.3e-168;
Matches 741; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy      1 TCGATGCAGAACTGCGGCTGCCAGCAAACTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Db      1 TCGATGCAGAACTGCGGCTGCCAGCAAACTTCTGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy      61 ACGACCGACAGTACTGCGGCGACGGGTGCCAGTGGGCCCGTCCGCTCGGGCGGCGGT 120
Db      61 ACGACCGACAGTACTGCGGCGACGGGTGCCAGTGGGCCCGTCCGCTCGGGCGGCGGT 120

Qy      121 GCGCGCGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGG 180
Db      121 GCGCGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGG 177

Qy      181 GTACCCGACGCGTTCTTCAACGGCATCAAGAAACAGAGCGGCGGAGCGGCGGCGGCAAG 240
Db      178 GTACCCGACGCGTTCTTCAACGGCATCAAGAAACAGAGCGGCGGAGCGGCGGCGGCAAG 237

Qy      241 AACTTCTACACCCGAGCGGTTCTCGAGGCGATGCGCGGCTACCCGGGCTTCGCGCAT 300
Db      238 AACTTCTACACCCGAGCGGTTCTCGAGGCGGTTCAAGGCGGTACCCAGGCTTCGCCCAT 297

Qy      301 GCGCGCTCGAGGTCAGGCGGAGCGGCGGAGTGGCGGCTTCTTCGCGCAGCGCAC 360
Db      298 GCGCGGTCACAGGTCAGGCGGAGCGGCGGAGTGGCGGCTTCTTCGCGCAGTGCACGCA 357

Qy      361 GAGACCGGCGCATTTCTGCTACATCAGCGAGTCAACAGAGCAACGCTTCTGCGACCGG 420
Db      358 GAGACCGGCGCATTTCTGCTACATCAGCGAGTCAACAGAGCAACGCTTCTGCGACCGG 417

Qy      421 ACCAAGAGCGAGTGGCCGTCGCGCGCGGCGGAGAGTACTACGGGCGGCGGCGGCTGCAG 480
Db      418 ACCAAGAGCGAGTGGCCGTCGCGCGCGGCGGAGAGTACTACGGGCGGCGGCGGCTGCAG 477

Qy      481 ATCTCGTGGAACTACAACCTACGGGCGCGGAGGCGGCGGCGGCGGCGGCGGCGG 540
Db      478 ATCTCGTGGAACTACAACCTACGGGCGCGGAGGCGGCGGCGGCGGCGGCGGCGG 537

Qy      541 GACCCCGCGAGGTCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
Db      538 GACCCCGCGAGGTCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 597

Qy      601 ATGAACAACAGTGCACCGTGTGATGCCGAGGCTTCGGGCGGCGGCGGCGGCGGCGGCGG 660
Db      598 ATGAACAACAGTGCACCGTGTGATGCCGAGGCTTCGGGCGGCGGCGGCGGCGGCGGCGG 657

Qy      661 GCGCGCTCGAGTGAACAGGGAACAAACCGCGGAGATGAACGCGGCGGCGGCGGCGGCGG 720
Db      658 GCGCGCTCGAGTGAACAGGGAACAAACCGCGGAGATGAACGCGGCGGCGGCGGCGGCGG 717

Qy      721 AGGCGAGTACTGCGGCGAGTGGCGGTGCAACCGGCGGCAACACCTTCACTGCTGA 774
Db      718 AGGCGAGTACTGCGGCGAGTGGCGGTGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGG 771
```

RESULT 12

US-10-692-367-37

; Sequence 37, Application US/10692367

```
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-37
```

```
Query Match      91.7%; Score 710; DB 19; Length 774;
Best Local Similarity 94.8%; Pred. No. 1.3e-168;
Matches 734; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy      1 TCGATGCAGAACTGCGGCTGCCAGCAAACTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Db      1 TCGATGCAGAACTGCGGCTGCCAGCAAACTATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy      61 ACGACCGACAGTACTGCGGCGACGGGTGCCAGTGGGCCCGTCCGCTCGGGCGGCGGT 120
Db      61 ACGACCGACAGTACTGCGGCGACGGGTGCCAGTGGGCCCGTCCGCTCGGGCGGCGGC 120

Qy      121 GCGCGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGG 180
Db      121 GCGCGCGCGCGCGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGG 180

Qy      181 GTACCCGACGCGTTCTTCAACGGCATCAAGAAACAGAGCGGCGGCGGCGGCGGCGGCAAG 240
Db      181 GTACCCGACGCGTTCTTCAACGGCATCAAGAAACAGAGCGGCGGCGGCGGCGGCGGCAAG 240

Qy      241 AACTTCTACACCCGAGCGGTTCTCGAGGCGCATTCGCGCGGCTACCCGGGCTTCGCGCAT 300
Db      241 AACTTCTACACCCGAGCGGTTCTCGAGGCGCGTCAAGGCGGTACCCAGGCTTCGCCCAT 300

Qy      301 GCGCGCTCGAGGTCAGGCGGAGCGGCGGAGATTCGCGCTTCTTCGCGCAGCGCACGCGAC 360
Db      301 GCGCGCTCGAGGTCAGGCGGAGCGGCGGAGATTCGCGCTTCTTCGCGCAGCGCACGCGAC 360

Qy      361 GAGACCGGCGCATTTCTGCTACATCAGCGAGTCAACAGAGCAACGCTTCTGCGACCGG 420
Db      361 GAGACCGGCGCATTTCTGCTACATCAGCGAGTCAACAGAGCAACGCTTCTGCGACCGG 420

Qy      421 ACCAAGAGCGAGTGGCGGCGGCGGCGGAGAGTACTACGGGCGGCGGCGGCGGCGGCGG 480
Db      421 ACCAAGAGCGAGTGGCGGCGGCGGCGGAGAGTACTACGGGCGGCGGCGGCGGCGGCGG 480

Qy      481 ATCTCGTGGAACTACAACCTACGGGCGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGG 540
Db      481 ATCTCGTGGAACTACAACCTACGGGCGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGG 540

Qy      541 GACCCCGCGAGGTCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
```

Db 541 GACCCAAACAGGTCGCGCAGAGACCCGTCGTGGTTCGAGGCGGCGCTCTGGTTCG 600  
Qy 601 ATGAACAAACGTCGACCGTCGTGATGCCGAGAGGCTTCGGCGGCACCATCAGGGCCATCAAC 660  
Db 601 ATGAACAAACGTCGACCGTCGTGATGCCGAGAGGCTTCGGCGGCACCATCAGGGCCATCAAC 660  
Qy 661 GCGGCCCTCGAGTGCAGCGGAAACAAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720  
Db 661 GCGGCCCTCGAGTGCAGCGGAAACAAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720  
Qy 721 AGGCAGTACTGCGCGCAGCTCGGCTCGACCGGGAACCAACCTCACCTGCTGA 774  
Db 721 AGGCAGTACTGCGCGCAGCTCGGCTCGACCGGGAACCAACCTCACCTGCTGA 774

## RESULT 13

US-10-389-432B-23  
; Sequence 23, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 48949200300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ. ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 771  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-389-432B-23

Query Match 91.6%; Score 708.6; DB 18; Length 771;  
Best Local Similarity 94.9%; Pred. No. 2.8e-168;  
Matches 732; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
Qy 1 TCGATGCAGAACTCGCGCTGCCAGCAACGATATCTGCAGCAAGTTGGCTACTGCGGC 60  
Db 1 TCGATGCAGAACTCGCGCTGCCAGCAACGATATCTGCAGCAAGTTGGCTACTGCGGC 60  
Qy 61 ACGACCGACGAGTACTGCGCGGACGCGGTGCCAGTCCGCGCGCTCGCGCGCGCGT 120  
Db 61 ACGACCGACGAGTACTGCGCGGACGCGGTGCCAGTCCGCGCGCTCGCGCGCGCGT 120  
Qy 121 GCG 180  
Db 121 GCG 180  
Qy 181 GTCACCGACGCGTCTTCAACGGCATCAAGACAGCGCGCGCGCGCGCGCGCGCGCG 240  
Db 181 GTCACCGACGCGTCTTCAACGGCATCAAGACAGCGCGCGCGCGCGCGCGCGCGCG 240  
Qy 241 AACTTCTACACCGCGCGCGTTCCTCGAGGCGCATCGCGCGTACCGCGGCTTCGCGCAT 300  
Db 241 AACTTCTACACCGCGCGCGTTCCTCGAGGCGCGTTCGAGCGCGTACCGCGGCTTCGCGCAT 300  
Qy 301 GCGCGCTCGAGGTTCGAGCGCAAGCGCGAGATTCGCGCTTCTTCGCGCAACCGCGCAC 360  
Db 301 GCGCGCTCGAGGTTCGAGCGCAAGCGCGAGATTCGCGCTTCTTCGCGCATGTCACGCGC 360  
Qy 361 GAGACCGCGCATTTCTGCTACTACGAGGTTCAACAGCGCGCGCGCGCGCGCGCGCG 420

Db 361 GAGACCGCGCATTTGCTGTACTCATCAACGAGTCAACAGAGCAACGCTTACTGCGACCCG 420  
Qy 421 ACCAAGAGGAGTCAGTCGCGCGCGCGCGCGAGAGTACTACGCGCGCGCGCGCGCTGCGAG 480  
Db 421 ACCAAGAGGAGTCAGTCGCGCGCGCGCGCGAGAGTACTACGCGCGCGCGCGCGCTGCGAG 480  
Qy 481 ATCTGTGGAACACTACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Db 481 ATCTGTGGAACACTACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Qy 541 GACCCCGCAGGTCG 600  
Db 541 GACCCCGCAGGTCG 600  
Qy 601 ATGAACAAACGTCACCGTCGTGATGCCGAGAGGCTTCGCGCGCACCATCAGGGCCATCAAC 660  
Db 601 ATGAACAAACGTCACCGTCGTGATGCCGAGAGGCTTCGCGCGCACCATCAGGGCCATCAAC 660  
Qy 661 GCGGCCCTCGAGTGCAGCGGAAACAAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720  
Db 661 GCGGCCCTCGAGTGCAGCGGAAACAAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720  
Qy 721 AGGCAGTACTGCGCGCAGCTCGGCTCGACCGGGAACCAACCTCACCTGCTGC 771  
Db 721 AGGCAGTACTGCGCGCAGCTCGGCTCGACCGGGAACCAACCTCACCTGCTGC 771

## RESULT 14

US-10-389-432B-59  
; Sequence 59, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 48949200300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 768  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-389-432B-59

Query Match 91.3%; Score 707; DB 18; Length 768;  
Best Local Similarity 95.7%; Pred. No. 7.1e-168;  
Matches 738; Conservative 0; Mismatches 30; Indels 3; Gaps 1;  
Qy 1 TCGATGCAGAACTCGCGCTGCCAGCAACGATATCTGCAGCAAGTTGGCTACTGCGGC 60  
Db 1 TCGATGCAGAACTCGCGCTGCCAGCAACGATATCTGCAGCAAGTTGGCTACTGCGGC 60  
Qy 61 ACGACCGACGAGTACTGCGCGGACGCGGTGCCAGTCCGCGCGCTCGCGCGCGCGT 120  
Db 61 ACGACCGACGAGTACTGCGCGGACGCGGTGCCAGTCCGCGCGCTCGCGCGCGCGT 120  
Qy 121 GCG 180  
Db 121 GCGCGCGCGT---GCGCGCGAGGCGCGAGGCGAGTGGCGGTGCGAAGCTGGCTAAATGTG 177  
Qy 181 GTCACCGACGCGTCTTCAACGGCATCAAGAAACAGAGCGCGCGCGCGCGCGCGCGCG 240  
Db 178 GTCACCGACGCGTCTTCAACGGCATCAAGAAACAGAGCGCGCGCGCGCGCGCGCG 237

```
Qy 241 AACTTCTACACCCGGAGCGGTTCTCTGAGGCCATGCGCGGTACCGGGGTTTCGCGCAT 300
Db 238 AACTTCTACACCCGGAGCGGTTCTCTGAGCGCGTCAAGGCGTACCCAGGCTTCGCCCAT 297
Qy 301 GGCGGCTCCGAGTTCGAGCGCAAGCGGAGATTGCGGCTTCTTCGGGCAAGCGCACGCGAC 360
Db 298 GGCGGCTCAAGTTCGAGGCGAAGCGGAGATTGCGGCTTCTTCGGGCAAGCGCACGCGAC 357
Qy 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGGTCAACAGAGCAACGCTTACTGCGACCCG 420
Db 358 GAGACCGGGCATTTCTGTCTACATCAGCGAGATCAACAGAGCAACGCTTACTGCGACCCG 417
Qy 421 ACCAAGGCGAGTGGCGGCTGCGCGCGGGGCGAGAGTACTAGGCGGGCGGCGCGCTGCGAG 480
Db 418 ACCAAGGCGAGTGGCGGCTGCGCGCGGGGCGAGAGTACTAGGCGGGCGGCGCGCTGCGAG 477
Qy 481 ATCTGTGGAACTCAACTACGAGGCGCGGGGCGAGGCGCATCGGCTTCGACGGGCTCGGG 540
Db 478 ATCTGTGGAACTCAACTACGAGGCGCGGGGCGAGGCGCATCGGCTTCGACGGGCTCGGG 537
Qy 541 GACCCCGGAGGTGGCGGGAAGCGCGTGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGG 600
Db 538 GACCCCGGAGGTGGCGGGAAGCGCGTGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGG 597
Qy 601 ATGAACACGTGCAACCGGTAATGATGCGCGAGGCGTTCGGCGGCGACCATCAGGGCCATCAAC 660
Db 598 ATGAACACGTGCAACCGGTAATGATGCGCGAGGCGTTCGGCGGCGACCATCAGGGCCATCAAC 657
Qy 661 GGCGGCTTCGAGTGCAGCGGAAACACCGCGCGGCGAGTGAACGGCGCGGCTCGGCTACTAC 720
Db 658 GGCGGCTTCGAGTGCAGCGGAAACACCGCGCGGCGAGTGAACGGCGCGGCTCGGCTACTAC 717
Qy 721 AGGCAGTACTGCGCGAGCTCGGCGTGCACCGGGCAACACCTCACCTGC 771
Db 718 AGGCAGTACTGCGCGAGCTCGGCGTGCACCGGGCAACACCTCACCTGC 768
```

## RESULT 15

```
US-10-389-432B-37
; Sequence 37, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 489492000300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: rl AH9 nucleic acid
US-10-389-432B-37
```

```
Query Match 91.3%; Score 707; DB 18; Length 771;
Best Local Similarity 94.8%; Pred. No. 7,1e-168;
Matches 731; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
```

```
Qy 1 TCGATGCGAAGTGGCGGTGCGAGCAACAGTATGCTCGAGCAAGTTGGCTACTGCGGC 60
Db 1 TCGATGCGAAGTGGCGGTGCGAGCAACAGTATGCTCGAGCAAGTTGGCTACTGCGGC 60
```

```
Qy 61 ACAGCCGACGAGTACTGCGCGCAGCGGTGCGAGTCCGGGCGCGTCCGCTCGGGCGCGGT 120
Db 61 ACAGCCGACGAGTACTGCGCGCAGCGGTGCGAGTCCGGGCGCGTCCGCTCGGGCGCGGC 120
Qy 121 GGCGGCGCGCGCGCGCGCGCGAGGCGCGGAGTGGCGGTGCGAACTGGTCTTAATGTG 180
Db 121 GGCGGCGCGCGCGCGCGCGCGAGGCGCGGAGTGGCGGTGCGAACTGGTCTTAATGTG 180
Qy 181 GTCAACGACGCGTCTTCAAGCGCATCAAGAACAGAGCGCGGAGCGGTGCGAGGGCAAG 240
Db 181 GTCAACGACGCGTCTTCAAGCGCATCAAGAACAGAGCGCGGAGCGGTGCGAGGGCAAG 240
Qy 241 AACTTCTACACCCGGAGCGGTTCTCTGAGGCCATCGCGCGTACCGGGGTTTCGCGCAT 300
Db 241 AACTTCTACACCCGGAGCGGTTCTCTGAGGCCATCGCGCGTACCGGGGTTTCGCGCAT 300
Qy 301 GGCGGCTTCGAGTTCGAGCGCAAGCGCGAATTGCCGCTTCTTCGGCGACGCGCACGCGAC 360
Db 301 GGCGGCTTCGAGTTCGAGCGCAAGCGCGAATTGCCGCTTCTTCGGCGACGCGCACGCGAC 360
Qy 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGTCAACAGAGCAACGCTTACTGCGACCCG 420
Db 361 GAGACCGGGCATTTCTGTCTACATCAGCGAGTCAACAGAGCAACGCTTACTGCGACCCG 420
Qy 421 ACCAAGAGGCGAGTGGCGGCGCGCGGCGAGAGTACTACGGGCGCGGCGCGCTCGCAG 480
Db 421 ACCAAGAGGCGAGTGGCGGCGCGCGGCGAGAGTACTACGGGCGCGGCGCGCTCGCAG 480
Qy 481 ATCTGTGGAACTCAACTACGAGGCGCGCGGCGAGGCGCATCGGCTTCGAGCGGCTCGGC 540
Db 481 ATCTGTGGAACTCAACTACGAGGCGCGCGGCGAGGCGCATCGGCTTCGAGCGGCTCGGC 540
Qy 541 GACCCCGGAGGTGGCGGCGCGCGTGTGCGGCTTCGAGGCGCGGCTCTGGTTCTGG 600
Db 541 GACCCCGAAGCGGTGGCGGCGCGGAGCGCGTGTGCGGCTTCGAGGCGGCGCTCTGGTTCTGG 600
Qy 601 ATGAACACGTGCAACCGTGTGATGCCGCGAGGCGTTCGGCGCGCACCATCAGGGCCATCAAC 660
Db 601 ATGAACACGTGCAACCGGTTGGTCCGCGAGGCGTTCGGCGCGCACCATCAGGGCCATCAAC 660
Qy 661 GGCGGCTTCGAGTGCAGCGGAAACACCGCGCGCGAGTGAACGGCGCGGCTCGGCTACTAC 720
Db 661 GGCGGCTTCGAGTGCAGCGGAAACACCGCGCGCGAGTGAACGGCGCGGCTCGGCTACTAC 720
Qy 721 AGGCAGTACTGCGCGAGCTCGGCGTGCACCGGGCAACACCTCACCTGC 771
Db 721 AGGCAGTACTGCGCGAGCTCGGCGTGCACCGGGCCCAACCTCACCTGC 771
```

Search completed: May 23, 2005, 17:32:09

Job time : 399.391 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 12:35:31 ; Search time 120.13 Seconds  
(without alignments)  
10542.593 Million cell updates/sec

Title: US-10-692-367-11

Perfect score: 774  
Sequence: 1 tcgatgcagactcggtg.....gcaacaacctcaactgtgta 774

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647.8	83.7	1094	4	US-09-522-714-1
2	377	48.7	881	4	US-09-522-714-29
3	373.2	48.2	1048	4	US-09-522-714-21
4	296.8	38.3	1116	4	US-09-522-714-31
5	174.6	22.6	1079	1	US-08-181-271A-37
6	174.6	22.6	1079	1	US-08-449-315-37
7	174.6	22.6	1079	1	US-08-444-803-37
8	174.6	22.6	1079	1	US-08-449-043-37
9	174.6	22.6	1079	1	US-08-456-285A-37
10	174.6	22.6	1079	1	US-08-455-416-37
11	174.6	22.6	1079	1	US-08-455-244-37
12	174.6	22.6	1079	1	US-08-454-876-37
13	174.6	22.6	1079	2	US-08-457-364-37
14	174.6	22.6	1079	2	US-08-456-282-37
15	174.6	22.6	1079	2	US-08-456-240-37
16	174.6	22.6	1079	2	US-08-455-736-37
17	174.6	22.6	1079	2	US-08-971-217-37
18	174.6	22.6	1079	3	US-09-350-600-37
19	174.6	22.6	1079	4	US-09-906-234-37
20	165	21.3	1318	3	US-09-125-891-1
21	162.6	21.0	816	4	US-09-266-965-73
22	162.6	21.0	53500	4	US-09-266-965-76
23	161.8	20.9	1151	1	US-07-704-288C-2
24	161.8	20.9	1151	1	US-08-093-372-1
25	161.8	20.9	1151	1	US-08-379-259-2
26	156	20.2	1218	4	US-09-902-540-4667
c 27	156	20.2	29384	4	US-09-902-540-1229

28 153.8 19.9 960 4 US-09-534-229C-8 Sequence 8, Appli  
29 135.4 17.5 1118 4 US-09-522-714-23 Sequence 23, Appli  
30 128.4 16.6 972 4 US-09-534-229C-7 Sequence 7, Appli  
31 125.2 16.2 1163 4 US-09-522-714-5 Sequence 5, Appli  
32 124.8 16.1 1002 1 US-08-457-797A-9 Sequence 9, Appli  
33 124.8 16.1 1002 1 US-08-812-025-9 Sequence 9, Appli  
34 124.8 16.1 1002 3 US-09-138-873A-9 Sequence 9, Appli  
35 121.2 15.7 1077 4 US-09-522-714-17 Sequence 17, Appli  
36 110.8 14.3 583 4 US-09-522-714-25 Sequence 25, Appli  
37 107.6 13.9 771 4 US-09-534-229C-6 Sequence 6, Appli  
38 103.2 13.3 1013 4 US-09-522-714-19 Sequence 19, Appli  
39 98.8 12.8 1619 4 US-09-522-714-11 Sequence 11, Appli  
40 84.8 11.0 2636 3 US-09-125-891-3 Sequence 3, Appli  
41 83.2 10.7 952 1 US-08-181-271A-38 Sequence 38, Appli  
42 83.2 10.7 952 1 US-08-449-315-38 Sequence 38, Appli  
43 83.2 10.7 952 1 US-08-444-803-38 Sequence 38, Appli  
44 83.2 10.7 952 1 US-08-449-043-38 Sequence 38, Appli  
45 83.2 10.7 952 1 US-08-456-265A-38 Sequence 38, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-522-714-1  
; Sequence 1, Application US/09522714  
; Patent No. 6563020  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Valpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100  
; CURRENT APPLICATION NUMBER: US/09/522.714  
; CURRENT FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/125,915  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (51)...(893)  
US-09-522-714-1

Query Match 83.7%; Score 647.8; DB 4; Length 1094;  
Best Local Similarity 91.8%; Pred. No. 3.1e-112;  
Matches 704; Conservative 0; Mismatches 42; Indels 21; Gaps 1;  
  
Qy 6 GCAGAACTGCGGCTGCCAGCCAAACGATGTCGACGAAGTTTGGCTACTCGCGGACGAC 65  
Db 149 GCAGAACTGCGGCTGCCAGCCAAACGATGTCGACGAAGTTTGGCTACTCGCGGACGAC 208  
Qy 66 CGACGAGTACTGCGGCGACCGGTCGACGTCGCGGCGCGTCCGCTCGCGCGCGTGGCGG 125  
Db 209 CGACGAGTACTGCGGCGACCGGTCGACGTCGCGGCGCGTCCGCTCGCGCGCGGCGG 268  
Qy 126 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185  
Db 269 CAGTGGCGGC-----GCTGGTGGCGAACGTCGCTAGCGTCGTCAC 307  
Qy 186 CGACGCGCTTCTTCAACGGCATCAAGAACCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 245  
Db 308 CGGCTCTCTTCTTCAACGGCATCAAGAACCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367  
Qy 246 CTACACCGGAGCGCGTTCCTCGAGGCGCATCGCGCGTACCCGGGCTTCGCGCATGGCGG 305  
Db 368 CTACACCGGAGCGCGTTCCTCGAGGCGCATCGAGGCGTACCCAGGCTTCGCGCATGGCGG 427  
Qy 306 CTCGAGGTGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 365

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Db 428 GTCCAGGTGCGAGGCGAGAGTCGCGCGCTTTCTTCGCGACGCCACGACGAGAC 487
Qy 366 CGGCAATTTCTGTACTACAGCGAGGTCAACAAGAGCAACGCCCTACTTGGACCCGACCAA 425
Db 488 CGGCAATTTCTGTACTACAGCGAGATCAACAAGAGCAACGCCCTACTTGGACCCGACCAA 547
Qy 426 GAGCAGTGGCGGTGCGCGCGGGGCGAGAGTACTACGGGCGCGCGGCTGCGAGATCTC 485
Db 548 GAGCAGTGGCGGTGCGCGCGGGGCGAGAGTACTACGGGCGCGCGGCTGCGAGATCTC 607
Qy 486 GTGCAACTACAACTACGGGCGCGCGGAGGCCCATCGGCTTCAGCGGGCTCGGGGACCC 545
Db 608 GTGGAATCAAACTACGGGCGCGCGGAGGGCCCATCGGCTTCAGCGGGCTCGGGGACCC 667
Qy 546 CGGAGGGTGGCGGGGACGCCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAA 605
Db 668 CGGAGGGTGGCGGGAGCGCGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAA 727
Qy 606 CAACGTGCACCGTGTGATGCGCGAGGGCTTGGGCGCCACCATCAGGGCCATCAACGGGC 665
Db 728 CAGCGTGCACGGGTGTGCGCGAGGGGTTCGGGCGCCACCATCAGGGCCATCAACGGGC 787
Qy 666 CCTCGAGTGCAACGGGAACACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGGCA 725
Db 788 CCTCGAGTGCGCGGGAAACACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGGCA 847
Qy 726 GTACTGCGCGCAGCTCGGCGGTGCGAGCCCGGGCAACAACTACCTGCT 772
Db 848 GTACTGCGCGCAGCTCGGCGGTGCGAGCCCGGGCCAACTACCTGCT 894
```

## RESULT 2

US-09-522-714-29

```
; Sequence 29, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 881
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(551)
US-09-522-714-29
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Query Match 48.7%; Score 377; DB 4; Length 881;

Best Local Similarity 80.7%; Pred. No. 9.4e-62;

Matches 453; Conservative 0; Mismatches 105; Indels 3; Gaps 1;

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Qy 215 AGGCGGGAGCGGTGCGAGGGCAAGACTTCTACCCCGGAGCGGTTCTCGAGGCA 274
Db 1 ATGCGGGAGCTGTGTGCGAGGGCAGACGCTTCTACACGGAAGCGGTTCTCGAGGCA 60
Qy 275 TCGCGCGTACCGGGCTTCGCGATGCGGCTCCGAGGTCGAGCGAAGCGAGATTG 334
Db 61 TCGCGCGTACCGGGCTTCGCGATGCGGCTCCGAGGTCGAGCGAAGCGAGATTG 120
Qy 335 CGGCTTCTTCGCGCAGCGCAGACGAGACGGGCTTCTGTACTACAGGAGTCA 394
Db 121 CGGCTTCTTCGCGCATGTCAAGCAGACCGGGCATTTGTGTACTACAGGAGTCA 180
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Qy 395 ACAAGAGCAACGCTACTTCGACCCCGACCAAGAGGCAAGTGGCGCGCGGGGCGAGA 454
Db 181 ACCTGGGGAAGTACTTGGGACTGGAGCAGTGAAGCAGTGGCCGCCACCCGAGGAGG 240
Qy 455 AGTACTACGGGCGCGGCGCGCTCGAGATCTGTGTGGAACATAAATAGGGGCGCGGGGA 514
Db 241 GTTACTACGGGCGCGGCGCGCTCGAGCTGTGTGTGAACATAAATAGGGGCGCGGGGA 300
Qy 515 GGGCCATCGGCTTCGAGCGGGCTCGGGAGCCCGGAGGGTGGCGGGAGCGCGTGTGG 574
Db 301 GAGGCTTCGGCTTCGAGCGGGCTGGGAGACCCGACAGACTGGGCGAGGACCCCGTGTGT 360
Qy 575 CGTTCAAGCGCGGCGCTCTGGTTCGTGATGAACAAACGTGACCGCTGTATGCCGAGGGCT 634
Db 361 CGTTCAAGTCGGGCTCTGGTACTGTGATGGAGAACATGCACAGCTCATGCCCGAGGGT 420
Qy 635 TCGGCGCCACCATCAGGGCCATCAACGGGCGCGCTCGAGTG---CAACGGGAACAAACCCG 691
Db 421 TCGGCGCCACCATCAGGGCCATCAACGGCTTCGACGAGTGTACGCGGGGAAACACGG 480
Qy 692 CCAGATGAACGCGGCTCGGCTACTTACAGGAGTACTGCGCGAGCTCGGGCTCGAC 751
Db 481 CCGAAATGAAGACCGGGTGGCTTCTACCTCGAGTACTGCCACCACTTCGGTTCACC 540
Qy 752 CGGCAACAACTCACCTGCT 772
Db 541 CCGGGCTCGACCTCAGTTGCT 561
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## RESULT 3

US-09-522-714-21

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; Sequence 21, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)...(854)
US-09-522-714-21
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Query Match 48.2%; Score 373.2; DB 4; Length 1048;

Best Local Similarity 71.3%; Pred. No. 4.9e-61;

Matches 555; Conservative 0; Mismatches 178; Indels 45; Gaps 3;

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Qy 6 GCAGAACTCGGCTGCCAGGCCAAACGATATGCTGCAGCAAGTTTGGCTACTGCGGACGAC 65
Db 116 GCAGAACTCGGCTGCCAGGCCCTGTGTGTGAGCGGTTTCGGGTACTGCGGGACGGG 175
Qy 66 CGAGAGTACTCGGCGGACGSGTGCCAGTCGGGCGCTGCGCTCGGCGCGCGGTGGCGG 125
Db 176 CGAGAGTACTGCGGCGCGGTTGCCAGTTCGGGCGCTGCG--- 215
Qy 126 CGGCGGCGGCGGCGGAGCGCGGAGGAGTGGCGGTGCGAACTGTGCTAATGTGGTCA 185
Db 216 -----GAGGTGCCGAGAGCCAAACACGCGTCCGTGCGCAGCATCGTCA 259
Qy 186 CGAGCGCTTCTTCAACGGCATCAAGAACCGGCGGAGCGGGTTCGAGGGCAAGACTT 245
Db 260 GCCGCGCTTCTTTCAGACGCGCTCTCTCGCGCAGGGCGCGCTCTGTCGAGGCGCAACGGCTT 319
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[illegible]

## RESULT 4

```

US-09-522-714-31
US-09-522-714-31
; Sequence 31, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: intron
; LOCATION: (445)...(512)
; NAME/KEY: CDS
; LOCATION: (42)...(444)
; NAME/KEY: CDS
; LOCATION: (513)...(922)
US-09-522-714-31

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D	b	116	GCAGAACTGCGGGTTCGGCCCTGTGTGTCAGCCGGTTTCGGGTACTCGCGGACGGG	17
Q	y	66	CGACGAGTACTGCGGCCGACGGTGCACTCGGGCCCCGTGCCCTCGGGCGCGGTGGCGC	125
D	b	176	CGAGGACTACTGCGGGCGGGTGCCAATCGGGCCCCTGC-----	215
Q	y	126	CGCGCGCGCGCGGAGCGCGCGGAGCAGTGGCGGTGCGAATGTTGGCTTAATGTGGTCAAC	185
D	b	216	-----GACGTGCCGAGACCACAAACACGCGTCCGTGGCGCAGCATCGTCGAC	259
Q	y	186	CGACGCGTTCTTCAACGSCATCAGAAACAGCGCCGGAGCGGTCGGAGGGCAAGAATT	245
D	b	260	GCCGGCCTTCTTCGACGCGCTCCTCGCGAGCGCCCGCGCTCGTGGAGGCCAACCGGCT	319
Q	y	246	CTACACCCGCGAGCGGTTCTCTCGAGGCCATCGCCCGCTACCCGCGGCTTCGCGCATGGCCG	305
D	b	320	CTACACCGCGCAGCGCTTCTCGCGCCCGCGGCTACTACCGGCGTTCGGCGCGCACCG	379
Q	y	306	CTCGAGGTGCGAGCGCAAGCGCGAGATTGCCGCTTCTTTCGGCGCACGCCACGACGAGAC	365
D	b	380	CACCGTCGACGACTCAAAGCGCGAGATCGCGCCTTCTTCGGCAACGCCCAACCAACGAGAC	439
Q	y	366	-----	365
D	b	440	CATAAGTAGTGGCGAACAACCGAAGCTGTCCTCAAGCTCTAGCTGCTACTAATCAAGTTT	499
Q	y	366	-----CGGGCAATTTCTGTACTACAGCGAGGTCAAC---AAGAGCAACGCCCTACTGC	414
D	b	500	CGACTGCTCGCAGATTCTGTACATCAACGAGATCGACGGCCGAGCAGAACTACTTGC	559
Q	y	415	GACCGCAACAGAGCAGTGGCCGTGCGCCCGCGGGCAGAAATCTACGCGCGCGGCCG	474
D	b	560	GACCGGAACAACACGCACTGCCCGTGCACGCGGGGAAGGGTACTACGCGCGCGCGCG	619
Q	y	475	CTCGAGATCTCGTGAATCAACAATAACGCGCGCGCGGGAGGGCCATCGGCTTCGACGG	534
D	b	620	CTCGAGATCTCTCGAACTTCAACTACGCGGCGCGCGGGCAGAGCATCGGCTTCGACGG	679
Q	y	535	CTCGGGGACCCCGCAGGGTGGCGGGACGCGCGGACGCGGTTCGAGGCGCGCTCTCG	594
D	b	680	CTGGCGHACCCGACGCGGTGGCGGACGCGCGGTCTCGGCTTCGCTCCGCTCTCG	739
Q	y	595	TTCGTGATGAACAACGTGSCACCGTGTGAT-----GCCGCAAGGCTTCGGGCGCACCATC	648
D	b	740	TACTGTGATGAACAACGTGCAACGGGCGCATCGTCTCGGCGCAGGGCTTCGGCGCCACCATC	799
Q	y	649	AGGGCCATCAACGGGGCCCTCGAGTGCAACGGGAACAACCCCGCCAGATGAACGGCGCG	708
D	b	800	CGGGCCATCAACGGCGCGCTCGAGTGCGACGCGCAAGAACCCCACTCCGTCAACAACCGC	859
Q	y	709	GTCGGCTACTACGSCAGTACTGCGCGCATCTCGGCGTTCGACCGGGAGCAACCTCTCAC	768
D	b	860	GTCGCTACTAAGAGAGTTCTGCCAGATTTCGGCGTTCGACCCGGGCAACAACTCTCAC	919
Q	y	769	TGCTGA 774	
D	b	920	TGCTGA 925	
 RESULT 5 US-08-181-271A-37 ; Sequence 37, Application US/08181271A ; Patent No. 5614395 ; GENERAL INFORMATION: ; APPLICANT: Ryals, John A. ; APPLICANT: Alexander, Danny C. ; APPLICANT: Beck, James J. ; APPLICANT: Duesing, John H. ; APPLICANT: Friedrich, Leslie B. ; APPLICANT: Goodman, Robert M. ; APPLICANT: Harms, Christian ; APPLICANT: Meins, Jr., Frederick ; APPLICANT: Montova, Alice				



APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericea C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/181,271A  
FILING DATE: 13-JAN-94  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-181-271A-37

Query Match 22.6%; Score 174.6; DB 1; Length 1079;  
Best Local Similarity 56.5%; Pred. No. 5.2e-24;  
Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;  
QY 7 CAGAACTGCGGTGCGCAGCAAAAGTATGCTGTCAGCAAGTTTGGCTACTGCGGCACGACC 66  
DB 93 CAAAACCTGCGGTGCGCTCCAAACCTCTGTTGCAGTCACTGCGTTACTGTTGTCGCGAC 152  
QY 67 GACGAGTACTGCGGCGACCGGTGCGAGTCCAGTCCGCGCCCGTCCGCTCGGCGCGGCGGTGGCGG 126  
DB 153 GATGCATACTGCGGTGTTGGATGCCGATCAGGTCTTGTA----- 192  
QY 127 GCGGCGCGCGCGAGGCGCGCGAGGCGAGTGGCGGTGCGAAACGTGGCTAATGTGGTCAACC 186  
DB 193 -----GAGGTAGTGGAAACCCGACCGGAGGGTGGTTCGTAGCATTTGTGACA 239  
QY 187 GACGCGTTCTTCAACCGCATCAAGAACCCAGGCGCGGAGCGGGTGGAGGCAAGAACTTC 246  
DB 240 CRAAGTTTCTTTAAACAATATATCAACCAAGCTGGTAATGTTGCGCGGGGAAAGATTC 299  
QY 247 TACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGCTACCGGGCTTCGGCGCATGGCGG 306  
DB 300 TACACCGGTGACTCTTTGTTAAACCGCGCTAATACATTTCCCAACTTGGCAATCTGTT 359  
QY 307 TCCGAGGTGAGCGCAAGCGCGAGATTGCGCGCTTCTTCGCGCACGCGCACGACGAGACC 366  
DB 360 AC-----CAGACGTGAAATTTGCTACCATGTTGCTCATTTCACTACGAGACC 407  
QY 367 GGGCATTTCTGTACATCAGCGAGGTCAAC---AAGACCAACCGCTTACTCGGACCGGACC 423  
DB 408 GGACATTTCTGTCTACATAGAGAGATTAAACGAGCAACACGTAACCTACTGCGAGAGCAGC 467  
QY 424 AAGAGCGAGTGGCGGCGCGCGCGAGAGTACTACGCGCGCGCGCGCTGCGAGATC 483  
DB 468 AACACCAATACCCATGTGACCGGGAAAGGCTACTTTCGTCGTGTCGATCCAACTA 527  
QY 484 TCGTGGAACTACAACTACGCGGCGCGGAGGCGCATCGGCTTCGACGCGGCTCGGGGAC 543  
DB 528 TCATGGNACTACAACTACGAGCGTGTGGTCAAGTCTCGGTCTTGACCTTCTACGCCAG 587  
QY 544 CCGCGCAGGTTGCGCGGAGACGCGGTGGTGGCTTCAAGCGCGGCGCTCTGGTTCTGGATG 603  
DB 588 CCGGAACTTGTGGGTAGCAACCCAACTGTAGCTTTTCAGGTTCGGGTTTGTGGTTGGATG 647  
QY 604 AACAACTGTCACCGTGTGATCGCGGCGCTTCGCGGCCACCATCAGGCGCATCAACGCG 663  
DB 648 AATAGCGTAAGCGCGGTTCTGAACCAAGGGTTTGGAGCGCCACCATTAGAGCTATTATGG- 706  
QY 664 GCGCTCGAGTGCACCGGAAACAAACCCCGCCCGAGATGAACCGCGCGCTCGGCTACTACAGG 723  
DB 707 --AATGGAAATGTAACGGTGGTAATTCCGGTGCAGTCAACCGCAAGGATGGATATAAGA 764  
QY 724 CAGTACTGCGCGCAGCTCGCGCTGCAGCCCGGGCAACACCTCACCTGCTGA 774  
DB 765 GACTATTGTGGACAGCTTGTGTGGACCCCTGGTCTTAACCTTAGTTGCTAA 815

RESULT 6  
US-08-449-315-37  
Sequence 37, Application US/08449315  
Patent No. 5650505

GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,315  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-449-315-37  
Query Match 22.6%; Score 174.6; DB 1; Length 1079;  
Best Local Similarity 56.5%; Pred. No. 5.2e-24;  
Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;  
QY 7 CAGAACTGGGGCTGCCAGCAACAGTATGCTGCAGCAAGTTTGGCTACTCGCGCAGCAGC 66  
DB 93 CAATACTGGGTGGCTCCAACTCTGTTGAGTCAGTTCGGTTACTTGTGTGATCCGAC 152  
QY 67 GACGAGTACTGGCGGACGGGTGCCAGTGGGGCCCTGTCGGCTCGGGCGCGGTGGCGGC 126  
DB 153 GATGCATACTGCGGTGTGGATGCCGATCAGGTCTTGTA----- 192  
QY 127 GCGCGCGCGCGGCGCGGAGCGAGTGGCGGTGGCAACCTGCTGCTGCTATGTTGTCACC 186  
DB 193 -----GAGGTAGTGGAAACCGGAGGGTTCGGTCGGTAGCATTTGTGACA 239  
QY 187 GACGCGTTCTTCAACGGCATCAAGAACACGAGCGCGGAGCGGGTCCGAGGCAAGAACTTC 246  
DB 240 CAAAGTTTCTTTAAACAATATTATCAACCAAGCTGGTAATGTTGCGGGGGAAGATTC 299  
QY 247 TACACCGGAGCGGCTTCTCGAGGCCATCGCGCGGTATCCCGGGCTTCGCGCATTGGCGGC 306  
DB 300 TACACCGGTGACTCTTTCTGTTAAACGCGGTAACTTTCCCAACTTTGCCAAATTTCTGTT 359  
QY 307 TCCGAGTTCGAGCGGCAAGCGGAGATTGCGGCTTCTTCCGCGCAGCGCAGCAGCAGC 366  
DB 360 AC-----CAGACGTGAAATTTGCTACCATGTTTGTCTCATTTCACTCAGAGAC 407  
QY 367 GGGCATTTCTGTACATCAGCAGGTCAAC---AAGAGCAACGCTTACTCGGACCCGAC 423  
DB 408 GGACATTTCTGTACATAGAGAGATTAAACGAGCAACACGTAACCTACTTCCAGAGCAGC 467  
QY 424 AAGAGCAGTGGCGGTCGCGCGGCGCAGAGTACTAGCGGCGCGCGCTTCGCGATC 483  
DB 468 AACACACAATACCCATGTGCACCGGGAAGAGGCTACTTCGGTGTGTCGATCCCACTA 527  
QY 484 TCGTGAACCTACAACTACGCGCGCGGAGGGCCATCGGCTTCGACGCGGCTCGGGGAC 543  
DB 528 TCATGGAACCTACAACTACGAGGCGTGTGGTCAAAAGTCTCGGCTTCACTTCAGCCAG 587  
QY 544 CCGGCGAGGTTGGCGGGAACGCGGTGGTGGCGCTTCAAGCGCGCGCTCTGTTTCTGATG 603  
DB 588 CCGGAATTTGTGGGTAGCAACCACTGTAGCTTTTCAAGTTCGGGTTTGTGTTTGGATG 647  
QY 604 AACACAGTGCAGCGTGTGATGCGCGGCTTCGCGCGCAACCATCAGGGCCATCAACGCGC 663  
DB 648 AATAGCGTAAGCGCGGTTCTGAACCAAGGTTTGGAGGCCACCATTAGAGCTAATAATGG- 706  
QY 664 GCGCTCGAGTGCNAACGGGAACACCCCGCCAGATGAACGCGCGGCTCGGCTACTACAGG 723

Db 707 --AATGAATGTAAACGGTGTAAATCCGGTGCAGTCAACGCAAGGATGATATAGA 764  
QY 724 CAGTACTGCCGCGAGCTCGCGTCGACCCCGGGCAACAACCTCACCTGCTGA 774  
Db 765 GACTATTGTGACAGCTTGTGTGGACCCCTGGTCCTTAACCTTAGTTGCTAA 815

## RESULT 7

US-08-444-803-37  
Sequence 37, Application US/08444803

Patent No. 5654414

## GENERAL INFORMATION:

APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Utnes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,803

FILING DATE: 19-MAY-1995

CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271

FILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566

FILING DATE: 6-FEB-1989

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/042,847

FILING DATE: 6-APR-1993

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-444-803-37

Query Match 22.6%; Score 174.6; DB 1; Length 1079;

Best Local Similarity 56.5%; Pred. No. 5.2e-24;

Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;

QY 7 CAGAACTGGCGGTGCCAGCAACAGTATGCTGCAGCAAGTTTGGCTACTCGCGCAGCACC 66

Db 93 CAAAACCTGGCGTTGCGCTCCAAACCTCTGTTGCAGTCAGTTTCGGTTACTTGTGTACCGAC 152

QY 67 GACGAGTACTGGCGGACGCGTCCAGTCGGGCGCCGTCGCCGCTCGGCGCGCGGTGGCGGC 126

Db 153 GATGCATATCTGCGGTGTGATGCCGATCAGGTCCTTGTGTA----- 192

QY 127 GCGCGCGCGCGGCGGCGGCGGAGGCGAGTGGCGGTGCGAACGTTGGCTAATGTGGTCACC 186

Db 193 -----GAGGTAGTGAACCCCGAGCGGTCGGTCGGTAGCATTTGTGACA 239

QY 187 GACCGGTTCTTCAACGGCATCAAGAACCGAGCGCGGAGCGGTCGAGGCGCAAGACTTC 246

Db 240 CAAGGTTTCTTTAAACAATATATCAACCAAGCTGGTAATGTTGCGCGGGGAAAGATTTC 299

QY 247 TACACCGGAGCGCGGTTCTTCGAGGCGCATCGCGCGGTACCGCGGCTTCGGCGCATGGCGGC 306

Db 300 TACACCGCGGACTCTTTTCGTTAAGCGCGCTAATACTTTCCCAACTTGGCAATTCGTTT 359

QY 307 TCGAGGTTCGAGCGCAAGCGCGGAGATTGCGCGCTTTCTTCGCGCAGCGCAGCAGAGACC 366

Db 360 AC-----CAGACGTGAATTTGCTACCATGTTTGTCTCATTTCACTCAGAGACC 407

QY 367 GGGCATTTCTGTACATACGAGGTTCAAC---AAGAGCAACGCTACTTCGGACCCGACC 423

Db 408 GGCACATTTCTGTCTACATAGAAGAGATTAAACGAGCAACACGTAACACTACTCCAGAGCAGC 467

QY 424 AAGAGGCGAGTGGCGCGTGGCGCGGCGGCAAGAACTACTACGCGCGCGCGCTGCGATC 483

Db 468 AACACACATATACCATGTGACCGGGGAAAGGCTACTTTCGTTGTTGGTCCGATCCCACTA 527

QY 484 TCGTGGAACTACAACTACGCGCGCGCGGAGGGCCATCGGCTTCGACGCGGCTCGGGGAC 543

528 TATGGAACAACTACGAGCGTGTGGTCAAAAGTCTCGGTCTTGACCTTCTACGCCAG 587  
544 CCCGCGAGGTGGCGGAGCCGCTGTGTGGCTTCAAGGCGCGCTCTGTTCTGGATG 603  
588 CCCGAACCTTGGGTAGCAACCCAACTGTAGCTTTCAGTGGGTGTGGTTTGGATG 647  
604 AACACGTGCACCGTGTGATGCCGAGCGCTTCGCGCCACCATCAGGCGCATCAAGCGC 663  
648 AATAGCGTAAGCGCGTCTCTGAACCAAGGTTTGGAGCCACCATTAGAGCTATTAATGG- 706  
664 GCCCTGAGTGAACGGGAACAACCCGCCAGATGAACGCGCGGTCTGCTACTACAGG 723  
707 --AATGGAATGAACGGTGGTAAATTCGGTGCAGTCAACGCAAGGATTGGATATAGA 764  
724 CAGTACTCCGCGACGTGGCGTGCAGCCCGGCAACACCTCACCCTGCTGA 774  
765 GACTATTGTGACAGCTTGGTGTGGACCTTGTCTTAACCTTAGTTGTTAA 815

RESULT 8

US-08-449-043-37  
Sequence 37, Application US/08449043  
Patent No. 5689044

GENERAL INFORMATION:

APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,043  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/053,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-449-043-37

Query Match 22.6%; Score 174.6; DB 1; Length 1079;  
Best Local Similarity 56.5%; Fred. No. 5.2e-24;  
Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;  
QY 7 CAGAACTCGGCTGCCAGCCAAACGATATGCTGCAGCAAGTTTGGCTACTTGGCGCACGACC 66  
Db 93 CAAAACTCGGTTGGCTCCAAAACCTCTGTTGCAGTCAGTTCCGTTACTTGTGTACCGAC 152  
QY 67 GACGAGTACTCGGCGAGCGGTGCAGTCGGGCCCGTCCCGCTCGGGCGCGCGTGGCGGC 126  
Db 153 GATGCATACTCGGCTGTTGGATGCCGATCAGGTCTCTTGA----- 192  
QY 127 GCGCGCGCGCGGCGCGGAGGAGTGGCGGAGTGGCGGTAATGTGTGTCACC 186  
Db 193 -----GAGGTAGTGGAAACCCCGAGGGGTGGTTCGGTAGCATTTGTGACA 239  
QY 187 GACGCTTCTTCAACCGCATCAAGAACCAAGCCGCGGAGCGGTGCGAGGGCAAGACTTC 246  
Db 240 CAAGTTTCTTTAACAATATATCAACCAAGCTGGTATGTTGCGCGGGAAGAAATTTC 299  
QY 247 TACACCCGAGCGGCTTCTCGAGGCCATCCCGCGGTACCCGGGGTTCGCGCATGGCGGC 306  
Db 300 TACACCCGCTGACTCTTTCGTTAAACCGCGCTAATACTTCCCAACTTTGCCAAATCTCTTT 359  
QY 307 TCCGAGGTGAGCGCGGAGGAGATTGCCCGCTTCTTCGCGCACGCCACGACGAGACC 366





Db 193 -----GAGGTAGTGGAAACCCGACGAGGGTTCGGTCGGTAGCATTTGTGACA 239  
Qy 187 GACCGGTTCTTCAACGGCATCAAGAACACAGCCCGGAGCGGGTTCGAGGGGCAAGACTTC 246  
Db 240 CAAGGTTCTTTAAACAATATTATCAACCAAGCTGTAATGGTTGCGGGGGAAGATTC 299  
Qy 247 TACACCCGGAGCGGTTCTTCTGAGGCCATCCCGGTTACCCGGGCTTCGCCATCGGGGC 306  
Db 300 TACACCCGGTACTCTTTGTTAAACGCGCTTAATCTTTCCCAACTTTGCCAAATCTGTT 359  
Qy 307 TCCGAGGTCGAGCGCAACGCGAGATTGCCCGCTTTCTTCCGCGCACGCCACCCAGAGACC 366  
Db 360 AC-----CAGAGGTGAATTTGCTACCATGTTTGTCTATTTCACTCACAGAGACC 407  
Qy 367 GGGGATTTCTGCTACATCAGCGAGGTCAAC---AAGAGCAAGCGCTTACTGCGACCCGAGC 423  
Db 408 GGACATTTCTGCTACATAGAAGAGATTAAACGAGCAACACGTAACCTACTTGCAGAGCAGC 467  
Qy 424 AAGAGGAGTGGCGTGGCGCGCGGCGAGAGTACTACGGGCGCGCGCGCTGCAGATC 483  
Db 468 AACACAAATACCATGTGCAACCGGGAAGGCTACTTCGGTCTGGTCCGATCCAACTA 527  
Qy 484 TCGTGGAACTACAACTACGGCGCGCGGAGGCGCATCGGCTTCGAGGGGCTCGGGAC 543  
Db 528 TCATGGAACTACAACTACGAGCGGTGTGTCAAAGTCTCGGTCTTGACCTTCTACGCCAG 587  
Qy 544 CCGGAGGTTGGCGCGGAGACCGCGTGTGGTTCAGGGCGGCTCTGTTCTGATG 603  
Db 588 CCGCAACTTGTGGGTAGCAACCAACTGTAGCTTTTCAGGTCGGGTTTGTGGTTTGGATG 647  
Qy 604 AACACGTGACCGTGTGATCCGCGGCTTCGCGCCACCATCAGGCGCATCAACGGC 663  
Db 648 AATAGCGTAAGCGCGGTCTCAACCAAGGTTTGAGCCACATTAGAGCTATTATAGG- 706  
Qy 664 GCCCTCGAGTCAACGGGAACAACCCCGCCAGATGAACGCGCGGCTCGGCTACTACAGG 723  
Db 707 --AATGAATGTAACGGTGGTAAATCCCGTGCAGTCAACGCAAGATTGGATCTATAGA 764  
Qy 724 CAGTACTCCCGCAGCTCGGCTGACCCCGGCAACACCTCAGCTGCTGTA 774  
Db 765 GACTATTGTGACAGCTTGGTGTGAGACCTTGGTCTTAACCTTAGTTGCTAA 815

RESULT 11  
US-08-455-244-37  
; Sequence 37, Application US/08455244  
; Patent No. 5789214  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr. Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne

; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,244  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-455-244-37

Query Match 22.6%; Score 174.6; DB 1; Length 1079;







; FILING DATE: 20-JUN-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/329,018  
 ; FILING DATE: 24-MAR-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/045,957  
 ; FILING DATE: 12-APR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Elmer, James Scott  
 ; REGISTRATION NUMBER: 36,129  
 ; REFERENCE/DOCKET NUMBER: S-19825/P1/CDC 1727  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919)541-8614  
 ; TELEFAX: (919)541-8689  
 ; INFORMATION FOR SEQ ID NO: 37:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1079 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-457-364-37

Query Match 22.6%; Score 174.6; DB 2; Length 1079;  
 Best Local Similarity 56.5%; Pred. No. 5.2e-24;  
 Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;

QY	7	CAGAACTGCGGCTGCAGCCAAA	CGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGACC	66
DB	93	CAAAACTCGGGTGGCTCCAAA	CTCTGTTGCAGTCAGTTCGGTTACTGTGGTACCGAC	152
QY	67	GACGAGTACTCGCGGACGGGTG	CGACGTGCGGCCCGTCCGCTCGGGCGCGGTGGCGGC	126
DB	153	GATGCATACTCGGCTGTGGATG	CCGATCAGGTCTCTTGTGTA-----	192
QY	127	GGCGGCGGCGGAGGCGGCGG	AGGAGGAGTGGCGGTGCGAACGTGGCTAATGTGGTCACC	186
DB	193	-----GAGGTAGTGGAAAC	CCCCCGACCGGAGGGTCCGTGCGTAGCATTTGTGACA	239
QY	187	GACGCGTTCTTCAACGGGATC	CAAGAACCAAGCCCGGAGCGGTGCGAGGCGCAAGACTTC	246
DB	240	CAAGTTTCTTTAACAATATTA	TATCAACCAAGCTGTAATGTTGCGGGGGAAGAATTC	299
QY	247	TACACCGGAGCGGGTTCTCT	CGAGGCCATCCGCGGTACCGGGGCTTCGCGCATCGGCGGC	306
DB	300	TACACCGTGACTCTTTCTG	TAAACGCGCTAATACTTTCCCCAACTTTGCCAATCTGTT	359
QY	307	TCCGAGTTCGAGCGCAAGCG	GAGATTGTCGCGCTTCTTTCGGGCGACGCCACGCAAGAGACC	366
DB	360	AC-----	CAGACGTGAATTTGCTACCATGTTTGTCTCATTTCACTCAGCAGACC	407
QY	367	GGGCATTTCTGTACATCAG	CGAGGTCAAC---AAGACCAACGCTACTTCGCGACCCGACC	423
DB	408	GGACATTTCTGCTACATAGA	AGAGATTAAACGAGCAACACGTAACTACTTCGCAGAGCAGC	467
QY	424	AAGAGGCAGTGGCGTGGCG	CGCGCGGGGAGAAAGTACTACGGGCGCGGCCCTCGCAGATC	483
DB	468	AACACAAATACCATGTGCA	CCGGGAAAAGGCTACTTTCGGTCTGGTCCGATCCACTA	527
QY	484	TCGTGGAACATAACAATA	CGGCGCCCGCGGGGAGGCGCATCGGCTTCGACGGGCTCGGGGAC	543
DB	528	TCATGGAACATAACAATA	CTACGAGCGTGTGGTCAAAAGTCTTCGGTCTTGACCTTCTACGCCAG	587
QY	544	CCCGGCAGGTGGCGCGGAC	CGCGTGGTGGCGTTCAAGGCGGCGCTCTGGGTTCTGGATG	603
DB	588	CCCGAACTTGTGGGTAGCA	ACCCAACTGTAGCTTTTCAGGTCCGGGTGTGGTGTTCGGATG	647
QY	604	AACAACTGTCACCGTGTG	TGATGCGCGCAGGGGCTTCGGCGCCACCATCAGGGCCCATCAACGCGC	663
DB	648	AATAGCGTAAGCCCGGTTC	TGAAACCAAGGGTTTGGAGGCCACATTAGAGCTATTATGG-	706
QY	664	GCCCTCGAGTCAACGGGAA	CAACCCCGCCAGATGAACGCGCGCGTTCGGCTACTACAGG	723

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; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-456-262-37

Query Match 22.6%; Score 174.6; DB 2; Length 1079;
Best Local Similarity 56.5%; Pred. No. 5.2e-24;
Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;

QY 7 CAGAACTCGCGTGCACGCAAAAGTATGTCGACGAAGTTGGCTACTGCGGACGACC 66
DB 93 CAAAACCTCGCGTTCGCTCCAAACCTCTGTTGCAGTCAGTTCCGTTACTGTTGTTACCGAC 152
QY 67 GACGAGTACTCGCGGACGGTGCAGTCGCGGCGCGCTCCGCTCGGCGCGGCGTGGCGGC 126
DB 153 GATGCATACTCGCGTGTGGATGCGCATCAGTCTCTGTA----- 192
QY 127 GCGCGCGCGCGGAGCGCGGAGCGAGTGGCGGTGCGAACGTGGCTTAATGTGTCAAC 186
DB 193 -----GAGGTAGTGGAAACCCCGACCGGAGGTCGCTCGGTAGCATTTGTGACA 239
QY 187 GACGGTTCTTCAACGGCATCAAGAACAGCGCGGAGCGGTTGGAGGGCAAGACTTC 246
DB 240 CAAGGTTTCTTTAAACAATATTTATCAACCAAGTGTGTAATGTTGCGCGGGAAGATTTC 299
QY 247 TACACCGCGAGCGGTTCTCGAGGCCATCGCGGTACCGCGCTTCGCGCATGGCGGC 306
DB 300 TACACCGGTGACTCTTTGTTAAACCGCTAATCTTTCCCAACTTTGCCAATCTGTT 359
QY 307 TCCGAGGTCGAGCGCAAGCGGAGATTGCCGCTTTCTTCGCGCAGCGCCACGCAAGAGACC 366
DB 360 AC-----CAGACGTGAATTTGCTACCATGTTTGTCTCACTTCACTCAGGAGACC 407
QY 367 GGGCATTTCTGTACTACGCGAGGTCAAC---AAGACCAAGCTACTGCGACCCGACC 423
DB 408 GGACATTTCTGTCTACATAGAAGATTAAACGAGCAACACGCTAACTACTGCGCAGGAGC 467
QY 424 AAGAGCGAGTGCCTGCGCGCGGAGAGTACTACGGCGCGGCGCGCTCGCAGATC 483
DB 468 AACACACATATCCATGTGCACCGGGAAGAGGCTACTTCGCTGCTGCTCGATCCACTA 527
QY 484 TCGTGGAACTACAACTACGCGGCCCGCGGAGGCGCATCGGCTTCGACGGGCTCGGGAC 543
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-456-262-37

528 TCATGGAACACAACTACGAGGCGGTGGTCAAAAGTCTCGGTCTTGACCTTCTACGCCAG 587
QY 544 CCGGCGAGGCGTGGCGCGGAGCGCGGTGGCGGTTCAAGGGCGGCTCTGGTTCTGATG 603
DB 588 CCGCAACTTGTGGGTAGCAACCAACTGTAGCTTTTCAAGTTCGGGTTTGTGGTTTGGATG 647
QY 604 AACAACTGTCACCGTGTGATGCGCGAGCGGCTTCGGCGCCACCATCAGGGCCATCAACGGC 663
DB 648 AATAGCGTAAGCGCGGTTCTGAACCAAGGGTTTGGAGCCACCATTAAGAGCTATTAAATGG- 706
QY 664 GCCCTCGAGTGCACACGGGAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGG 723
DB 707 --AATGGAATGTAACGGTGGTAAATTCGGGTGCACTCAACGCAAGGATTGGATACTATAGA 764
QY 724 CAGTACTGCGCGCAGCTCGGCGTGCACCGGCGCAACCACTCACCTCTGTA 774
DB 765 GACTATTGTGACAGCAGCTTGGTGGACCCCTGGTCTTAACCTTAGTTGCTAA 815

RESULT 15
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; Sequence 37, Application US/08456240
; Patent No. 5856154
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,240
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; APPLICATION NUMBER: US 07/305,566
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; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
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; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CSC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-456-240-37

Query Match 22.6%; Score 174.6; DB 2; Length 1079;
Best Local Similarity 56.5%; Pred. No. 5.2e-24;
Matches 436; Conservative 0; Mismatches 284; Indels 51; Gaps 4;

QY 7 CAGAACTGCGGTGCGCAAGCAAAAGTATGCTGCGAGCAAGTTTGGCTACTGCGGCAAGCACC 66
DB 93 CAAAACTGCGGTGCGCTCCAAACCTCTGTTGCGAGTCAGTTCCGGTTACTGTTGGTACCGAC 152
QY 67 GACGAGTACTGCGGCGAGCGGTGCGAGTCGCGGCCCGCTGCGCGCGCGGTGCGCGGC 126
DB 153 GATGCATACTGCGGTGTTGGATGCGCGATCAGGTCTCTGTA----- 192
QY 127 GCGCGCGCGCGGAGCGCGGAGGAGGAGTGGCGGTGCGAAGCTGCGTAAATGTTGCTACC 186
DB 193 -----GAGGTAGTGGAAACCCCGGAGGGTGGTGGTAGCAITGTTGACA 239
QY 187 GACGCGTTCTTTCAAGCGCATCAAGAACAGGCGGAGCGGTGCGAGGCGCAAGAACTTC 246
DB 240 CAAGGTTCTTTAACAATATTATCAACCAAGCTGGTAATGTTGCGCGGGAAGATTC 299
QY 247 TACACCGGAGCGGTCTCTGAGGCCATTCGCGCGGTACCCGCGGTTTCGCGCATGCGCGC 306
DB 300 TACACCGGTGACTCTTTGTTAAACCGCGCTAATCTTTCCCAACTTTGCCAATTTCTGTT 359
QY 307 TCCGAGGTCGAGCGCAAGCGGAGATTGCGCGCTTCTTTCGCGCAGCGCCAGCAGAGACC 366

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DB 360 AC-----CAGACGTGAATTTGCTACCATGTTTGTCTCATTTTCACTCACGAGACC 407
QY 367 GGGCAATTTCTGCTACATCAGCGAGGTCAAC---AAGAGCAACGGCTACTTGCAGCCCGACC 423
DB 408 GGACATTTCTGCTACATAGAGAGATTTAACGGAGCAACACCTAACTACTGCGCAGAGCAGC 467
QY 424 AAGAGGCAAGTGGCGGTGCGCGCGGCGAGAAAGTACTACGGGCGGCGCGCTGCAGATC 483
DB 468 AACACAAATACCCATGTGCAACCGGGAAGGCTACTTCGGTCTGGTCCGATCCAACTA 527
QY 484 TCGTGGAACTACAACTACGGGCCCGCGGAGGCGCATCGGCTTTCGAGCGGCTCGGGGAC 543
DB 528 TCATGGAACTACAACTACGGGAGCGGTGGTCAAAAGTCTCGGTCTTGACCTTCTACGCCAG 587
QY 544 CCCGGCAGGGTGGCGCGGAGCGCGGTGGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATG 603
DB 588 CCCGAACTTGTGGGTAGCAACCCCAACTGTAGCTTTTCAGGTGCGGTTTGTGGTGGATG 647
QY 604 AACCAAGTGCACCGTGTGATGCGCGGAGGCTTTCGGCGCCACCATCAGGCGCATCAACGCG 663
DB 648 AATAGCGTAAAGGCGCGTTCGAAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAAATGG- 706
QY 664 GCCCTCGAGTGCACCGGAAACAACCCCGCCCGAGATGAACGCGCGCTCGGCTACTACAGG 723
DB 707 --AATGGAAATGAACGGTGGTAATTCGGTGCACTCAACGCAAGGATTGGATATATAGA 764
QY 724 CAGTACTGCGCGCCAGCTGCGCGTGCACCCGCGGCAACAACTCACTGCTGA 774
DB 765 GACTATTGTGGACAGCTTGGTGTGGACCTTGGTCTTAACCTTAGTTGCTAA 815

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Search completed: May 23, 2005, 15:37:14  
Job time : 125.13 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:11:31 ; Search time 360.896 Seconds  
(without alignments)  
12695.850 Million cell updates/sec

Title: US-10-692-367-11

Perfect score: 774

Sequence: 1 tcgatgagaactcgcgctg.....gcaacaacctcaactgctga 774

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 16Dec04.\*

1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002as.\*

7: geneseqn2002bs.\*

8: geneseqn2003as.\*

9: geneseqn2003bs.\*

10: geneseqn2003cs.\*

11: geneseqn2003ds.\*

12: geneseqn2004as.\*

13: geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	774	100.0	774	13	AdS92627 Chitinase
2	761.2	98.3	774	13	AdS92645 Chitinase
3	759.6	98.1	774	13	AdS92649 Chitinase
4	727.6	94.0	774	13	AdS92687 Chitinase
5	714.8	92.4	774	13	AdS92661 Chitinase
6	711.6	91.9	774	13	AdS92639 Chitinase
7	710	91.7	774	13	AdS92675 Chitinase
8	706.8	91.3	774	13	AdS92653 Chitinase
9	706.8	91.3	774	13	AdS92677 Chitinase
10	703.6	90.9	774	13	AdS92681 Chitinase
11	702	90.7	774	13	AdS92679 Chitinase
12	692.4	89.5	774	13	AdS92663 Chitinase
13	692.4	89.5	774	13	AdS92689 Chitinase
14	690.8	89.3	840	11	AdJ12126 Maize cDN
15	686.8	88.7	765	13	AdS92683 Chitinase
16	686	88.6	774	13	AdS92699 Chitinase
17	682.8	88.2	774	13	AdS92623 Chitinase
18	680.4	87.9	753	13	AdS92659 Chitinase
19	678	87.6	780	13	AdS92691 Chitinase
20	677.2	87.5	765	13	AdS92641 Chitinase

21	676.4	87.4	780	13	AdS92655	Chitinase
22	674.8	87.2	771	13	AdS92657	Chitinase
23	674.6	87.2	777	13	AdS92631	Chitinase
24	669.4	86.5	777	13	AdS92619	Chitinase
25	662.8	85.6	753	13	AdS92697	Chitinase
26	659.6	85.2	753	13	AdS92667	Chitinase
27	658	85.0	753	13	AdS92651	Chitinase
28	653.2	84.4	753	13	AdS92685	Chitinase
29	648.4	83.8	753	13	AdS92671	Chitinase
30	647.8	83.7	1094	3	AAA96222	cDNA enco
31	646.8	83.6	753	13	AdS92647	Chitinase
32	646.8	83.6	753	13	AdS92693	Chitinase
33	645.6	83.4	750	13	AdS92695	Chitinase
34	645.2	83.4	753	13	AdS92673	Chitinase
35	638.8	82.5	753	13	AdS92637	Chitinase
36	637.2	82.3	753	13	AdS92665	Chitinase
37	635.6	82.1	753	13	AdS92669	Chitinase
38	630.8	81.5	753	13	AdS92643	Chitinase
39	600.2	77.5	756	13	AdS92621	Chitinase
40	598.6	77.3	756	13	AdS92629	Chitinase
41	597	77.1	756	13	AdS92625	Chitinase
42	495.6	64.0	636	9	ADA49298	Maize gen
43	495.6	64.0	636	12	ADJ44871	Plant cDN
44	465	60.1	843	8	ADA70140	Rice gene
45	465	60.1	843	11	ADJ11575	Rice DNA

## ALIGNMENTS

## RESULT 1

AdS92627  
ID AdS92627 standard; DNA; 774 BP.

XX AdS92627;

XX 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #5.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
XX Heterodera.

XX Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

XX 06-NOV-2002; 2002US-00290086.

XX 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

XX (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-PSDB; AdS92628.

XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.

XX Disclosure; SEQ ID NO 11; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The





QY 421 ACCAAGGCGAGTGGCGGTGCGCGCGGGGAGAACTACTACGGCGGGCGCGCGCGTGCAG 480  
 Db 421 ACCAAGGCGAGTGGCGGTGCGCGCGGGGAGAACTACTACGGCGGGCGCGCGCGTGCAG 480  
 QY 481 ATCTCGTGGAACTCAACTACGGGCGCGGGGAGGGGCATCGGCTTCGACGGGCTCGGG 540  
 Db 481 ATCTCGTGGAACTCAACTACGGGCGCGGGGAGGGGCATCGGCTTCGACGGGCTCGGG 540  
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 Db 541 GACCCCGGACGGGTGGCGGGAGCGCGGTGGTGGCTTCAAGGGCGGCGCTCTGGTTCTGG 600  
 QY 601 ATGAACACGTGACCGGTGATGTCGGCAGGGCTTCGGCGGCACATCAGGGCCATCAAC 660  
 Db 601 ATGAACACGTGACCGGTGATGTCGGCAGGGCTTCGGCGGCACATCAGGGCCATCAAC 660  
 QY 661 GCGCGCTTCGAGTCAACCGGAAACAACCCCGCCAGATGAACGGCGCGCTCGGTACTAC 720  
 Db 661 GCGCGCTTCGAGTGGGGGGAACAACCCCGCCAGATGAACGGCGCGCTCGGTACTAC 720  
 QY 721 AGGCAGTACTGCCCGCAGCTCGGCGTGCAGCCCGGGCAACACCTCACTGCTGA 774  
 Db 721 AAGCAGTACTGCCCGCAGCTCGGCGTGCAGCCCGGGCAACACCTCACTGCTGA 774

## RESULT 3

ADS92649  
 ID ADS92649 standard; DNA; 774 BP.

AC ADS92649;

DT 02-DEC-2004 (first entry)

DE Chitinase variant polynucleotide #14.

KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 Heterodera.

OS Synthetic.

FN WO2004037194-A2.

XX 06-MAY-2004.

PD 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420656P.

PR 06-NOV-2002; 2002US-00290086.

PR 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

PA (PTON-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-PSDB; ADS92650.

XX New chitinase polynucleotides and polypeptides, useful in producing

PT plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 33; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.

XX

SQ Sequence 774 BP; 138 A; 251 C; 278 G; 107 T; 0 U; 0 Other;  
 Query Match 98.1%; Score 759.6; DB 13; Length 774;  
 Best Local Similarity 98.8%; Pred. No. 3e-119;  
 Matches 765; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 TCAGTGCAGAACTGCGGCTGCCAGCCAAACGTATGCTGACGAAGTTTGGCTACTGCGGC 60  
 Db 1 TCAGTGCAGAACTGCGGCTGCCAGCCAAACGTATGCTGACGAAGTTTGGCTACTGCGGC 60  
 QY 61 ACAGACGACAGTACTGCGCGGACGGGTGCAGTCCGGGCCCGCTCCCGCTCGGGCGGGCGGT 120  
 Db 61 ACAGACGACAGTACTGCGCGGACGGGTGCAGTCCGGGCCCGCTCCCGCTCGGGCGGGCGGT 120  
 QY 121 GCGCGCGCGCGCGCGCGGAGCGCGGAGGAGTGGCGGTGCGAACTGCTGCTTAATGTG 180  
 Db 121 GCGCGCGCGCGCGCGCGGAGCGCGGAGGAGTGGCGGTGCGAACTGCTGCTTAATGTG 180  
 QY 181 GTCAACGACCGGTTCCTCAACGGGATCAAGAACAGGCCGGGAGCGGGTGGAGGGCAAG 240  
 Db 181 GTCAACGACCGGTTCCTCAACGGGATCAAGAACAGGCCGGGAGCGGGTGGAGGGCAAG 240  
 QY 241 AACTTCTACACCGGAGCGGTTCCTCGAGGCCATCGCCGGCTACCGGGCTTCGCGCAT 300  
 Db 241 AACTTCTACACCGGAGCGGTTCCTCGAGGCCATCGCCGGCTACCGGGCTTCGCGCAT 300  
 QY 301 GCGCGCTCCGAGGTTCGAGCGCAAGCGCGAGATTCGCGCCCTTCTTCGCGCACCGCACGCAC 360  
 Db 301 GCGCGCTCCGAGGTTCGAGCGCAAGCGCGAGATTCGCGCCCTTCTTCGCGCACCGCACGCAC 360  
 QY 361 GAGACCGGGCATTTCTGTACATCAGCGAGGTCAACAAGAGCAACGCTACTGCGACCCG 420  
 Db 361 GAGACCGGGCATTTCTGTACATCAGCGAGGTCAACAAGAGCAACGCTACTGCGACCCG 420  
 QY 421 ACCAAGAGGCGAGTGGCGCGCGGGGAGAGTACTACGGGGCGGCGCGCGCTGCGTGCAG 480  
 Db 421 ACCAAGAGGCGAGTGGCGCGCGGGGAGAGTACTACGGGGCGGCGCGCGCTGCGTGCAG 480  
 QY 481 ATCTCGTGGAACTACAACTACCGGCGCGGGGAGGCGCATCGGCTTCGACGGGCTCGGG 540  
 Db 481 ATCTCGTGGAACTACAACTACCGGCGCGGGGAGGCGCATCGGCTTCGACGGGCTCGGG 540  
 QY 541 GACCCCGGACGGGTGGCGGGAGCGCGGTGGTGGCTTCAAGGGCGGCGCTCTGGTTCTGG 600  
 Db 541 GACCCCGGACGGGTGGCGGGAGCGCGGTGGTGGCTTCAAGGGCGGCGCTCTGGTTCTGG 600  
 QY 601 ATGAACAACTGTCACCGTGTGATGCCGAGGGCTTCGGCGGCACCATCAGGGCCATCAAC 660  
 Db 601 ATGAACAACTGTCACCGTGTGATGCCGAGGGCTTCGGCGGCACCATCAGGGCCATCAAC 660  
 QY 661 GCGCGCTTCGAGTCAACCGGAAACAACCCCGCCAGATGAACGGCGCGCTCGGTACTAC 720  
 Db 661 GCGCGCTTCGAGTGGGGGGAACAACCCCGCCAGATGAACGGCGCGCTCGGTACTAC 720  
 QY 721 AGGCAGTACTGCCCGCAGCTCGGCGTGCAGCCCGGGCAACACCTCACTGCTGA 774  
 Db 721 AAGCAGTACTGCCCGCAGCTCGGCGTGCAGCCCGGGCAACACCTCACTGCTGA 774

## RESULT 4

ADS92687

ID ADS92687 standard; DNA; 774 BP.

XX ADS92687;

XX 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #33.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

XX Heterodera.

XX Synthetic.



Qy 1 TCGATGCAAGACTGGCTGCCAGCCAAACGATATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db |||||  
Qy 1 TCGATGCAAGACTGGCTGCCAGCCAAACGATATGCTGCAGCCGTTTGGCTACTGCGGC 60  
Db |||||  
Qy 61 ACACCCGACGAGTACTGGCGGAGCGGTTGCCAGTCCGAGTCCGCTCGCGGCGCGGT 120  
Db |||||  
Qy 61 ACACCCGACGAGTACTGGCGGAGCGGTTGCCAGTCCGAGTCCGCTCGCGGCGCGGT 120  
Db |||||  
Qy 121 GCGCGCGCGCGCGCGCGGAGCGGAGCGAGTGGCGGTGCGAACTGGCTAAATGTG 180  
Db |||||  
Qy 121 GCGCGCGCGCGCGCGGAGCGGAGCGAGTGGCGGTGCGAACTGGCTAAATGTG 180  
Db |||||  
Qy 181 GTCACCGACGCGTTCTTCAACGCGCATCAAGCAACGAGCCGCGGAGCGGTGCGAGGCAAG 240  
Db |||||  
Qy 181 GTCACCGACGCGTTCTTCAACGCGCATCAAGCAACGAGCCGCGGAGCGGTGCGAGGCAAG 240  
Db |||||  
Qy 241 AACTTCTACCCGCGCGCGGAGCGGAGCGGAGCGAGTGGCGGTGCGAACTGGCTAAATGTG 300  
Db |||||  
Qy 241 AACTTCTACCCGCGCGCGGAGCGGAGCGGAGCGAGTGGCGGTGCGAACTGGCTAAATGTG 300  
Db |||||  
Qy 301 GCGCGCTCCGAGGTGCGAGCGCAAGCGCGGAGTTGCGCGCTTCTTTCGCGCAGCCACGCGAC 360  
Db |||||  
Qy 301 GCGCGCTCCGAGGTGCGAGCGCAAGCGCGGAGTTGCGCGCTTCTTTCGCGCAGCCACGCGAC 360  
Db |||||  
Qy 361 GAGACCGGCGATTTCTGCTACATCAGCGGAGTCAACAGAGCAACGCGCTACTGCGACCG 420  
Db |||||  
Qy 421 ACCAAGAGCGAGTGGCGCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCGCTGCGAC 480  
Db |||||  
Qy 421 ACCAAGAGCGAGTGGCGCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCGCTGCGAC 480  
Db |||||  
Qy 481 ATCTCGTGAATCAACTACGCGCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCGCTGCG 540  
Db |||||  
Qy 481 ATCTCGTGAATCAACTACGCGCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCGCTGCG 540  
Db |||||  
Qy 541 GACCCCGCAACAGGTTGGCGCGGAGCGCGGTGCGGTTCAAGGCGCGCGCTCTGCTTCTG 600  
Db |||||  
Qy 541 GACCCCGCAACAGGTTGGCGCGGAGCGCGGTGCGGTTCAAGGCGCGCGCTCTGCTTCTG 600  
Db |||||  
Qy 601 ATGAACAGCGTCCGCGGTGATCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCGCTGCGAC 660  
Db |||||  
Qy 601 ATGAACAGCGTCCGCGGTGATCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCGCTGCGAC 660  
Db |||||  
Qy 661 GCGCGCTCCGAGTGCACGCGGAAACACCCCGCGCGAGTGAACGCGCGCGCTGCGCTACTAC 720  
Db |||||  
Qy 661 GCGCGCTCCGAGTGCACGCGGAAACACCCCGCGCGAGTGAACGCGCGCGCTGCGCTACTAC 720  
Db |||||  
Qy 721 AGGCGAGTACTCGCGCGAGTGGCGGTGCGACCGCGGAGCAACCTCACTGCTGA 774  
Db |||||  
Qy 721 AAGCAGTACTCGCGCGAGTGGCGGTGCGACCGCGGAGCAACCTCACTGCTGA 774  
Db |||||

RESULT 6

AD92639  
ID AD92639 standard; DNA; 774 BP.

XX AC AD92639;

XX AC AD92639;

DT 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #9.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
XX Heterodera.

OS Synthetic.

XX WO2004037194-A2.

XX PD 06-MAY-2004.

PP 22-OCT-2003; 2003WO-US033588.  
XX 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX Muller ML, True T, Simmons CR, Yalpani N;  
PI WPI; 2004-365417/34.  
DR P-PSDB; ADS92640.  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
PT Claim 4; SEQ ID NO 23; 197pp; English.  
XX The invention relates to chitinase polypeptides and the polynucleotides  
PS encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
SQ Sequence 774 BP; 146 A; 246 C; 271 G; 111 T; 0 U; 0 Other;

Query Match 91.9%; Score 711.6; DB 13; Length 774;  
Best Local Similarity 95.0%; Pred. No. 3.7e-111;  
Matches 735; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 TCGATGCAAGACTGGCTGCCAGCCAAACGATATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db |||||  
Qy 1 TCGATGCAAGACTGGCTGCCAGCCAAACGATATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db |||||  
Qy 61 ACACCCGACGAGTACTGGCGGAGCGGTTGCCAGTCCGAGTCCGCTCGCGGCGCGGT 120  
Db |||||  
Qy 61 ACACCCGACGAGTACTGGCGGAGCGGTTGCCAGTCCGAGTCCGCTCGCGGCGCGGT 120  
Db |||||  
Qy 121 GCGCGCGCGCGCGCGGAGCGGAGCGAGTGGCGGTGCGAACTGGCTAAATGTG 180  
Db |||||  
Qy 121 GCGCGCGCGCGCGGAGCGGAGCGAGTGGCGGTGCGAACTGGCTAAATGTG 180  
Db |||||  
Qy 181 GTCACCGACGCGTTCTTCAACGCGCATCAAGCAACGAGCCGCGGAGCGGTGCGAGGCAAG 240  
Db |||||  
Qy 181 GTCACCGACGCGTTCTTCAACGCGCATCAAGCAACGAGCCGCGGAGCGGTGCGAGGCAAG 240  
Db |||||  
Qy 241 AACTTCTACCCGCGCGCGGAGCGGAGCGGAGTGGCGGTGCGAACTGGCTAAATGTG 300  
Db |||||  
Qy 241 AACTTCTACCCGCGCGCGGAGCGGAGTGGCGGTGCGAACTGGCTAAATGTG 300  
Db |||||  
Qy 301 GCGCGCTCCGAGGTGCGAGCGCAAGCGCGGAGTTGCGCGCTTCTTTCGCGCAGCCACGCGAC 360  
Db |||||  
Qy 301 GCGCGCTCCGAGGTGCGAGCGCAAGCGCGGAGTTGCGCGCTTCTTTCGCGCAGCCACGCGAC 360  
Db |||||  
Qy 361 GAGACCGGCGATTTCTGCTACATCAGCGGAGTCAACAGAGCAACGCGCTACTGCGACCG 420  
Db |||||  
Qy 361 GAGACCGGCGATTTCTGCTACATCAGCGGAGTCAACAGAGCAACGCGCTACTGCGACCG 420  
Db |||||  
Qy 421 ACCAAGAGCGAGTGGCGCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCTGCGAC 480  
Db |||||  
Qy 421 ACCAAGAGCGAGTGGCGCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCTGCGAC 480  
Db |||||  
Qy 481 ATCTCGTGAATCAACTACGCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCTGCG 540  
Db |||||  
Qy 481 ATCTCGTGAATCAACTACGCGCGCGGAGCGGAGTACTACGCGCGCGCGCGCTGCG 540  
Db |||||  
Qy 541 GACCCCGCAACAGGTTGGCGCGGAGCGCGGTGCGGTTCAAGGCGCGCGCTCTGCTTCTG 600  
Db |||||

Db 541 GACCCGACAGACTGGCGCAGGACCCCGTGTGTGTTCAAGTCCGGCGCTCTGTTCTGG 600  
Qy 601 ATGAACAACGTGCAACCGTGTGATGCCGACGGGCTTCGGCGCCACCATCAAGGCGCATCAAC 660  
Db 601 ATGAACAACGTGCAACCGTGTGATGCCGACGGGCTTCGGCGCCACCATCAAGGCGCATCAAC 660  
Qy 661 GGGCCCTCGAGTGCACAGCGGAACACCCCGCCAGATGAACGCGCGGTGGCTACTAC 720  
Db 661 GGGCCCTCGAGTGCAGCGGGAACACCCCGCCAGATGAACGCGCGGTGGCTACTAC 720  
Qy 721 AGGCACTACTGCCCGAGCTCGGCGTGCAGCCCGGCAACCACTCACTGCTGA 774  
Db 721 AGGCACTACTGCCCGAGCTCGGCGTGCAGCCCGGCAACCACTCACTGCTGA 774

RESULT 7  
ADS92675  
ID ADS92675 standard; DNA; 771 BP.  
XX  
AC ADS92675;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #27.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
FN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
XX  
PI (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
DR P-PSDB; ADS92676.  
XX  
PT New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 4; SEQ ID NO 59; 197pp; English.  
XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX  
SQ Sequence 771 BP; 139 A; 247 C; 274 G; 111 T; 0 U; 0 Other;

Query Match 91.7%; Score 710; DB 13; Length 771;  
Best Local Similarity 95.7%; Pred. No. 6.9e-111;  
Matches 741; Conservative 0; Mismatches 30; Indels 3; Gaps 1;  
Qy 1 TCGATGCAACTGGCGGTGCCAGCAACGATGCTGCGAGCAAGTTGGCTACTGCGGC 60  
Db 1 TCGATGCAACTGGCGGTGCCAGCAACGATGCTGCGAGCAAGTTGGCTACTGCGGC 60

Qy 61 ACCACCGACGAGTACTGCGCGCAGCGGTGCCAGTCCGGGCCCGCTCGCGCGCGCGGT 120  
Db 61 ACCACCGACGCGCTACTGCGCGCAGCGGTGCCAGTCCGGGCCCGCTCGCGCGCGCGGT 120  
Qy 121 GCG 180  
Db 121 GCGCGCGCGTG- --GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 177  
Qy 181 GTACACGACGCGTCTTCTCAACGCGCATCAAGAACGAGCGCGGAGCGGTCGAGGGCAAG 240  
Db 178 GTACACGACGCGTCTTCTCAACGCGCATCAAGAACGAGCGCGGAGCGGTCGAGGGCAAG 237  
Qy 241 AACTTCTACACCGGAGCGGTTCTCTCGAGGCCATCGCCGCGTACCGCGGCTTCGCGCAT 300  
Db 238 AACTTCTACACCGGAGCGGTTCTCTCGAGGCCGCTCAAGCGGTACCCAGGCTTCGCCCAT 297  
Qy 301 GCGCGCTCCGAGTTCGAGCGCAAGCGCGAGATTGTCGCGCTTCTTCGCGCAAGCGCAC 360  
Db 298 GCGCGGTCAACGCTGCAAGGCAAGCGCGAGATTGTCGCGCTTCTTCGCGCATGTCACGCAC 357  
Qy 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAAAGAGCAACGCTACTGCGACCG 420  
Db 358 GAGACCGGCGCATTTCTGCTACATCAGCGAGATCAACAAAGAGCAACGCTACTGCGACCG 417  
Qy 421 ACCAAGAGGAGTGGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
Db 418 ACCAAGAGGAGTGGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 477  
Qy 481 ATCTCGTGGAACTACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Db 478 ATCTCGTGGAACTACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 537  
Qy 541 GACCCGCGAGGTTGGCG 600  
Db 538 GACCCGCGAGGTTGGCG 597  
Qy 601 ATGAACAACGTCACCGTGTGATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Db 598 ATGAACAACGTCACCGTGTGATGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 657  
Qy 661 GCGCGCTTCGAGTGCACCGGGAACACCCCGCCAGATGAACGCGCGCGCGCGCGCGCG 720  
Db 658 GCGCGCTTCGAGTGCACCGGGAACACCCCGCCAGATGAACGCGCGCGCGCGCGCGCG 717  
Qy 721 AGGCACTACTGCCCGAGCTCGGCGTGCAGCCCGGCAACCACTCACTGCTGA 774  
Db 718 AGGCACTACTGCCCGAGCTCGGCGTGCAGCCCGGCAACCACTCACTGCTGA 771

RESULT 8  
ADS92653  
ID ADS92653 standard; DNA; 774 BP.  
XX  
AC ADS92653;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #16.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
FN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.





Db 118 GCGCGCGTGGCGCGCGAGGCGGAGGCGAGTGGCGGTGGAACGTGGCTAGCGTC 177  
Qy 181 GTACCCACGCGTTCTTCAACCGCATCAAGAACAGCCGCGGAGCGGGTGCAGGCGAAG 240  
Db 178 GTCACCGGCTCTTCTTCAACCGCATCAAGAACAGCCGCGGAGCGGGTGCAGGCGAAG 237  
Qy 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCCGCGTACCGGGCTTCGCGCAT 300  
Db 238 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCCGCGTACCGGGCTTCGCGCAT 297  
Qy 301 GCGCGCTCCGAGGTCGAGCGCAAGCGGAGATTCCCGCTTCTTTCGCGCAGCCACGCGAC 360  
Db 298 GCGCGCTCCGAGGTCGAGCGCAAGCGGAGATTCCCGCTTCTTTCGCGCAGCCACGCGAC 357  
Qy 361 GAGACCGGCGCATTTCTGTATCATCAGCGAGGTCAACAGAGCAACGCTACTTCGACCCG 420  
Db 358 GAGACCGGCGCATTTCTGTATCATCAACGAGATCAACAGAGCAACGCTACTTCGACCCG 417  
Qy 421 ACCAAGGCGAGTGGCGCGCGCGGCGGAGGAGTACTACGGCGGCGGCGCGCTGCAG 480  
Db 418 ACCAAGGCGAGTGGCGCGCGCGGCGGAGGAGTACTACGGCGGCGGCGCGCTGCAG 477  
Qy 481 ATCTCTGGAACTACAACTACGCGCCCGCGGAGGCGCATCGGCTTCGACGGCTCGCG 540  
Db 478 ATCTCTGGAACTACAACTACGCGCCCGCGGAGGCGCATCGGCTTCGACGGCTCGCG 537  
Qy 541 GACCCCGCAGGGTGGCGCGGAGCGCGCTGTGTGCGTTCGAGCGGCGCTTCGTTCTGG 600  
Db 538 GACCCCGCAGGGTGGCGCGGAGCGCGCTGTGTGCGTTCGAGCGGCGCTTCGTTCTGG 597  
Qy 601 ATGAACAACGTGCACCGTGTGATGCGCGCAGGCGCTTCGCGCGCACCATCAGGCGCATCAAC 660  
Db 598 ATGAACAACGTGCACCGTGTGATGCGCGCAGGCGCTTCGCGCGCACCATCAGGCGCATCAAC 657  
Qy 661 GCGCGCTTCGAGTGCACCGGAAACAAACCCCGCCAGATGAACGCGCGCTTCGCGCGCACCATCAGGCGCATCAAC 720  
Db 658 GCGCGCTTCGAGTGCAGGCGGAGAAACAAACCCCGCCAGATGAACGCGCGCTTCGCGCGCACCATCAGGCGCATCAAC 717  
Qy 721 AGGAGATATCCCGCAGCTCGGCGTGCACCGGCGCAACCCGCGCGCAACCTCACTCTGCTGA 774  
Db 718 AAGCAGTACTCGCGCAGCTCGGCGTGCACCGGCGCAACCTCACTCTGCTGA 771

RESULT 10  
ADS92681  
ID ADS92681 standard; DNA; 774 BP.  
XX  
AC ADS92681;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #30.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
XX (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.  
DR P-PSDB; ADS92682.  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
XX Claim 4; SEQ ID NO 65; 197pp; English.  
XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX  
SQ Sequence 774 BP; 142 A; 250 C; 272 G; 110 T; 0 U; 0 Other;  
Query Match 91.3%; Score 706.8; DB 13; Length 774;  
Best Local Similarity 94.6%; Pred. No. 2.4e-110;  
Matches 732; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
Qy 1 TCGATGCGAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Db 1 TCGATGCGAGAACTGCGGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
Qy 61 ACAGACCGACGAGTACTGCGGCGAGCGGTGCCAGTCCGCGCCCGTCCGCGCGCGGT 120  
Db 61 ACAGACCGACGAGTACTGCGGCGAGCGGTGCCAGTCCGCGCCCGTCCGCGCGCGGT 120  
Qy 121 GCG 180  
Db 121 GCG 180  
Qy 181 GTACCCGACGCTCTTCTTCAACCGCATCAAGAACCGAGCGCGGTTCGCGCGCGCGCG 240  
Db 181 GTACCCGACGCTCTTCTTCAACCGCATCAAGAACCGAGCGCGGTTCGCGCGCGCGCG 240  
Qy 241 AACTTCTACACCGGAGCGGCTTCTTCGAGGCGCATCGCCGCGTACCGGCGGTTCGCGCAT 300  
Db 241 AACTTCTACACCGGAGCGGCTTCTTCGAGGCGCGGTTCGAGGCGGTTCGCGCAT 300  
Qy 301 GCGCGCTCCGAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
Db 301 GCGCGGTTCGAGGTCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
Qy 361 GAGACCGGCGCATTTCTGTATCATCAGCGAGGTCAACAGAGCAACGCTACTTCGCGACCCG 420  
Db 361 GAGACCGGCGCATTTCTGTATCATCAGCGAGGTCAACAGAGCAACGCTACTTCGCGACCCG 420  
Qy 421 ACCAAGGCGAGTGGCG 480  
Db 421 ACCAAGGCGAGTGGCG 480  
Qy 481 ATCTCTGGAACTACAACTACGCGCCCGCGGAGGCGCATCGGCTTCGAGCGCGCTCGCG 540  
Db 481 ATCTCTGGAACTACAACTACGCGCCCGCGGAGGCGCATCGGCTTCGAGCGCGCTCGCG 540  
Qy 541 GACCCCGCAGGGTGGCG 600  
Db 541 GACCCCGCAGGGTGGCG 600  
Qy 601 ATGAACAACGTCGACCGTGTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Db 601 ATGAACAACGTCGACCGTGTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
Qy 661 GCGCGCTTCGAGTGCACCGGAAACAAACCCCGCCAGATGAACGCGCGCGGTTCGCGCTAC 720  
Db 661 GCGCGCTTCGAGTGCACCGGAAACAAACCCCGCCAGATGAACGCGCGCGGTTCGCGCTAC 720



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Qy 721 AGCAGTACTGCGCCAGCTCGCGTCGACCCGGGCAACAACCTCACTGCTGA 774
Db 721 AAGCAGTACTGCGCCAGCTCGCGTCGACCCGGGCAACAACCTCACTGCTGA 774

RESULT 11
AD92679
ID ADS92679 standard; DNA; 774 BP.
XX
AC ADS92679;
XX
XX 02-DEC-2004 (first entry)
XX
XX Chitinase variant polynucleotide #29.
XX
XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
XX Synthetic.
XX
XX WO2004037194-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033588.
XX
XX 22-OCT-2002; 2002US-0420666P.
XX
XX 06-NOV-2002; 2002US-00290086.
XX
XX 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Muller ML, True T, Simmons CR, Yalpani N;
XX
XX WPI; 2004-365417/34.
XX
XX P-PSDB; ADS92680.
XX

New chitinase polynucleotides and polypeptides, useful in producing
plants with enhanced resistance against a fungus or a nematode.

Claim 4; SEQ ID NO 63; 197pp; English.

The invention relates to chitinase polypeptides and the polynucleotides
encoding them. A method of enhancing plant resistance to a fungus or
nematode comprises introducing into a plant a recombinant expression
cassette comprising a promoter operably linked to a chitinase
polynucleotide of the invention. The plant is maize or soybean. The
fungus is from the genus Fusarium. The nematode is from the genus
Heterodera. The polynucleotides and polypeptides are useful in enhancing
plant resistance to a fungus or nematode. This sequence represents a
chitinase variant polynucleotide of the invention.

XX
XX Sequence 774 BP; 144 A; 256 C; 269 G; 105 T; 0 U; 0 Other;

Query Match 90.9%; Score 703.6; DB 13; Length 774;
Best Local Similarity 94.3%; Pred. No. 8.3e-110;
Matches 730; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 1 TCGATGACAGAACTCGCGCTGCAGCCAAACCTATGCTGCAGCAAGTTTGCTACTGCGGC 60
Db 1 TCGATGACAGAACTCGCGCTGCAGCCAAACCTATGCTGCAGCAAGTTTGCTACTGCGGC 60
Qy 61 ACACACGACAGTACTCGCGGACGGGTGCCAGTCCGGCCCGTCCCGCTCGGGCGCGGT 120
Db 61 ACACACGACAGTACTCGCGGACGGGTGCCAGTCCGGCCCGTCCCGCTCGGGCGCGGC 120
Qy 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 181 GTCAACGACGCGTTCTTCAACGGCATCAAGAACCCAGCGCGCGCGCGCGCGCGCGCG 240

```

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Db 181 GTCAACGACGCGTTCTTCAACGGCATCAAGAACCCAGCGCGCGCGCGCGCGCGCGCG 240
Qy 241 AACTTCTACACCCGGAGCGGTTCTCTCGAGGCCATCGCCCGGTACCCGGGCTTCGCGCAT 300
Db 241 AACTTCTACACCCGGAGCGGTTCTCTCGAGGCCATCGCCCGGTACCCGGGCTTCGCGCAT 300
Qy 301 GCGGCTCCGAGTTCGAGCGCGAGATTCGCGGCTTCGCGGCGCGCGCGCGCGCGCGCG 360
Db 301 GCGGCTTCACAGGTGCGAGGCCAAGCGCGAGATTCGCGGCTTCGCGGCGCGCGCGCG 360
Qy 361 GAGACCGGGCATTTCTCTACATCAGCGAGGTCAACAAGAGCAACGCTTACTGCGACCGG 420
Db 361 GAGACCGGGCATTTCTCTACATCAGCGAGATCAACAAGAGCAACGCTTACTGCGACCGG 420
Qy 421 ACCAAGAGCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db 421 ACCAAGAGCAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Qy 481 ATCTCGTGGAACTACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db 481 CTGTGTGGAACTACAACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Qy 541 GACCCCGGCGAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 541 GACCCCGGCGAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Qy 601 ATGAACAACTGTCACCGTGTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 601 ATGAACAACTGTCACCGTGTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Qy 661 GCGCGCTTCAGTGCAGCGGAAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db 661 GCGCGCTTCAGTGCAGCGGAAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Qy 721 AGCAGTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 774
Db 721 AAGCAGTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 774

RESULT 12
AD92663
ID ADS92663 standard; DNA; 771 BP.
XX
XX ADS92663;
XX
XX 02-DEC-2004 (first entry)
XX
XX Chitinase variant polynucleotide #21.
XX
XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
XX Synthetic.
XX
XX WO2004037194-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033588.
XX
XX 22-OCT-2002; 2002US-0420666P.
XX
XX 06-NOV-2002; 2002US-00290086.
XX
XX 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Muller ML, True T, Simmons CR, Yalpani N;
XX
XX WPI; 2004-365417/34.
XX
XX P-PSDB; ADS92664.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing

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PT	plants with enhanced resistance against a fungus or a nematode.
XX	Claim 4; SEQ ID NO 47; 197pp; English.
XX	The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.
XX	Sequence 771 BP; 137 A; 251 C; 277 G; 106 T; 0 U; 0 Other;
SQ	
Query Match	90.7%; Score 702; DB 13; Length 771;
Best Local Similarity	95.1%; Pred. No. 1.5e-109;
Matches 736; Conservative	0; Mismatches 35; Indels 3; Gaps 1;
Qy	1 TCGATGCAGAACTCGCGCTGCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Db	1 TCGATGCAGAACTCGCGCTGCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
Qy	61 ACGACCGACGAGTACTCGGCGACGGGTGCCAGTCCGGCCCGTCCGCGCGCGGT 120
Db	61 ACGACCGACGAGTACTCGGCGACGGGTGCCAGTCCGGCCCGTCCGCGCGCGGT 117
Qy	121 GCGCGCGCGCGCGCGCGCGCGCGCGAGTGCAGTCCGCTGCAGCAAGTTTGGCTACTGTCG 180
Db	118 GCGCGCGCGCGCGCGCGCGCGCGAGTGCAGTCCGCTGCAGCAAGTTTGGCTACTGTCG 177
Qy	181 GTCAACCGACGCTTCTTCAACCGCATCAAGAACCAAGCCAGCGCGGTGCAGGGCAAG 240
Db	178 GTCAACCGACGCTTCTTCAACCGCATCAAGAACCAAGCCAGCGCGGTGCAGGGCAAG 237
Qy	241 AACTTCTACACCGCGAGCGCGTTCCTCGAGGCCATCGCGCGTACCCAGGCTTCCGCCAT 300
Db	238 AACTTCTACACCGCGAGCGCGTTCCTCGAGGCCATCGCGCGTACCCAGGCTTCCGCCAT 297
Qy	301 GCGCGCTCCGAGGTGCAGCGCAAGCGCGAGATTCGCGCTTCTTTCGCGCAGCCACGCGAC 360
Db	298 GCGCGGTCAAGGTGCAGCGCAAGCGCGAGATTCGCGCTTCTTTCGCGCAGTGCAGCGAC 357
Qy	361 GAGACCGCGCATTTCTGTATCATAGCAGGTTCACAGAGCAACGCTTACTGCGACCGC 420
Db	358 GAGACCGCGCATTTCTCGCTACATCAGCGAGGTTCACAGAGCAACGCTTACTGCGACCGC 417
Qy	421 ACCAGAGGCGAGTGGCGGTGCGCGCGCGCGAGTACTACGCGCGCGCGCGCGCGCGCG 480
Db	418 ACCAGAGGCGAGTGGCGGTGCGCGCGCGCGAGTACTACGCGCGCGCGCGCGCGCGCG 477
Qy	481 ATCTCGTGAACCTACAACTACGCGCGCGCGCGAGGCGCATCGGCTTCGACGGGTCTCGGG 540
Db	478 ATCTCGTGAACCTACAACTACGCGCGCGCGAGGCGCATCGGCTTCGACGGGTCTCGGG 537
Qy	541 GACCCCGCAGGGTGGCGCGGACCGCGTGTGGCGTTCAAGGGCGCGCTCTGTGTTCTGG 600
Db	538 GACCCCGCAGGGTGGCGCGGACCGCGTGTGGCGTTCAAGGGCGCGCTCTGTGTTCTGG 597
Qy	601 ATGACACGTCGACCGGTGTATGCGCGAGGCTTCGCGCGCGCGCGCGCGCGCGCGCATCAAC 660
Db	598 ATGACACGTCGACCGGTGTATGCGCGAGGCTTCGCGCGCGCGCGCGCGCGCGCGCATCAAC 657
Qy	661 GCGCGCTTCGAGTGCAGCGGAACACCCCGCGCAGATGAACGCGCGGTTCGGCTACTTAC 720
Db	658 GCGCGCTTCGAGTGCAGCGGAACACCCCGCGCAGATGAACGCGCGGTTCGGCTACTTAC 717
Qy	721 AGGCGAGTACTCGCGCGAGTTCGGCGTTCGACCGCGCGCAACACCTTCACTTGTGA 774
Db	718 AGGCGAGTACTCGCGCGAGTTCGGCGTTCGACCGCGCGCAACACCTTCACTTGTGA 771





Result No.	Score	Query #			DB	ID	Description
		Match	Length	Time			
1	687	88.8	843	6	MZECHTTA	M84164	Zea mays ch
2	647.8	83.7	1094	8	AR321624	AR321624	Sequence
3	637.8	82.4	810	8	MZECRIIB	M84165	Zea mays ch
4	581.8	75.2	1094	8	AY532775	AY532775	Zea mays
5	562	72.6	1115	8	AY532768	AY532768	Zea mays
6	558.4 <sup>4</sup>	72.2	1101	8	AY532770	AY532770	Zea mays
7	554.4 <sup>4</sup>	71.6	1128	8	AY532740	AY532740	Zea diplo
8	552.4	71.4	1094	8	AY532778	AY532778	Zea mays
9	552.4	71.4	1094	8	AY532779	AY532779	Zea mays
10	550.8	71.2	1118	8	AY532773	AY532773	Zea mays
11	548.4	70.9	1107	8	AY532781	AY532781	Zea diplo
12	548.4	70.9	1110	8	AY532783	AY532783	Zea diplo
13	548.4	70.9	1110	8	AY532784	AY532784	Zea diplo
14	548.4	70.9	1110	8	AY532785	AY532785	Zea diplo
15	548.4	70.9	1110	8	AY532786	AY532786	Zea diplo
16	548.4	70.9	1110	8	AY532787	AY532787	Zea diplo
17	548.4	70.9	1110	8	AY532788	AY532788	Zea diplo
18	546.6	70.6	1132	8	AY532774	AY532774	Zea mays
19	541.2	69.9	1131	8	AY532780	AY532780	Zea mays

FEATURES	source
	Location/Qualifiers
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	/tissue_type="seed"
	/tissue_lib="lamda GT 10 corn seed (imbibed)"
Gene	1..843
	/gene="seed chitinase"

[illegible]

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NLIC"

ORIGIN  
Query Match 88.8%; Score 687; DB 8; Length 843;  
Best Local Similarity 93.5%; Pred. No. 1.1e-79;  
Matches 717; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 6 GCAGAACTGCGGTCGCGGCAAACTGATGTCGAGCAAGTTTGGCTACTGCGGACGAC 65  
Db 75 GCAGAACTGCGGTCGCGGCAAACTTCTGCTGCGAGCAAGTTTGGCTACTGCGGACGAC 134  
Qy 66 CGACGAGTACTGCGGCGAGCGGTCGAGTCGCGGCGGTCGCGGCGGTCGCGGCGG 125  
Db 135 CGACGCTTACTGCGGCGAGCGGTCGAGTCGCGGCGGTCGCGGCGGTCGCGGCGG 194  
Qy 126 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185  
Db 195 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 254  
Qy 186 CGACGCTTCTTCAACGCGATCAAGAACACGCGGCGGAGCGGTCGCGGCGGCAAGAACTT 245  
Db 255 CGACGCTTCTTCAACGCGATCAAGAACACGCGGCGGAGCGGTCGCGGCGGCAAGAACTT 314  
Qy 246 CTACACCGGAGCGGCTTCTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 305  
Db 315 CTACACCGGAGCGGCTTCTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 374  
Qy 306 CTCGAGGTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 365  
Db 375 GACGAGGTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 434  
Qy 366 CGGCGATTTCTGTACATCAGCGAGGTCAACAAGAGCAAGCGCTACTGCGACCGGACAA 425  
Db 435 CGGCAATTTCTGTACATCAGCGAGATCAACAAGAGCAAGCGCTACTGCGACCGGAGCA 494  
Qy 426 GAGCGAGTGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 485  
Db 495 CAGGCGAGTGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 554  
Qy 486 GTGGAACTTCAACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 545  
Db 555 GTGGAACTTCAACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 614  
Qy 546 CGGCGAGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 605  
Db 615 CAACAGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 674  
Qy 606 CAACGTGCAACCGTGTGATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 665  
Db 675 CAACGTGCAACCGTGTGATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 734  
Qy 666 CTTGAGTGCAACGCGGCAACACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 725  
Db 735 CTTGAGTGCAACGCGGCAACACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 794  
Qy 726 GTACTGCGGCGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 772  
Db 795 GTACTGCGGCGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 841

RESULT 2  
AR321624  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

Sequence 1 from patent US 6563020.  
AR321624  
AR321624.1 GI:33706864  
Unknown.  
Unclassified.  
1 (bases 1 to 1094)  
Simmons, C.R. and Valpani, N.

TITLE  
JOURNAL  
FEATURES  
source  
ORIGIN

Maize chitinases and their use in enhancing disease resistance in crop plants  
Patent: US 6563020-A 1 13-MAY-2003;  
Location/Qualifiers  
1. 1094  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 83.7%; Score 647.8; DB 6; Length 1094;  
Best Local Similarity 91.8%; Pred. No. 1.2e-74;  
Matches 704; Conservative 0; Mismatches 42; Indels 21; Gaps 1;

Qy 6 GCAGAACTGCGGTCGCGGCAAACTGATGTCGAGCAAGTTTGGCTACTGCGGACGAC 65  
Db 149 GCAGAACTGCGGTCGCGGCAAACTGATGTCGAGCAAGTTTGGCTACTGCGGACGAC 208  
Qy 66 CGACGAGTACTGCGGCGAGCGGTCGAGTCGCGGCGGTCGCGGCGGTCGCGGCGG 125  
Db 209 CGACGAGTACTGCGGCGAGCGGTCGAGTCGCGGCGGTCGCGGCGGTCGCGGCGG 268  
Qy 126 CGGCGGCGGCGGCGGAGCGGCGGAGGCAAGTCGCGGTCGCGAACTGTGCTTAATGTGTCAC 185  
Db 269 CAGTGGCGGC-----GGTGGTGGCAACGTCGCTAGCGCTGCTGCTAC 307  
Qy 186 CGACGCTTCTTCAACGCGATCAAGAACACGCGGCGGAGCGGTCGCGGCGGCAAGAACTT 245  
Db 308 CGGCTCTTCTTCAACGCGATCAAGAACACGCGGCGGAGCGGTCGCGGCGGCAAGAACTT 367  
Qy 246 CTACACCGGAGCGGCTTCTCGAGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGG 305  
Db 368 CTACACCGGAGCGGCTTCTCGAGGCGGTCGCGGCGGTCGCGGCGGTCGCGGCGG 427  
Qy 306 CTCGAGGTCGAGCGGCAAGCGCGAGATTGCGGCTTCTTTCGCGACCGCGGCGGCGG 365  
Db 428 GTGCGAGTGTGCGGCGGCAAGCGCGAGATCGCGGCTTCTTTCGCGCAAGCGGCGG 487  
Qy 366 CGGCGATTTCTGTACTACATCAGCGAGGTCAACAAGAGCAAGCGCTACTGCGACCGGACAA 425  
Db 488 CGGCGATTTCTGTACTACATCAGCGAGATCAACAAGAGCAAGCGCTACTGCGACCGGACAA 547  
Qy 426 GAGCGAGTGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 485  
Db 548 GAGCGAGTGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 607  
Qy 486 GTGGAATCAACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 545  
Db 608 GTGGAATCAACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 667  
Qy 546 CGGCGAGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 605  
Db 668 CGGCGAGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 727  
Qy 606 CAACGTGCAACCGTGTGATGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 665  
Db 728 CAGGTCGACGCGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 787  
Qy 666 CTTGAGTGCAACGCGGCAACACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 725  
Db 788 CTTGAGTGCAACGCGGCAACACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847  
Qy 726 GTACTGCGGCGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 772  
Db 848 GTACTGCGGCGGCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 894

RESULT 3  
MZECHITB  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS

MZECHITB  
Zea mays chitinase B (seed chitinase) gene, 3' end.  
M84165  
M84165.1 GI:168442  
chitinase B.





Query Match		75.2%; Score 581.8; DB 8; Length 1094;
Best Local Similarity		83.2%; Pred. No. 3.9e-66;
Matches		715; Conservative 0; Mismatches 52; Indels 92; Gaps 1;
QY	6	GCAGAACTCGGGCTGCCAGCCAAACGATGCTGCAGCAAGTTTGGCTACTTGGCGCAGCAC 65
DB	98	GCAGAACTCGGGCTGCCAGCCAAACGATGCTGCAGCAAGTTTGGCTACTTGGCGCAGCAC 157
QY	66	CGACGAGTACTTGGCGGCGAGCGGGTGCAGTTCGGGCGCCGTCGCGCTCGGGCGCGCGTGGCGG 125
DB	158	CGACGCTACTTGGCGGCGAGCGGGTGCAGTTCGGGCGCCGTCGCGCTCGGGCGCGCGTGGCGG 217
QY	126	CGGCGGCGCGCGCGGCGAGCGCGAGGAGTGGCGGTGCGAACCTGCTTAATGTGGTCAC 185
DB	218	CGGCGGCGCGCGCGGCGAGCGCGAGGAGTGGCGGTGCGAACCTGCTTAATGTGGTCAC 277
QY	186	CGACGCGTTCCTCAACGGCATCAAGAACCGAGCGCGGCGGGTGCAGGGCGCAAGAACTT 245
DB	278	CGACGCGTTCCTCAACGGCATCAAGAACCGAGCGCGGCGGGTGCAGGGCGCAAGAACTT 337
QY	246	CTACACCGGAGCGCGTTCCTCGAGGCGCATCGCCGCTTACCCGGCTTCGCGCATGCGGG 305
DB	338	CTACACCGGAGCGCGTTCCTCGAGGCGCATCGCCGCTTACCCGGCTTCGCGCATGCGGG 397
QY	306	CTCCGAGGTTCGAGCGGAGCGGAGTTCGCGCTTCTTCGCGCACGCCACGCGCAGGAGAC 365
DB	398	GACGAGGTTCGAGCGGAGCGGAGTTCGCGCTTCTTCGCGCACGCCACGCGCAGGAGAC 457
QY	366	CGGGC----- 370
DB	458	CGGAGCTAAGTTATTACACCTAAGTACGATGACGAGGACCTTTGATCTGAGCGACG 517
QY	371	-----ATTTCTGCTACATCAGCGAGTTC 393
DB	518	ATCATCGTTCGCTGACCATGATTTTCGATCAGATTTCTGCTACATCAGCGAGATC 577
QY	394	AACAGAGCAAGCTTACTGCGACCCGACCAAGAGGAGTGGCGTTCGCGCGCGGCGAG 453
DB	578	AACAGAGCAAGCTTACTGCGACCCGACCAAGAGGAGTGGCGTTCGCGCGCGGCGAG 637
QY	454	AAGTACTACGGCGCGGCGCTGCGAGATCTCTGCGAATCACTACGCGGCGCGCGGG 513
DB	638	AAATACTACGGCGCGGCGCTGCGAGATCTCTGCGAATCACTACGCGGCGCGCGGG 697
QY	514	AGGGCCATTCGGCTTCGACGCGGCTCGGGACCCCGCGCAGGTGGCGCGGAGCGCGTGGTG 573
DB	698	AGGACATTCGGCTTCGACGCGGCTCGCGACCCCGCAACAGGGTGGCGCAGGACGCGGTGATC 757
QY	574	CGGTTCAAGCGGCGGCTCTGGTTCTGGATGAACACGTCGACCGTGTGATGCGCGAGGGC 633
DB	758	CGGTTCAAGCGGCGGCTCTGGTTCTGGATGAACACGTCGACCGTGTGATGCGCGAGGGC 817
QY	634	TTCCGCGCCACCATCAGGGCCATCAACCGCGCCCTTCGAGTGCACCGGAAACAACCCGCC 693
DB	818	TTCCGCGCCACCATCAGGGCCATCAACCGCGCCCTTCGAGTGCACCGGAAACAACCCGCC 877
QY	694	CAGATGAACGCGCGCTTCGCTTACTACAGGCGAGTACTGCGCGCAGCTCGGCGTGCACCG 753
DB	878	CAGATGAACGCGCGCTTCGCTTACTACAGGCGAGTACTGCGCGCAGCTCGGCGTGCACCG 937
QY	754	GGCAACAACTCACCCTGCT 772
DB	938	GGCCCAACTCACCCTGCT 956

RESULT 5  
AY532768  
LOCUS  
DEFINITION  
Zea mays subsp. parviglumis isolate pl chitinase (ch1A) gene,  
complete cds.  
ACCESSION  
AY532768  
VERSION  
AY532768.1  
KEYWORDS  
1115 bp DNA linear PLN 29-JUL-2004

SOURCE		Zea mays subsp. parviglumis
ORGANISM		Zea mays subsp. parviglumis
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE		1 (bases 1 to 1115)
AUTHORS		Tiffin, P.
TITLE		Comparative evolutionary histories of chitinase genes in the genus
JOURNAL		Genetics 167 (3), 1331-1340 (2004)
PUBMED		15280246
REFERENCE		2 (bases 1 to 1115)
AUTHORS		Tiffin, P.
TITLE		Direct Submission
JOURNAL		Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
FEATURES		Location/Qualifiers
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ORIGIN		
Query Match		72.6%; Score 562; DB 8; Length 1115;
Best Local Similarity		82.7%; Pred. No. 1.4e-63;
Matches		711; Conservative 0; Mismatches 50; Indels 99; Gaps 2;
QY	6	GCAGAACTCGGGCTGCCAGCCAAACGTAATGCTGAGCAAGTTTGGCTACTTGGCGCAGCAC 65
DB	98	GCAGAACTCGGGCTGCCAGCCAAACGTAATGCTGAGCAAGTTTGGCTACTTGGCGCAGCAC 157
QY	66	CGACGAGTACTTGGCGGCGAGCGGTCAGTTCGGGCGCCGTCGCGCTCGGGCGCGGTGGCGG 125
DB	158	CGACGCTACTTGGCGGCGAGCGGTGCCAGTTCGGGCGCCGTCGCGCTCGGGCGCGGTGGCGG 217
QY	126	CGGCGGCGCGCGCGGAGCGCGGAGGCGAGTGGCGGTGCGAACCTGTCGCTAAATGTGGTCAC 185
DB	218	CGGCACTGGCGCGGAGGCGG-----CAGTGGCGGTGCGAACCTGTCGCTAACTGGTTCAC 271
QY	186	CGACGCGTTCCTCAACGGCATCAAGAACCGAGCGCGGAGCGGGTTCGAGGGCGCAAGAACTT 245
DB	272	CGACGCGTTCCTCAACGGCATCAAGAACCGAGCGCGGAGCGGGTTCGAGGGCGCAAGAACTT 331
QY	246	CTACACCGGAGCGCGTTCCTCGAGGCGATCGCGCGTACCCGGGCTTCGCGCATGGCGG 305
DB	332	CTACACCGGAGCGCGTTCCTCGAGGCGGTTCCTGAGCGCGTCAACGCGTACCCGGGCTTCGCGCATGGCGG 391
QY	306	CTCCGAGGTTCGAGCGGAGCGCGAGATTCGCGCTTCTTCGCGCACGCCACGCGCAGGAGAC 365
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QY	366	CGGGC----- 370





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ASNRQWPCAGQKYKYGRLQISWNTYGPAGRDIFGNGLADPNRVAQDAVIAFKTAL
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TC"
ORIGIN
Query Match 71.4%; Score 552.4; DB 8; Length 1094;
Best Local Similarity 82.0%; Pred. No. 2.4e-62;
Matches 707; Conservative 0; Mismatches 51; Indels 104; Gaps 2;
Qy 6 GCAGAACTGCGGCTGCCAGCCAAACGATGTCGAGCAAGTTTCGGCTACTGCGGCACGAC 65
Db 101 GCAGAACTGCGGCTGCCAGCTTAATCTGCTGAGCAGATTCGGCTACTGCGGCACGAC 160
Qy 66 CGACGAGTACTGCGGCGAGCGGTGCCAGTCCGAGTCCGCGCCGCTGCGGCGCGGTGCGG 125
Db 161 CGACGAGTACTGCGGCGAGCGGTGCCAGTCCGCGCCGCTGCGGCTCG-----GGCGG 211
Qy 126 CGCGCGGCGGCGGAGCGCGGAGCGAGTGGCGGTGCGAGTGGCGTCCGAACTGCTAATGTGTCAC 185
Db 212 CGCGCGGCGGCGGAGCGGAGCGAGCGAGTGGCGGTGCGAACTGCTAATGTGTCAC 271
Qy 186 CGACGCGTCTTCAACGGCATCAAGAACACGAGCGCGGAGCGGCTGCGAGGCGCAAGAACTT 245
Db 272 CGACGCGTCTTCAACGGCATCAAGAACACGAGCGCGGAGCGGCTGCGAGGCGCAAGAACTT 331
Qy 246 CTACACCGGAGCGGTTCTCGAGGCGCATGCGCGCGTACCGCGGCTTCGCGCATGCGCG 305
Db 332 CTACACCGGAGCGGTTCTCGAGGCGCGTCAACAGTACCGCGGCTTCGCGCATGCGCG 391
Qy 306 CTCCGAGTTCGAGCGGCGAGCGGAGTGGCGGCTTCTTCGCGCAGCGCGCAGCGACGAC 365
Db 392 GACGAGGTCGAGGCGCAAGCGGAGTGGCGGCTTCTTCGCGCAGCGTCAACGCGCAGGAC 451
Qy 366 CGGCG-----370
Db 452 CGGAGCTAAGTTATTACACCTAACAATACGGAATAGTAGTGCAGGACCTTTGATCTGAC 511
Qy 371 -----ATTTCCTCATCAGCGAG 390
Db 512 CGACCGATCATGCTCATGACCATGTTTATTCAGATTTCTGCTATCATCAGCGAG 571
Qy 391 GTCACAGAGCAACGCTACTGCGACCGCCAGCAAGGAGCGAGTGGCGTGGCGCGCGGG 450
Db 572 ATCAACAGAGCAACGCTACTGCGACCGCGAGCAACGAGGAGTGGCGTGGCGCGCGGG 631
Qy 451 CAGAAGTACTACGGGCGGCGCGCTGCAGATCTCGTGGAATCAACACTACGAGCGCGCG 510
Db 632 CAGAAGTACTACGGGCGGCGCGCTGCAGATCTCGTGGAATCAACACTACGAGCGCGCG 691
Qy 511 GGGAGGCGCATGCGCTTCGAGCGGCTCGGGAGCCCGCGGCAAGGTGGCGCGGAGCGCGTG 570
Db 692 GGGAGGCGCATGCGCTTCGAGCGGCTCGGGAGCCCGCGACCGCGAGGTTGGCGGAGGACGCGGTG 751
Qy 571 GTGCGCTCAAGGCGGCGCTCTGTTCTTGATGAAACAAAGTGCACCGTGTGATGCGCGCAG 630
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Db 752 ATGCGGTTCAAGACGGCGCTCTGTTCTTGGATGAACAAACGTCACCGTGTGATCCGCGAG 811
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AV532779
LOCUS
DEFINITION
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complete cds.
ACCESSION
AV532779
VERSION
AV532779.1 GI:48093339
KEYWORDS
Zea mays subsp. parviglumis
ORGANISM
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 1094)
Tiffin,P.
TITLE
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
JOURNAL
Genetics 167 (3), 1331-1340 (2004)
PUBMED
15280246
REFERENCE
2 (bases 1 to 1094)
Tiffin,P.
AUTHORS
Direct Submission
TITLE
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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Best Local Similarity 82.0%; Pred. No. 2.4e-62;
Matches 707; Conservative 0; Mismatches 51; Indels 104; Gaps 2;
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DEFINITION	1107 bp DNA linear PLN 29-JUL-2004
ACCESSION	Zea diploperennis isolate d1 chitinase (chiA) gene, complete cds.
VERSION	AY532781.1 GI:48093343
KEYWORDS	.
SOURCE	Zea diploperennis
ORGANISM	Zea diploperennis
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REFERENCE	1 (bases 1 to 1107)
AUTHORS	Tiffin,P.
TITLE	Comparative evolutionary histories of chitinase genes in the genus zea and family poaceae
JOURNAL	Genetics 167 (3), 1331-1340 (2004)
PUBMED	15280246
REFERENCE	2 (bases 1 to 1107)
AUTHORS	Tiffin,P.
TITLE	Direct Submission
JOURNAL	Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA

## ORIGIN

Query Match	70.9%	Score 548.4	DB 8	Length 1107
Best local Similarity	81.6%	Pred. No. 7.9e-62		
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Qy	246	CTACACCCGAGCGCGTTCTCTCGAGGCCATTCGCGCGGTACCCGGGCTTCCG	CGCATGCG	305
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Qy	306	CTCGAGGTGCGAGCGAACGGCGGAGATTGGCGGCTTCTTCGCGCAACGCA	CGCAGAGC	365
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Qy	366	CGGGC-----	-----	370
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Qy	371	-----	-----	386
Db	506	TGACCGACCGATCATCGTCACTGCTGACCATGCAATTTTCGATCAGATTT	CTGCTACATCAG	565
Qy	387	CGAGGTCAACAGAGCAACGCTACTTGCACCCGACCAAGAGGCACTGGCCGT	GGCGCGC	446
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Db	806	GCAGGGCTTCGGCGCACCATCAGGGCCATCAACGGCGCCTCGAGTGA	CAACGGGAACA	865
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Qy	747	CGACCGGGGCAACACTCACTGCT		772
Db	926	CGACCGGGGCAACACTCACTGCT		951

RESULT 12  
AY532783  
LOCUS

1110 bp DNA linear PLN 29-JUL-2004



DEFINITION Zea diploperennis isolate d3 chitinase (chiA) gene, complete cds.  
ACCESSION AY532783  
VERSION AY532783.1 GI:48093347  
KEYWORDS  
SOURCE  
ORGANISM  
Zea diploperennis  
Zea diploperennis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 1110)  
AUTHORS Tiffin,P.  
TITLE Comparative evolutionary histories of chitinase genes in the genus  
JOURNAL Genetics 167 (3), 1331-1340 (2004)  
PUBMED 15280246  
AUTHORS Tiffin,P.  
TITLE Direct Submission  
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
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ORIGIN  
Query Match 70.9%; Score 548.4; DB 8; Length 1110;  
Best Local Similarity 81.6%; Pred. No. 7.9e-62;  
Matches 707; Conservative 0; Mismatches 51; Indels 108; Gaps 2;  
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DEFINITION Zea diploperennis isolate d4 chitinase (chiA) gene, complete cds.  
ACCESSION AY532784  
VERSION AY532784.1 GI:48093349  
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SOURCE Zea diploperennis  
ORGANISM Zea diploperennis  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 1110)  
AUTHORS Tiffin,P.  
TITLE Comparative evolutionary histories of chitinase genes in the genus  
JOURNAL Genetics 167 (3), 1331-1340 (2004)  
PUBMED 15280246  
AUTHORS Tiffin,P.  
TITLE Direct Submission  
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
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AY532786			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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Zea diploperennis			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD			
clade; Panicoideae; Andropogoneae; Zea.			
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Tiffin,P.			
Comparative evolutionary histories of chitinase genes in the genus			
zea and family poaceae			
Genetics 167 (3), 1331-1340 (2004)			
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Tiffin,P.			
Direct Submission			
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,			
JOURNAL			
1445 Gortner Ave., St. Paul, MN 55108-1095, USA			
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Query Match			
Best Local Similarity			
Matches			
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81.6%; Pred. No. 7.9e-62;			
Conservative			
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Qy	687	CCCCGCCAGATGAACGGCGGTCGGCTACTACAGGCAGTACTGCCGCCAGCTCGGGGT	746
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GenCore version 5.1.6  
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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*

1: /cgm2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgm2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgm2\_6/ptodata/1/ina/FACTUS\_COMB.seq:\*  
6: /cgm2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1297.5	89.4	1094	4	US-09-522-714-1
2	861.5	59.3	1048	4	US-09-522-714-21
3	825.5	56.9	1079	1	US-08-181-271A-37
4	825.5	56.9	1079	1	US-08-449-315-37
5	825.5	56.9	1079	1	US-08-444-803-37
6	825.5	56.9	1079	1	US-08-449-043-37
7	825.5	56.9	1079	1	US-08-456-265A-37
8	825.5	56.9	1079	1	US-08-455-416-37
9	825.5	56.9	1079	1	US-08-455-244-37
10	825.5	56.9	1079	1	US-08-454-876-37
11	825.5	56.9	1079	1	US-08-457-364-37
12	825.5	56.9	1079	2	US-08-456-262-37

13	825.5	56.9	1079	2	US-08-456-240-37	Sequence 37, Appl
14	825.5	56.9	1079	2	US-08-455-736-37	Sequence 37, Appl
15	825.5	56.9	1079	2	US-08-971-217-37	Sequence 37, Appl
16	825.5	56.9	1079	3	US-09-350-600-37	Sequence 37, Appl
17	825.5	56.9	1079	4	US-09-906-234-37	Sequence 37, Appl
18	825.5	56.9	1116	4	US-09-522-714-31	Sequence 31, Appl
19	727.5	50.1	881	4	US-09-522-714-29	Sequence 29, Appl
20	622.5	42.9	943	2	US-08-475-427-15	Sequence 15, Appl
21	622.5	42.9	943	2	US-07-842-165-15	Sequence 15, Appl
22	619.5	42.7	1152	1	US-08-047-413-10	Sequence 10, Appl
23	619.5	42.7	1152	3	US-08-229-050-10	Sequence 10, Appl
24	619.5	42.7	1152	3	US-08-801-563-10	Sequence 10, Appl
25	605	41.7	1225	1	US-08-286-020-1	Sequence 1, Appl
26	605	41.7	1225	1	US-08-603-919-1	Sequence 1, Appl
27	585.5	40.3	905	2	US-08-475-427-14	Sequence 14, Appl
28	585.5	40.3	905	2	US-07-842-165-14	Sequence 14, Appl
29	581.5	40.0	1151	1	US-07-704-288C-2	Sequence 2, Appl
30	581.5	40.0	1151	1	US-08-093-372-1	Sequence 2, Appl
31	581.5	40.0	1151	1	US-08-379-259-2	Sequence 4, Appl
32	579	39.9	1153	2	US-08-475-427-4	Sequence 4, Appl
33	579	39.9	1153	2	US-07-842-165-4	Sequence 4, Appl
34	579	39.9	1153	3	US-08-448-398-6	Sequence 6, Appl
35	579	39.9	1163	2	US-08-475-427-12	Sequence 12, Appl
36	579	39.9	1163	2	US-07-842-165-12	Sequence 12, Appl
37	579	39.9	1863	1	US-08-525-507-16	Sequence 16, Appl
38	579	39.9	1863	2	US-08-475-427-9	Sequence 9, Appl
39	579	39.9	1863	2	US-07-842-165-9	Sequence 9, Appl
40	578.5	39.8	960	4	US-09-534-229C-8	Sequence 8, Appl
41	573	39.5	972	4	US-09-534-229C-7	Sequence 7, Appl
42	543	37.4	1163	4	US-09-522-714-5	Sequence 5, Appl
43	538	37.1	3012	2	US-08-475-427-5	Sequence 5, Appl
44	538	37.1	3012	2	US-07-842-165-5	Sequence 5, Appl
45	532	36.6	1318	3	US-09-125-891-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-522-714-1  
; Sequence 1, Application US/09522714  
; Patent No. 6563020  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Rasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100  
; CURRENT APPLICATION NUMBER: US/09/522,714  
; CURRENT FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/125,915  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (51)...(893)  
US-09-522-714-1

Alignment Scores:  
Pred. No.: 2.26e-121 Length: 1094  
Score: .1297.50 Matches: 229  
Percent Similarity: 93.33% Conservative: 9  
Best Local Similarity: 89.80% Mismatches: 10  
Query Match: 89.36% Indels: 7  
DB: 4 Gaps: 1

US-10-692-367-12 (1-257) x US-09-522-714-1 (1-1094)

Qy 3 GlnAnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22

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Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42
Db 210 GACGAGTACTCGCGGACGAGCGGTGCGAGTCGCGGCCGCTGCGCGCGCGGCGGCGAGC 269
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62
Db 270 AGTGGCGGC-----GCTGTGCGAAGCGTGTAGCGTCTGTACCC 308
Qy 63 AspAlaPhePheAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82
Db 309 GGCCTCTCTTCAACGGCATCAGAGCCAGCGCGGAGCGGTGCGAGGGCAAGACTTC 368
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 102
Db 369 TACACCGGAGCGGTTCCTGAGCGCGCTCAAGGCGTACCCAGGCTTCGCCCATGCGGG 428
Qy 103 SerGluValGluArgLysArgGluAlaAlaPhePheAlaHisAlaThrHisGluThr 122
Db 429 TCGCAGGTGAGGCAAGCGGAGATCGCCGCTTCTTCGCGCAGCGCCACGACGAGACC 488
Qy 123 GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrIys 142
Db 489 GGGCATTTCTGCTACATCAGCGAGATCAACAAGAGCAACGCTACTGCGACCCGACCAAG 548
Qy 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGlnIleSer 162
Db 549 AGGCAGTGGCGGTGCGCGCGGCGAGAACTACTACGCGCGCGCGCGCTGCGATCTCG 608
Qy 163 TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182
Db 609 TGGAACTACAACTACGCGCGCGGAGGCGCATCGCTTCGACGGGCTCGGGAGCCCC 668
Qy 183 GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn 202
Db 669 GGCAGGTGGCGCGGACGCGTGTGCGTTCAGGCGCGCTCTGGTCTCGATGAAC 728
Qy 203 AsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla 222
Db 729 AGCGTGCAAGCGGTGCTGCGCGAGGGTTCGCGCGCCACACGAGGGCCATCAACGCGGCC 788
Qy 223 LeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrArgGln 242
Db 789 CTCGAGTCCGCGGGAACACCCGCCGAGATGAACGCGCGCGTCCGGTACTACAGGAG 848
Qy 243 TyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 849 TACTGCCCGCAGCTCGCGGTGCGACCCCGGCGCCCACTCACCTGC 893
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## RESULT 2

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US-09-522-714-21
; Sequence 21, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (42)...(854)
US-09-522-714-21
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Score: 861.50 Matches: 155
Percent Similarity: 71.71% Conservative: 30
Best Local Similarity: 60.08% Mismatches: 58
Query Match: 59.33% Indels: 15
DB: 4 Gaps: 3
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US-10-692-367-12 (1-257) x US-09-522-714-21 (1-1048)

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Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42
Db 177 GAGGACTACTGCGCGCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG 215
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62
Db 216 -----GAGGTGCGGAGCAACACGCTCCGTGCGGAGCATCGTGACG 260
Qy 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82
Db 261 CCGGCTCTTTCGAGCGGCTCTCTCGCGAGCGCGCGCTCGTGCGAGGCCCAACGCGCTC 320
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
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Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
Db 381 ACCGTGACGACTCAACGCGGAGATCGCGCTTCTTCGCGCAACGCGCAACACGAGACC 440
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
Db 441 ATAAAGTTCTGCTACATCAACGAGATCGAGCGCGCGGAGCAAGACTACTGCGACCGGAAC 500
Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 501 AACACGCGAGTGGCGGTGCGAGCGGAGGAGGCTACTACGCGCGCGCGCGCTGCAGATC 560
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 561 TCCTGGAACTTCAACTACGCGCGCGCGGAGGAGATCGGCTTCGAGCGGCTGGCGGAC 620
Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 201
Db 621 CCGACGCGGTGGCGCGCGCGGTGCTGCGGTTCGCTCGCGCTCGGTACTGGATG 680
Qy 202 AsnAsnValHisArg-----ValMetProGlnGlyPheGlyAlaThrIleArgAlaIle 219
Db 681 AACAACTGACGCGGCGCATGCTCTCGCGCGCGGCTTCGCGCGCACCATCCGCGGCATC 740
Qy 220 AsnGlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 239
Db 741 AACGCGCGGTGCGAGTGGCGGCAAGACCCCACTCCCGTCAACACCGCGGTGCGCTAC 800
Qy 240 TyrArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
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## RESULT 3

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US-08-181-271A-37
; Sequence 37, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
```

APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/181,271A  
FILING DATE: 13-JAN-94  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-181-271A-37  
Alignment Scores:  
Pred. No.: 7,89e-74 Length: 1079  
Score: 825.50 Matches: 146  
Percent Similarity: 69.92% Conservative: 33  
Best Local Similarity: 57.03% Mismatches: 60  
Query Match: 56.85% Indels: 17  
DB: 1 Gaps: 4  
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Qy 3 GlnAsnGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAACCTGCGGTTCGCTCCAAACCTCTGTTGAGTCAGTTCGTTACTGTTGTTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 153 GATGCATACCTGCGGTTCGATGCGATCAGTTCCTTTGTAGA----- 194  
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62  
Db 195 -----GGTAGTGGAAACCCCGACCGAGGGTCGGTCGTAGCATTTGTGACA 239  
Qy 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
Db 240 CAAGTTTCTTTTAAACATATTATCAACACAGCTGTTGTTGTTGCGGGGGAAGAATTC 299  
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
Db 300 TACACCGTGACTCTTTGTTAAACGCGCTAACTTTCCCAACTTTGCCAATTTCTGTT 359  
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122  
Db 360 ACC-----AGACGTGAATTTGCTACCATGTTTCTCATTTTCACCTCACGAGACC 407  
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141  
Db 408 GGACATTTCTGTACATAGAGAGATTACGGAGCAACAGTAACCTACTGTCACGAGCAGC 467  
Qy 142 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161  
Db 468 AACACACAATACCATGTCACCGGGAAGAGCTACTTCGTTGTTGTCGATCCAACTA 527  
Qy 162 SerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181  
Db 528 TCATGGAACTACAACTACGAGGCGTGTGGTCAAAAGTCTCGGTCCTTGACCTTCTACGCCAG 587  
Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaLeuAlaLeuTyrPheTyrMet 201  
Db 588 CCGAACTTGTGGTACCAACCACTGAGCTTTAGGTCGGGTTTGTGGTTTGTGATG 647  
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221  
Db 648 AATAGCGTAAGCGCGTTCTGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAAATGA 707  
Qy 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg 241



Db 708 ---ATGGAATGTAAACGGTGGTAATTCGGTGCAGTCAACGCAGGATGGATACTATAGA 764  
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAenAsnLeuThrCys 257  
Db 765 GACTATTGTGGACAGCTTGGTGGACCTGGTCTCAACCTTACTTGC 812

## RESULT 4

US-08-449-315-37  
; Sequence 37, Application US/08449315  
; Patent No. 5650505  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Heins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericea C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,315  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504

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1 FILING DATE: 20-OCT 1989
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: US 07/848,506
4 FILING DATE: 6-MAR-1992
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 07/768,122
7 FILING DATE: 27-SEP-1991
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: US 07/580,431
10 FILING DATE: 7-SEP-1990
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 07/368,672
13 FILING DATE: 20-JUN-1989
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 07/329,018
16 FILING DATE: 24-MAR-1989
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 08/045,957
19 FILING DATE: 12-APR-1993
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Elmer, James Scott
22 REGISTRATION NUMBER: 36,129
23 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (919)541-8614
26 TELEFAX: (919)541-8689
27 INFORMATION FOR SEQ ID NO: 37:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 1079 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: DNA
34 US-08-449-315-37
35
36 Alignment Scores:
37 Pred. No.: 7,89e-74 Length: 1079
38 Score: 825.50 Matches: 146
39 Percent Similarity: 69.92% Conservative: 33
40 Best Local Similarity: 57.03% Mismatches: 60
41 Query Match: 56.85% Indels: 17
42 DB: 1 Gaps: 4
43
44 US-10-692-367-12 (1-257) x US-08-449-315-37 (1-1079)
45
46 Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
47 Db 93 CAAAACTCGCGGTTCGGCTCCAAACCTCTGTGTGCAGTCAGTTCGGTTACTGTGTGTAACCGAC 152
48 Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42
49 Db 153 GATCATCTACTCGGTGTGGATCGCATCAGGTCTCTGTAGA----- 194
50 Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62
51 Db 195 -----GGTAGTGGAAACCCCGACCGAGGGTCGCTAGCATTTGTGACA 239
52 Qy 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82
53 Db 240 CAAGGTTTCTTTAAACAATATTATCAACCAAGCTGGTAATGGTTGCGCGGGGAAAAAGATTTC 299
54 Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 102
55 Db 300 TACACCGGTGACTCTTTCGTTAAACGCCCGCTAATCTTTCCCACTTTTGCACAACTTCTGT 359
56 Qy 103 SerGluValGluArgLysGluGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
57 Db 360 ACC-----AGACGTGAATTTGCTACCATTTTCACTTCACTCACCAGACC 407
58 Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
59 Db 408 GGACATTTCTGCTCATATAGAGAGATTAACCGAGCAACAGTAACCTACTCTGCCAGACGAGC 467

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Qy	142	LysArgGlnTrpProCysAlaIaGlyGlnIysTyrGlyArgGlyProLeuGlnIle	161
Db	468	AAACACAAATACCCATGTCACCGGGAAAAGCTACTTTCGGTCGTGTGCGTCACTCAACTA	527
Qy	162	SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp	181
Db	528	TCATGGAACTACAACCTACGGAGCGTGTGGTCAAAAGTCTTCGGTCTTGACCTTCTACGCCAG	587
Qy	182	ProGlyArgValAlaArgAspAlaValAlaAlaPheLysAlaAlaLeuTrpPheTrpMet	201
Db	588	CCCGAACTTGTGGTAGCAACCAACTGTAGCTTTCAGTTCGGGTTTGTGTTTGGATG	647
Qy	202	AsnAsnValIleArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly	221
Db	648	AATAGCGTAAAGCCGGTCTCGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAAATGGA	707
Qy	222	AlaLeuGlnCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg	241
Db	708	---ATGGAATGTAAACGGTGGTAAATTCGGTGCAGTCAACCGCAGAGATTGGATCTATAGA	764
Qy	242	GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys	257
Db	765	GACTATTGTGGACAGCTTGGTGTGACCGCTGCTCTCAACCTTACTTGC	812

## RESULT 5

US-08-444-803-37  
; Sequence 37, Application US/084444803  
; Patent No. 5654414

GENERAL INFORMATION:

APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
 ;  
 ; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 106

NUMBER OF INQUIRIES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA

```

;
;
; ZIP: 10532
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;

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CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/444,803  
 FILING DATE: 19-MAY-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992

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Qy 63 AspAlaPheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82
Db 240 CAAGGTTCTTTAACAATATTATCAACAAGCTGGTAATGGTTCGGCGGGAAGAATTC 299
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaLalaTyrProGlyPheAlaHisGlyGly 102
Db 300 TACACCGTGACTCTTTCGTTAACCGCGCTAATACTTCCCAACTTTGCCAATTCGTGT 359
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 360 ACC-----AGACGTGAATTTGCTACCAATGTTTGTCTATTTCACTCAGCAGACC 407
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
Db 408 GGACATTTCTCTACATAGAGAGATTAAACGAGCAACACGTAATACTACTGCCAGACAGC 467
Qy 142 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACAAATACCCATGTGCACCGGGAAGAGCTACTTCGGTCTGTCGATCCAACTA 527
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACAACACTACGAGCGGTGTGTCCTCAAAAGTCTCGGTCTTGACCTTCTACGCCAG 587
Qy 182 ProGlyArgValAlaArgAspAlaValAlaAlaPheLysAlaAlaLeuTyrPheTyrMet 201
Db 588 CCCGAAGTGTGGTAGACCAACCACTGTACTTTCAGTCCGGTGTGTGGTTTGGATG 647
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
Db 648 AATAGCGTAAGCGCGTTCTGAACCAAGGTTTGGAGCCACCAATTAGAGCTATTAAATGA 707
Qy 222 AlaLeuGluCysAsnGlyValMetProGlnGlyPheGlyAlaThrIleArgValGlyTyrArg 241
Db 708 ---ATGGAATGTAAACGGTGGTAATTCCTCGTCCAGTCAACGCAAGGATTGGATCTATAGA 764
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 765 GACTATTGTGACAGCTTGGTGTGAGACCTCTGCTTAACCTTAGTTGC 812

RESULT 6
US-08-449-043-37
; Sequence 37, Application US/08449043
; Patent No. 5689044
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-449-043-37

Alignment Scores: 7.89e-74 Length: 1079
Pred. No.: 825.50 Matches: 146
Score: 69.92% Conservative: 33
Percent Similarity:
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Alignment Scores: 7.89e-74 Length: 1079  
Pred. No.: 825.50 Matches: 146  
Score: 69.92% Conservative: 33  
Percent Similarity: 57.03% Mismatches: 60  
Best Local Similarity: 56.85% Indels: 17  
Query Match: 1 Gaps: 4  
DB: 1

US-10-692-367-12 (1-257) x US-08-456-265A-37 (1-1079)

Qy 3 GlnAsnGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThr 22  
Db 93 CAAAACTGCGGTTCGCTCCAACTCTCTGTCAGTCAGTTCGTTGTTGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyCysArgSerGlyGlyGlyGly 42  
Db 153 GATCATACTGCGGTTCGTTGGATGCGATCAGTTCCTTTGTAGA----- 194  
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValThr 62  
Db 195 -----GGTAGTGGAAACCCGACCGAGGTCGTCGTCAGTTCGAC 239  
Qy 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
Db 240 CAAGGTTTCCTTAAACAATATTATCAACCAAGCTGTAATGTTGCGCGGGAAGATTC 299  
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaLalaTyrProGlyPheAlaHisGlyGly 102  
Db 300 TACACCGGTGACTCTTCGTTGTAACCGCTAATACTTTCCCACTTTGGCAATTCGTT 359  
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122  
Db 360 ACC-----AGAGTGGAATTCCTACCATGTTTGTCTCACTTCACGAGACC 407  
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141  
Db 408 GGACATTTCCTACATAGAGAGATTAAACGGACCAACACGCTAACTACTGCCAGCAGC 467  
Qy 142 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161  
Db 468 AACACAAATACCATGTCACCGGAAAGGCTACTTCGTCGTGTCGATCCAACTA 527  
Qy 162 SerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181  
Db 528 TCATGGAACTCACTACGAGCGTGTGTCAAAGTCTCGTCTTGACCTTCTAGCCAG 587  
Qy 182 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTyrPheTyrMet 201  
Db 588 CCGCAACTTGTGGGTAGCAACCACTAGTCTTTCAGTTCGCGGTTCGTTGTTGGATG 647  
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221  
Db 648 AATAGCGTAAACCGCGGTTCGAAACAGGTTTGGAGCCACCATTAGAGCTATTAAATGGA 707  
Qy 222 AlaLeuGluCysAsnGlyAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg 241  
Db 708 ---ATGGAAATGTAACGGTGTGAATTCGTCAGTCACGCAAGGATTGGATCTATAGA 764  
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 765 GACTATTGTGCAGACGTTGGTGTGGACCTTCGTCCTACCTTAGTTGC 812

RESULT 8  
US-08-455-416-37  
; Sequence 37, Application US/08455416  
; Patent No. 577200  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.

APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,416  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-455-416-37

Alignment Scores:
Pred. No.: 7,89e-74 Length: 1079
Score: 825.50 Matches: 146
Percent Similarity: 69.92% Conservative: 33
Best Local Similarity: 57.03% Mismatches: 60
Query Match: 56.85% Indels: 17
DB: 1 Gaps: 4

US-10-692-367-12 (1-257) x US-08-455-416-37 (1-1079)

Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThr 22
Db 93 CAAAACTGGGTTGGCTCCAACTCTGTTGCGAGTCAGTTCGGTTACTGGTACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 42
Db 153 GATCATACTCGGTGTGGATCGGATCAGTCTCTGTGTA-----194
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62
Db 195 -----GGTAGTGGAAACCCCGACCGGCGGTCTCGGTAGCATTTGTGACA 239
Qy 63 AspAlaPheAenGlyIleLysAenGlnAlaGlySerGlyCysGlyLysAenPhe 82
Db 240 CAAGTTTCTTAAATATATATACCACTGTAATGTTGCGGGGAAAGATTC 299
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGly 102
Db 300 TACACCGGTGACTCTTCTTTAAGCGCGCTAATACTTTCCCAACTTTGCCAATTCGTT 359
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 360 ACC-----AGACGTGAATTTGCTACCATGTTTGTCTATTTCACTCACGAGACC 407
Qy 123 GlyHisPheCysTyrIleSerGluValAen--LysSerAenAlaTyrCysAspProThr 141
Db 408 GGACATTTCTGTACATAGAGAGATTTAAGGACCAACACTACTACTGCGCAGCAGC 467
Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACACAATACCATGTGACCGCGGAAAGGCTACTTCCGTGCTGTCGATCAACTA 527
Qy 162 SerTrpAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACAACTACGGAGCGGTGTGGTCAAAAGTCTCGGTCTTGACCTTCTACGCGCAG 587
Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 201
Db 588 CCCGAATTGCGGTAGCAACCACTGTAGCTTTCAGTTCGGGTTTGTGTTTGTGATG 647
Qy 202 AenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGly 221
Db 648 AATAGCGTAAGCGCGTTCTGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAATGA 707
Qy 222 AlaLeuGluCysAenGlyAenAenProAlaGlnMetAenAlaArgValGlyTyrArg 241
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Db 708 ---ATGGAATGTACGGTGTAAATTCGGTGCAGTCAACGCAAGGATTGGATCTATAGA 764
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257
Db 765 GACTATTGTGACAGCTTGTGTGGACCCCTGGTCTTAACCTTAGTTGC 812

RESULT 9
US-08-455-244-37
; Sequence 37, Application US/08455244
; Patent No. 5789214
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,244
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; APPLICATION NUMBER: US 07/425,504
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; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-244-37

Alignment Scores:
Pred. No.: 7,89e-74 Length: 1079
Score: 825.50 Matches: 146
Percent Similarity: 69.92% Conservative: 33
Best Local Similarity: 57.03% Mismatches: 60
Query Match: 56.85% Indels: 17
DB: 1 Gaps: 4

US-10-692-367-12 (1-257) x US-08-455-244-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerIlySphGlyTyrCysGlyThr 22
Db 93 CAAAACTGCGGTTCGCTCCAAACCTCTGTTGCAGTCAGTTTCGTTACTGTTGGTACCGAC 152

Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 42
Db 153 GATGCATACGCGGTGTTGGATGCGGATCAGTCTTGTAGA----- 194

Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyAlaAsnValAlaAsnValThr 62
Db 195 -----CGTAGTGAACCCCGACCGAGGTCGTCGTCGATGTCGATGTCGAC 239

Qy 63 AsplalaphaAsnGlyIleLysAsnGlnAlaGlySerGlyGlyLysAsnPhe 82
Db 240 CAAGGTTTCTTTTAAACAATATTATCAACCAAGCTGTTAATGTTGCGCGGAAAGATTC 299

Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
Db 300 TACACCGTGACTCTTTCGTTAAGCGCGCTAATACTTCCCACTTTGCCAATTCCTGTT 359

Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 360 ACC-----AGACGTGAATTTGCTACCATGTTTGTCTATTTCACTTCACGAGACC 407

Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
Db 408 GGACATTCTGCTACATAGAGATTATACGGCAACAGTAACCTACTACTGCGAGAGCAGC 467

142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACACAATACCATCTGTGCACCGGAAAGGCTACTTCGGTCTGTCGATCCAACTA 527

Qy 162 SerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACCACTACGAGCGGTGTGGTCAAGTCTCTGGTCTTGACCTTCTACGCCAG 587

Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 201
Db 588 CCCGAACCTTGTGGTAGCAACCACTGTAGCTTTAGTTCGGTTCGTTTGGATG 647

Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
Db 648 AATAGCGTAAGCGCGGTTCCTGAACCAAGGTTTGGAGCCACCATTAATGGA 707

Qy 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrArg 241
Db 708 ---ATGGAATGTAACGCTGTTAATTCGGTGTGTCAGTCAACGCAAGGATTTGGATACATAGA 764

Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 765 GACTATTGTGCACAGCTTGTGTGGACCCCTGCTTAACCTTAGTTGC 812

RESULT 10
US-08-454-876-37
; Sequence 37, Application US/08454876
; Patent No. 5804693
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA: US 07/937,197
FILING DATE: 6-NOV-1992
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-454-876-37

Alignment Scores:
Pred. No.: 7,896-74 Length: 1079
Score: 825.50 Matches: 146
Percent Similarity: 69.92% Conservative: 33
Best Local Similarity: 57.03% Mismatches: 60
Query Match: 56.85% Indels: 17
DB: 1 Gaps: 4

US-10-692-367-12 (1-257) x US-08-454-876-37 (1-1079)

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Db 93 CAAACTCGGCTGGCTCCAACTCTGTTGCAGTCAGTTCGGTACTGTTGTTACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 42
Db 153 GATGCATACCTCGGCTGGTGGATCGCATCGATCCCTCTGTAGA----- 194
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62
Db 195 -----GGTAGTGAACCCCGAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 239

63 AspAlaPhePheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyAenPhe 82
240 CAAGGTTTCTTTAAACAATATTATCAACCAAGCTGTAATGTTGCGGGGAAAGATTTC 299
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaLysProGlyPheAlaHisGlyGly 102
Db 300 TACACCGGTGACTCTTTGTTAACCGCGCTAATCTTCCCAACTTTGCCAATCTGTT 359
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122
Db 360 ACC-----AGACGTGAAATTGCTACCATGTTTGTCTCATTTCACTCAGCAGACC 407
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaLysCysAspProThr 141
Db 408 GGACATTTCTGTCTACATAGAGAGATTAAACGGAGCAACACGTAACCTACTGCCAGAGCAGC 467
Qy 142 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACACAATACCCATGTGCACCGGAAAGGCTACTTCGGTCTGGTCCGATCCACTA 527
Qy 162 SerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACAACTACGGAGCGTGGTCAAGTCTCGTCTTGACCTTCTAGCCAG 587
Qy 182 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTyrMet 201
Db 588 CCCGAACCTGTGGGTAGCACCACTGTTAGCTTTCAGTCTGGGTTTGGTGGATG 647
Qy 202 AsnAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
Db 648 ANTAGCGTAGGCGGTTCTGAACCAAGGGTTGGAGCCACCATTAGAGCTATTATGGA 707
Qy 222 AlaLeuGluCysAenGlyAsnAenProAlaGlnMetAenAlaArgValGlyTyrTyrArg 241
Db 708 ---ATGGAATGTAACGGTGGTAATTCGGTGCAGTCAGCAACGCAAGGATTGGATATAGA 764
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAenLeuThrCys 257
Db 765 GACTATTGTGGACAGCTTGGTGGACCCCTGGTCTCAACCTTAGTTAGTTGC 812

RESULT 11
US-08-457-364-37
; Sequence 37, Application US/08457364
; Patent No. 5847258
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Utnes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; CORRESPONDENCE ADDRESS:
; ADDRESS: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
```



APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,262  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-456-262-37  
Alignment Scores:  
Pred. No.: 7,89e-74 Length: 1079  
Score: 825.50 Matches: 146  
Percent Similarity: 69.92% Conservative: 33  
Best Local Similarity: 57.03% Mismatches: 60  
Query Match: 56.85% Indels: 17  
Gaps: 4  
US-10-692-367-12 (1-257) x US-08-456-262-37 (1-1079)  
Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAAACTGCGGTGCGCTCCAAACCTCTGTTCAGTCAGTTCGGTTACTGTTGTTACCCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 153 GATGCATACCTGCGGTGTTGGATGCGATCCGATCAGGTCTCTGTGTA----- 194  
Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
Db 195 -----GGTAGTGGAAACCCCGACCGGAGGGTCGGTCGGTAGCATTTGTGACA 239  
Qy 63 AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe 82  
Db 240 CAAGGTTTCTTTAAACAATATTTATCAACAGCTGTTGTTGTTGCGGGGGAAGAATTC 299  
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
Db 300 TACACCGTGACTCTTTTCGTTAAGCGCGCTAATCTTTCCCAACTTTTCCCAATTTCTGT 359  
Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122  
Db 360 ACC-----AGACGTGAAATTTGCTACCATGTTTGTCTCATTTTCACCTCACGAGACC 407  
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141  
Db 408 GGACATTTCTGTACATAGAGAGATTAAACGGACCAACACGTAACCTACTCTCCAGAGCAGC 467  
Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161  
Db 468 AACACACAATACCCATGTGCACCGGGAAGAGCTTCTCGTCTGTTGTCGATCCAACTA 527  
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181  
Db 528 TCATGGAACTACACTACGAGCGGTGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 587  
Qy 182 ProGlyArgValAlaAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 201  
Db 588 CCCGAATTTGGGTAGCAACCCCACTGTAGCTTTCAGGTTCGGGTTTGTGTTTGGATG 647  
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221  
Db 648 AATAGCGTAAGCGCGGTTCGAACCAAGGGTTTGGAGCCACCATTAGAGCTATTAAATGA 707  
Qy 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrArg 241  
Db 708 ---ATGGAATGTAACGGTGGTAAATTCGGGTGCAGTCAACGACGAGGATGGATATAGATA 764  
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257

Db 765 GACTATTGTGACAGCTTGGTGTGGACCCCTGGTCTTAACCTTAGTTGC 812

## RESULT 13

US-08-456-240-37

; Sequence 37, Application US/08456240

; Patent No. 5856154

## GENERAL INFORMATION:

APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

## CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,240

FILING DATE: 31-MAY-1995

CLASSIFICATION: 800

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271

FILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566

FILING DATE: 6-FEB-1989

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/042,847

FILING DATE: 6-APR-1993

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-OCT 1989

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/848,506

FILING DATE: 6-MAR-1992

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-456-240-37

## Alignment Scores:

Pred. No.:	7.89e-74	Length:	1079
Score:	825.50	Matches:	146
Percent Similarity:	69.92%	Conservative:	33
Best Local Similarity:	57.03%	Mismatches:	60
Query Match:	56.85%	Indels:	17
DB:	2	Gaps:	4

US-10-692-367-12 (1-257) x US-08-456-240-37 (1-1079)

Qy	3	GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr	22
Db	93	CAAACTGCGGTTGCGCTCCAAACCTCTGTTCAGTCAGTTCGGTTACTGTGGTACCGAC	152
Qy	23	AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly	42
Db	153	GATGCATACCTGCGGTGTGGATCCGATCAGTCTTGTAGA-----	194
Qy	43	GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly	62
Db	195	-----GGTAGTGGAAACCCCGAGGCGGTGCGTGGTAGCATTTGTGACA	239
Qy	63	AspAlaPheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPhe	82
Db	240	CAAGGTTTCTTTAAATAATATTATCAACCAAGCTGGTAATGTTGCGGGGAAAGATTC	299
Qy	83	TyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle	102
Db	300	TACACCGGTGACTCTTTCGTTAACCGCGCTAATACTTTCCTCCCACTTTGCCAATTCGTT	359
Qy	103	SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr	122
Db	360	ACC-----AGACGTGAATTTGCTACCATGTTTGTCTCATTTCACTCAGGAGACC	407
Qy	123	GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr	141
Db	408	GGACATTTCTGTACATAGAGAGATTAAACGAGCAACACACGTAATACTACTGCGAGAGACG	467
Qy	142	LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle	161
Db	468	AACACACAATACCATGTGACCGGAAAGGCTACTTTCGGTCGTGGTCCCATCTCACTA	527
Qy	162	SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp	181





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Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62
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Db 240 CAAGGTTTCTTTAACAAATATTATCAACCAAGCTGGTAATGGTTGCCGGGGAAAGATTTC 299
Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102
Db 300 TACACCCGCTACTTTCGTTAAACGCCGCTAATACTTTCCCAACTTTGCCCAATTCGTGT 359
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Db 360 ACC-----AGACGTGAATTCGTACCAATGTTTGCTCATTTTCACCTCACGAGACC 407
Qy 123 GlyHisPheCysTyrIleSerGluValAsn---LysSerAsnAlaTyrCysAspProThr 141
Db 408 GGACATTTCTGTACTATAGAGAGATTAAACGGAGCAACACGTAACCTACTGCCAGAGCAGC 467
Qy 142 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 161
Db 468 AACACACAATACCCCATGTGCACCGGAAAAGGCTACTTCGGTGGTGGTCCGATCCAACTA 527
Qy 162 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAsp 181
Db 528 TCATGGAACTACAACTACCGGACGCGTGTGGTCAAAAGTCTCGGTCTTGACCTTCTACGCCAG 587
Qy 182 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 201
Db 588 CCGMACTTGTGGTAGACCAACCACTGTAGCTTTCAGGTGGGTTTGTGGTTTGGATG 647
Qy 202 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 221
Db 648 AATAGCGTAAGCGCGTTCTGAACCAAGSGTTTGGAGCCACCATTAGAGCTATTAAATGGA 707
Qy 222 AlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArg 241
Db 708 ---ATGGAATGTAACGGTGGTAATTCCCGGTGCAGTCAACGCAAGGATTGGATACTATAGA 764
Qy 242 GlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 765 GACTATTGTGACACAGCTTGGGTGGACCCCTGGTCTCTAACCTTAGTTGC 812
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Job time : 135.26 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: May 23, 2005, 19:25:43 ; Search time 414.647 Seconds  
(without alignments)  
3800.840 Million cell updates/sec

Title: US-10-692-367-12

Perfect score: 1452

Sequence: 1 SMQNCQPNVCCSKFGYCG.....GYRQYRQLGVDGNLTC 257

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -OPMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10692367 @CGN 1.1 456 @runat 20052005 172257 20130  
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgm2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgm2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgm2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq.\*  
4: /cgm2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgm2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgm2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgm2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgm2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgm2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgm2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgm2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgm2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgm2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgm2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgm2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgm2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgm2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgm2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgm2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
20: /cgm2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgm2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgm2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1452	100.0	771	18	US-10-389-432B-11	Sequence 11, Appl
2	1452	100.0	771	19	US-10-692-367-11	Sequence 11, Appl
3	1435	98.8	771	18	US-10-389-432B-29	Sequence 29, Appl
4	1435	98.8	771	18	US-10-389-432B-33	Sequence 33, Appl
5	1435	98.8	771	19	US-10-692-367-29	Sequence 29, Appl
6	1435	98.8	771	19	US-10-692-367-33	Sequence 33, Appl
7	1405	96.8	771	18	US-10-692-367-71	Sequence 71, Appl
8	1382.5	95.2	768	19	US-10-389-432B-59	Sequence 59, Appl
9	1382.5	95.2	771	19	US-10-692-367-59	Sequence 59, Appl
10	1382	95.2	771	19	US-10-389-432B-45	Sequence 45, Appl
11	1382	95.2	771	19	US-10-692-367-45	Sequence 45, Appl
12	1377	94.8	771	18	US-10-389-432B-65	Sequence 65, Appl
13	1377	94.8	771	19	US-10-692-367-65	Sequence 65, Appl
14	1373.5	94.6	768	18	US-10-389-432B-61	Sequence 61, Appl
15	1373.5	94.6	771	19	US-10-692-367-61	Sequence 61, Appl
16	1366.5	94.1	768	18	US-10-389-432B-47	Sequence 47, Appl
17	1366.5	94.1	771	19	US-10-692-367-47	Sequence 47, Appl
18	1365.5	94.0	771	19	US-10-692-367-73	Sequence 73, Appl
19	1363	93.9	771	18	US-10-389-432B-63	Sequence 63, Appl
20	1363	93.9	771	18	US-10-692-367-63	Sequence 63, Appl
21	1361	93.7	771	18	US-10-389-432B-23	Sequence 23, Appl
22	1361	93.7	771	18	US-10-389-432B-37	Sequence 37, Appl
23	1361	93.7	771	19	US-10-692-367-23	Sequence 23, Appl
24	1361	93.7	771	19	US-10-692-367-37	Sequence 37, Appl
25	1356.5	93.4	765	19	US-10-692-367-37	Sequence 67, Appl
26	1353.5	93.2	750	18	US-10-389-432B-43	Sequence 43, Appl
27	1353.5	93.2	753	19	US-10-692-367-43	Sequence 43, Appl
28	1351.5	93.1	771	19	US-10-692-367-83	Sequence 83, Appl
29	1342	92.4	777	18	US-10-389-432B-39	Sequence 39, Appl
30	1342	92.4	780	19	US-10-692-367-39	Sequence 39, Appl
31	1339	92.2	780	19	US-10-692-367-75	Sequence 75, Appl
32	1338.5	92.2	753	19	US-10-692-367-81	Sequence 81, Appl
33	1333.5	91.8	762	18	US-10-389-432B-25	Sequence 25, Appl
34	1333.5	91.8	765	19	US-10-692-367-25	Sequence 25, Appl
35	1333	91.8	840	15	US-10-259-165-762	Sequence 762, App
36	1333	91.8	1138	17	US-10-425-114-30480	Sequence 30480, A
37	1333	91.8	1530	18	US-10-425-115-135817	Sequence 135817,
38	1332	91.7	774	19	US-10-692-367-7	Sequence 7, Appl
39	1332	91.7	845	18	US-10-389-432B-7	Sequence 7, Appl
40	1323.5	91.2	750	18	US-10-389-432B-51	Sequence 51, Appl
41	1323.5	91.2	753	19	US-10-692-367-51	Sequence 51, Appl
42	1318.5	90.8	753	19	US-10-692-367-69	Sequence 69, Appl
43	1318.5	90.8	768	18	US-10-389-432B-41	Sequence 41, Appl
44	1318.5	90.8	771	19	US-10-692-367-41	Sequence 41, Appl
45	1315.5	90.6	750	18	US-10-389-432B-35	Sequence 35, Appl

#### ALIGNMENTS

RESULT 1  
US-10-389-432B-11  
; Sequence 11, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmonds, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Naseer  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 489492000300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 771

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; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-389-432B-11

Alignment Scores:
Pred. No.:      1.17e-166      Length:      771
Score:          1452.00      Matches:      257
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      18          Indels: 0
DB:              18          Gaps: 0

US-10-692-367-12 (1-257) x US-10-389-432B-11 (1-771)
QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTGCGGCTGCCAGCAAACTGATGCTGCGGCGCGGCTGCGGCGGCGG 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
DB 61 ACGACCGACGAGTACTGCGGCGGACGGGTGCCAGTGCAGCAAGTATGCTGCGGCGGCGG 120
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB 121 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ValThrAspAlaPhePheAsnGlyLeuLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
DB 181 GTCACCGACGCGTCTTCAACGGCATCAAGAACACGAGCGGCGGCGGCGGCGGCGGCAAG 240
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaAlaTyrProGlyPheAlaHis 100
DB 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGTACCGCGGCTTCCGCGAT 300
QY 101 GlyGlySerGluValGluArgLysArgGluLeuAlaAlaPhePheAlaHisAlaThrHis 120
DB 301 GCGGCGCTCCGAGGTCCGAGCGCAGCGGAGGATTCGCGCTTCTTCGCGACGCCACGCGAC 360
QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
DB 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAAGAGCAACGCTACTGCGACCCG 420
QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
DB 421 ACCAAGAGCGAGTGGCGCGTGGCGCGCGGCGAGAGTACTACGGGCGCGCGCGCGCGCG 480
QY 161 IleSerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaAlaIleGlyPheAspGlyLeuGly 180
DB 481 ATCTCTGTGAATACTACATACGGGCGCGCGGCGGAGGCGCATCGGCTTCAGCGGCTCGGG 540
QY 181 AppProGlyArgValAlaArgAspAlaValAlaAlaPheLysAlaAlaLeuTyrPheTyr 200
DB 541 GACCCCGGCGAGGTGGCGGCGGACCGCGTGGTGGCGGTTCAAGGCGCGCGCTCTGTTCTGG 600
QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaLeuAsn 220
DB 601 ATGAACAACGTCACCGTGTGATGCGCGAGGGCTTCGGCGGCCACCATCAGGGCCATCAAC 660
QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
DB 661 GCGGCGCTCCAGTGTGACCGGAGCAACCCCGCCAGATGAACCGCGCGGCTGCGGCTACTAC 720
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
DB 721 AGGCGAGTACTGCGCGCAGCTCGCGCTCGACCCCGGCAACAACCTCACCTGC 771

RESULT 2
US-10-692-367-11
; Sequence 11, Application US/10692367
; Publication No. US20050050595A1
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; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-11

Alignment Scores:
Pred. No.:      1.17e-166      Length:      774
Score:          1452.00      Matches:      257
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      19          Indels: 0
DB:              19          Gaps: 0

US-10-692-367-12 (1-257) x US-10-692-367-11 (1-774)
QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTGCGGCTGCCAGCAAACTGATGCTGCGGCGCGGCTGCGGCGGCGG 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
DB 61 ACGACCGACGAGTACTGCGGCGGACGGGTGCCAGTGCAGCAAGTATGCTGCGGCGGCGG 120
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB 121 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ValThrAspAlaPhePheAsnGlyLeuLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
DB 181 GTCACCGACGCGTCTTCAACGGCATCAAGAACACGAGCGGCGGCGGCGGCGGCGGCAAG 240
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaAlaTyrProGlyPheAlaHis 100
DB 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGTACCGCGGCTTCCGCGAT 300
QY 101 GlyGlySerGluValGluArgLysArgGluLeuAlaAlaPhePheAlaHisAlaThrHis 120
DB 301 GCGGCGCTCCGAGGTCCGAGCGCAGCGGAGGATTCGCGCTTCTTCGCGACGCCACGCGAC 360
QY 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
DB 361 GAGACCGGCGCATTTCTGCTACATCAGCGAGGTCAACAAGAGCAACGCTACTGCGACCCG 420
QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
DB 421 ACCAAGAGCGAGTGGCGCGTGGCGCGCGGCGAGAGTACTACGGGCGCGCGCGCGCGCG 480
QY 161 IleSerTyrAsnTyrAsnTyrGlyProAlaGlyArgAlaAlaIleGlyPheAspGlyLeuGly 180
DB 481 ATCTCTGTGAATACTACATACGGGCGCGCGGCGGAGGCGCATCGGCTTCAGCGGCTCGGG 540
QY 181 AppProGlyArgValAlaArgAspAlaValAlaAlaPheLysAlaAlaLeuTyrPheTyr 200
DB 541 GACCCCGGCGAGGTGGCGGCGGACCGCGTGGTGGCGGTTCAAGGCGCGCGCTCTGTTCTGG 600
QY 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaLeuAsn 220
DB 601 ATGAACAACGTCACCGTGTGATGCGCGAGGGCTTCGGCGGCCACCATCAGGGCCATCAAC 660
QY 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
DB 661 GCGGCGCTCCAGTGTGACCGGAGCAACCCCGCCAGATGAACCGCGCGGCTGCGGCTACTAC 720
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
DB 721 AGGCGAGTACTGCGCGCAGCTCGCGCTCGACCCCGGCAACAACCTCACCTGC 771
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Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGGAACTACAATACGGGGCCCGGGAGGGCCATCGGCTTCGACGGGCTCGGG 540

Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 541 GACCCCGGAGGGTGGCGGGGACCGCTGTGGGTTCGAGGGCGCTCTGGTTCGG 600

Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 601 ATGAACAACGTGCACCGTGTATCGCGAGGCTTCGGCGGCACCATCAGGGCCATCAAC 660

Qy 221 GlyAlaLeuGluCysAsnGlyAsnValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 240
Db 661 GCGGCCCTCGAGTGCACGGGAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720

Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 721 AGGCAGTACTGCCGCGACGCTCGGCTGCAGCCGCGGCAACACCTCACCTGC 771

RESULT 3
US-10-389-432B-29
; Sequence 29, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 489492000300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: r1 AD4 nucleic acid
US-10-389-432B-29

Alignment Scores:
Pred. No.: 1,376-164 Length: 771
Score: 1435.00 Matches: 254
Percent Similarity: 99.22% Conservative: 1
Best Local Similarity: 98.83% Mismatches: 2
Query Match: 98.83% Indels: 0
DB: 18 Gaps: 0

US-10-692-367-12 (1-257) x US-10-389-432B-29 (1-771)

Qy 1 SerMetGlnAsnGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGGTGCAGCAACGATGCTGCAGCAAGTTTGGCTACTCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGAGTACTCGCGGACGGGTGCCAGTCGGCGCGCTCGCGCGCGCGGT 120

Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTCACCGACGCGTCTTCAACGGCATCAAGAACGAGCGCGGAGCGGCTGCGAGGGCAAG 240
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```
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleTyrProGlyPheAlaHis 100
Db 241 AACTTCTACACCCGGAGCGGCTTCTCGAGGCCATCGCCGGGTACCCGGGCTTCGCGCAT 300

Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
Db 301 GCGCGCTCGAGGTCGAGCGCAAGCGCGAGATTGCCGCTTCTTCGCGCACGCGCAC 360

Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140
Db 361 GAGACCGCGCATTTCTGCTCATCAGCGAGGTCAACAAGAGCAACGCTACTCTCGCACCG 420

Qy 141 ThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGGAGTGGCGCTGCGCGCGCGGCGAGACTACGCGCGCGCGCGCTGCGAG 480

Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGGAACTACAATACGGCGCCCGGGAGGGCCATCGGCTTCGACGGGCTCGGG 540

Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 541 GACCCCGGAGGGTGGCGGGACCGCTGTGGGTTCGAGGGCGGCTCTGGTTCGG 600

Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 601 ATGAACAACGTGCACCGTGTATCGCGAGGCTTCGGCGGCACCATCAGGGCCATCAAC 660

Qy 221 GlyAlaLeuGluCysAsnGlyAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
Db 661 GCGGCCCTCGAGTGCAGCGGGAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTAC 720

Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 721 AAGCAGTACTGCCGCGACGCTCGGCTGCAGCCGCGGCAACACCTCACCTGC 771

RESULT 4
US-10-389-432B-33
; Sequence 33, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 489492000300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: r1 AG9 nucleic acid
US-10-389-432B-33

Alignment Scores:
Pred. No.: 1,376-164 Length: 771
Score: 1435.00 Matches: 254
Percent Similarity: 99.22% Conservative: 1
Best Local Similarity: 98.83% Mismatches: 2
Query Match: 98.83% Indels: 0
DB: 18 Gaps: 0

US-10-692-367-12 (1-257) x US-10-389-432B-33 (1-771)
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```
QY 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAAACTGCGGCTGTCAGCAAAAGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
DB 61 ACAACCGACGAGTACTGCGCGGACGCGGTGTCAGTCCGCGCCGCTCGCGGCGCGGT 120
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ValThrAspAlaPhePheAsnGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLys 80
DB 181 GTCACCGACGCGTCTTCAACCGCATCAAGCAACGAGCGCGGAGCGGTGCGAGGCGAAG 240
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaHis 100
DB 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGGTACCGCGGCTTCGCGCAT 300
QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
DB 301 GCGCGCTCGAGGTGCGAGCGAGCGAGATGCGCGCTTCTTCGCGCAACGCGCACGCGAC 360
QY 121 GluThrGlyHisPheCysTyrIleSerGluValAenLysSerAsnAlaTyrCysAspPro 140
DB 361 GAGACCGGCGCATTTCTGTCTACATCAGCGAGGTCAAGCAACGAGCGCGGTGCGAGGCGAAG 420
QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160
DB 421 ACCAAGAGCGAGTGGCGCGTTCCTCGAGGCGCATCGCGCGGTACCGCGGCTTCGCGCAT 480
QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
DB 481 ATCTCGTGAACATCAACCTACGAGGTGAGCGGAGGCGCATCGCGGCTTCGAGCGGCTCGGG 540
QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200
DB 541 GACCCCGGACGGGTGGCGGGAGCGCGCTGTGGTGGCGTTCAGGCGGCGCTCTGGTTCGTGG 600
QY 201 MetAenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
DB 601 ATGAACAACGTCACCGCTGTGTATCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAAC 660
QY 221 GlyAlaLeuGluCysAenGlyAsnProAlaGlnMetAenAlaArgValGlyTyrTyr 240
DB 661 GCGCGCTTCGAGTGGCGGGGAAACACCCCGCCAGATGAACGCGCGGTGCGGTACTACTAC 720
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAsnLeuThrCys 257
DB 721 AAGCAGTACTGCGCGCAGCTCGCGCTCGACCCAGGCGCCACCTTCACCTTGC 771
```

## RESULT 5

US-10-692-367-29

; Sequence 29, Application US/10692367

; Publication No. US2005005059A1

; GENERAL INFORMATION:

; APPLICANT: Muller, Mathias L.

; APPLICANT: True, Thom

; APPLICANT: Simmons, Carl R.

; APPLICANT: Yalpani, Nasser

; TITLE OF INVENTION: Novel compositions with chitinase

; FILE REFERENCE: 549162000320

; CURRENT APPLICATION NUMBER: US/10/692,367

; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/389,432

; PRIOR FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: 10/290,086

; PRIOR FILING DATE: 2002-11-06

; PRIOR APPLICATION NUMBER: 60/337,029

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: 60/420,666

```
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (774)
US-10-692-367-29
```

## Alignment Scores:

Pred. No.:	1.37e-164	Length:	774
Score:	1435.00	Matches:	254
Percent Similarity:	99.22%	Conservative:	1
Best Local Similarity:	98.83%	Mismatches:	2
Query Match:	98.83%	Indels:	0
DB:	19	Gaps:	0

US-10-692-367-12 (1-257) x US-10-692-367-29 (1-774)

```
QY 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAAACTGCGGCTGTCAGCAAAAGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
DB 61 ACAGCCAGCAGTACTGCGCGGACGCGGTGCGAGTCCGCGCCGCTCGCGGCGCGGT 120
QY 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ValThrAspAlaPhePheAsnGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLys 80
DB 181 GTCACCGACGCGTCTTCAACCGCATCAAGCAACGAGCGCGGTGCGAGGCGAAG 240
QY 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaHis 100
DB 241 AACTTCTACACCGGAGCGGCTTCTCGAGGCGCATCGCGCGGTACCGCGGCTTCGCGCAT 300
QY 101 GlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 120
DB 301 GCGCGCTCGAGGTGAGCGGAGGCGCATCGCGGCTTCGCGCGCACCATCAGGCGCATCAAC 360
QY 121 GluThrGlyHisPheCysTyrIleSerGluValAenLysSerAsnAlaTyrCysAspPro 140
DB 361 GAGACCGGCGCATTTCTGTCTACATCAGCGAGGTCAAGCAACGAGCGCGGTGCGAGGCGAAG 420
QY 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160
DB 421 ACCAAGAGCGAGTGGCGCGTTCCTCGAGGCGCATCGCGCGGTACCGCGGCTTCGCGCAT 480
QY 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
DB 481 ATCTCGTGAACATCAACCTACGAGGTGAGCGGAGGCGCATCGCGGCTTCGAGCGGCTCGGG 540
QY 181 AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrp 200
DB 541 GACCCCGGACGGGTGGCGGGAGCGCGCTGTGGTGGCGTTCAGGCGGCGCTCTGGTTCGTGG 600
QY 201 MetAenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
DB 601 ATGAACAACGTCACCGCTGTGTATCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAAC 660
QY 221 GlyAlaLeuGluCysAenGlyAsnProAlaGlnMetAenAlaArgValGlyTyrTyr 240
DB 661 GCGCGCTTCGAGTGGCGGGGAAACACCCCGCCAGATGAACGCGCGGTGCGGTACTACTAC 720
QY 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAsnLeuThrCys 257
```

Db 721 AAGCAGTACTGCCGCGTGGCGTGCACCCAGGGCCCAACCTCCTTGC 771  
 ::

## RESULT 6

US-10-692-367-33  
 ; Sequence 33, Application US/10692367  
 ; Publication No. US20050050595A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Muller, Mathias L.  
 ; APPLICANT: True, Thom  
 ; APPLICANT: Simmons, Carl R.  
 ; APPLICANT: Yalpani, Nasser  
 ; TITLE OF INVENTION: Novel compositions with chitinase  
 ; TITLE OF INVENTION: activity  
 ; FILE REFERENCE: 549162000320  
 ; CURRENT APPLICATION NUMBER: US/10/692,367  
 ; CURRENT FILING DATE: 2003-10-22  
 ; PRIOR APPLICATION NUMBER: 10/389,432  
 ; PRIOR FILING DATE: 2003-03-14  
 ; PRIOR APPLICATION NUMBER: 10/290,086  
 ; PRIOR FILING DATE: 2002-11-06  
 ; PRIOR APPLICATION NUMBER: 60/337,029  
 ; PRIOR FILING DATE: 2001-11-07  
 ; PRIOR APPLICATION NUMBER: 60/420,666  
 ; PRIOR FILING DATE: 2002-10-22  
 ; NUMBER OF SEQ ID NOS: 84  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 33  
 ; LENGTH: 774  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(774)  
 US-10-692-367-33

## Alignment Scores:

Pred. No.:	1.37e-164	Length:	774
Score:	1435.00	Matches:	254
Percent Similarity:	99.22%	Conservative:	1
Best Local Similarity:	98.83%	Mismatches:	2
Query Match:	98.83%	Indels:	0
DB:	19	Gaps:	0

US-10-692-367-12 (1-257) x US-10-692-367-33 (1-774)

Qy 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrcysgly 20  
 Db 1 TCGATGCAGAACTGCGGCTGCCAGCAACAGTATGCTGAGCAAGTTTGGCTACTGCGGC 60  
 Qy 21 ThrThrAspGluTyrcysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40  
 Db 61 ACNACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGCGCGCGTCCGCTCGGGCGCGGT 120  
 Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
 Db 121 GCG 180  
 Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLys 80  
 Db 181 GTCACCGACGCGTCTTCAACGGCATCAAGAACCGAGCGGAGCGGTGGCGAGGCAAG 240  
 Qy 81 AenPheTyThrArgSerAlaPheLeuGluAlaIleAlaIleAlaTyProGlyPheAlaHis 100  
 Db 241 AACTTCTACACCGAGGCGGTCTCTCGAGCCATCGCGGTACCGCGGTTCGCGCAT 300  
 Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaPheAlaHisAlaThrHis 120  
 Db 301 GCGCGCTCCGAGTCCAGCGCAAGCGGAGATTGCGGCTTCTTCCGCGCAGCGCAC 360  
 Qy 121 GluThrGlyHisPheCysTyIleSerGluValAenLysSerAsnAlaTyrcysaspPro 140

Db 361 GAGACCGGCGCATTTCTGCTATCATGCGAGGTCAACAGAGCAACGCTTACTGCGACCG 420  
 Qy 141 ThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyTyTyTyTyTyTyTyTyTyTy 160  
 Db 421 ACCAAGAGGCACTGCGCGTGGCGCGGAGTACTACGGGCGCGCGCGCGCGCTGCAG 480  
 Qy 161 IleSerTrpAenTyAsnTyGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
 Db 481 ATCTGTGGAACATAACTACGGGCGCGCGGAGGCGCATCGGCTTCGACGGGCTCGGG 540  
 Qy 181 AspProGlyArgValAlaAtqAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
 Db 541 GACCCCGGCGAGGTGGCGGAGCGCGTGTGGGTTCAGAGCGCGCGCTCTGGTCTGG 600  
 Qy 201 MetAenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220  
 Db 601 ATGAACACAGTGCACCGTGTGATGCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 660  
 Qy 221 GlyAlaLeuGluCysAenGlyAsnAenProAlaGlnMetAenAlaAatqValGlyTyTyTy 240  
 Db 661 GCGCGCTTCGAGTCCGCGGAGCAACCGCGCCAGATGAACGCGCGCTCGGCTACTAC 720  
 Qy 241 ArgGlnTyrcysArgGlnLeuGlyValAspProGlyAenAenLeuThrCys 257  
 Db 721 AAGCAGTACTGCCGCGAGCTCGGCTGCACCGGCGCCAACTCCTCCTTGC 771

## RESULT 7

US-10-692-367-71  
 ; Sequence 71, Application US/10692367  
 ; Publication No. US20050050595A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Muller, Mathias L.  
 ; APPLICANT: True, Thom  
 ; APPLICANT: Simmons, Carl R.  
 ; APPLICANT: Yalpani, Nasser  
 ; TITLE OF INVENTION: Novel compositions with chitinase  
 ; TITLE OF INVENTION: activity  
 ; FILE REFERENCE: 549162000320  
 ; CURRENT APPLICATION NUMBER: US/10/692,367  
 ; CURRENT FILING DATE: 2003-10-22  
 ; PRIOR APPLICATION NUMBER: 10/389,432  
 ; PRIOR FILING DATE: 2003-03-14  
 ; PRIOR APPLICATION NUMBER: 10/290,086  
 ; PRIOR FILING DATE: 2002-11-06  
 ; PRIOR APPLICATION NUMBER: 60/337,029  
 ; PRIOR FILING DATE: 2001-11-07  
 ; PRIOR APPLICATION NUMBER: 60/420,666  
 ; PRIOR FILING DATE: 2002-10-22  
 ; NUMBER OF SEQ ID NOS: 84  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 71  
 ; LENGTH: 774  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(774)  
 US-10-692-367-71

Alignment Scores:	6.15e-161	Length:	774
Pred. No.:	1405.00	Matches:	245
Score:	98.44%	Conservative:	8
Percent Similarity:	95.33%	Mismatches:	4
Best Local Similarity:	96.76%	Indels:	0
Query Match:	19	Gaps:	0

US-10-692-367-12 (1-257) x US-10-692-367-71 (1-774)

Qy 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrcysgly 20

Db 1 TCGATGCAAGTCTGGGCTGCAGCCAACTATGCTGCACCAAGTTTCGGCTACTGCGGC 60  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACAGCCGACGAGTACTGCGGCGAGCGGTGCGAGTGCAGTCCGGCCCGCTGCGCTCGGGCGGGT 120  
Qy 41 Gly 60  
Db 121 GCG 180  
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
Db 181 GTCCACCGAGCGTCTTCAACCGCATCAAGAGCCAGCGCGCGCGCGCGCGCGCGCGCG 240  
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100  
Db 241 AACTTCTACACCGCGCGCGTTCCTGAGCGCGCTCAAGCGCGTACCCAGGCTTCGCCCAT 300  
Qy 101 GlyGlySerGluValGluArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
Db 301 GCGCGGTACAGGTGCGAGGCGAGCGCGAGATCGCGCTTCTTCGCGCAGCGCGCGCAC 360  
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
Db 361 GAGACCGCGCATTTCTGTACATCAGCGAGATCAACAGAGCAACGCGCTACTGCGACCG 420  
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160  
Db 421 ACCAAGAGCGAGTGGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
Db 481 ATCTCGTGGAACTACACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
Qy 181 AspProGlyArgValAlaAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 541 GACCCCGCGAGGTGGCGCGGAGCGCGTGGTGGCGTTCAAGGGCGCGCTCTGGTTCTGG 600  
Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaIleArgAlaIleAsn 220  
Db 601 ATGAACAACGTCACCGTGTATGCGCGAGGGCTTCGCGCGCGCACCCATCAGGGCCATCAAC 660  
Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240  
Db 661 GCGCGCGTCTGAGTGCAGCGGGAACAACCCCGCGCGAGATGAACGCGCGCATCGGTACTAC 720  
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 721 AAGCAGTACTGCGCGCAGCTCGCGCTGCAGCCAGGCGCCCAACCTTCACTTGC 771

RESULT 8  
US-10-389-432B-59  
; Sequence 59, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; TITLE OF INVENTION: ACTIVITY  
; FILE REFERENCE: 48942000300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 768  
; TYPE: DNA  
; ORGANISM: Unknown

FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; OTHER INFORMATION: 4N1/33\_P4 nucleic acid  
US-10-389-432B-59  
Alignment Scores: 3.33e-158 Length: 768  
Pred. No.: 1382.50 Matches: 244  
Score: 96.89% Conservatives: 5  
Percent Similarity: 94.94% Mismatches: 7  
Best Local Similarity: 95.21% Indels: 1  
Query Match: 18 Gaps: 1  
US-10-692-367-12 (1-257) x US-10-389-432B-59 (1-768)  
Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
Db 1 TCGATGCAAGTCTGGGCTGCAGCCAACTATGCTGCACCAAGTTTCGGCTACTGCGGC 60  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACNACCGAGCGCTACTGCGGCGAGCGGTGCGAGTGCAGTCCGGCCCGCTCGCGCTCG 117  
Qy 41 Gly 60  
Db 118 GGTGCGCGGTGCG 177  
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
Db 178 GTCAACCGAGCGTCTTCAACCGCATCAAGAACCGCGCGCGCGCGCGCGCGCGCG 237  
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis 100  
Db 238 AACTTCTACACCGCGAGCGCGTTCCTGAGCGCGCTCAAGGGGTACCCAGGCTTCGCCCAT 297  
Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaPheAlaHisAlaThrHis 120  
Db 298 GCGCGGTACAGGTGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 357  
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
Db 358 GAGACCGCGCATTTCTGCTATCATCAGCGAGATCAACAGAGCAACGCGCTACTGCGACCG 417  
Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGln 160  
Db 418 ACCAAGAGCGAGTGGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 477  
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
Db 478 ATCTCGTGGAACTACAACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 537  
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 538 GACCCCGCGAGGTGGCG 597  
Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
Db 598 ATGAACAACGTCACCGTGTATGCGCGAGGGCTTCGCGCGCGCACCCATCAGGGCCATCAAC 657  
Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240  
Db 658 GCGCGCGTCTGAGTGCAGCGGGAACAACCCCGCGCGAGATGAACGCGCGCGCTCGGTACTAC 717  
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257  
Db 718 AGGCACTACTGCCCGCAGCTCGCGGTGCACCCAGGCGCCCAACCTTCACTTGC 768

RESULT 9  
US-10-692-367-59  
; Sequence 59, Application US/10692367  
; Publication No. US2005005059A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.



```
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(771)
US-10-692-367-59

Alignment Scores:
Pred. No.: 3,35e-158 Length: 771
Score: 1382.50 Matches: 244
Percent Similarity: 96.89% Conservative: 5
Best Local Similarity: 94.94% Mismatches: 7
Query Match: 95.21% Indels: 1
DB: 19 Gaps: 1

US-10-692-367-12 (1-257) x US-10-692-367-59 (1-771)
Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGTGCAGCCAACTTCTGCTGCAGCAAGTTTGGCTACTGCGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGCTACTGCGGCGACGGGTGCCAGTCCGCGCGCTCG---GGCGGC 117
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 118 GGTGGCGCGGTGGCGGCGGAGCGGCGGAGGCGAGTGGCGGTGCGAACTGGCTTAATGTG 177
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 178 GTACCCGACGGTCTTCAACGGCATCAAGAACCCAGCGCGGAGCGGTGCGAGGGCAG 237
Qy 81 AenPheTyrThrArgSerAlaPheLeuGluAlaIleAlaTyrProGlyPheAlaHis 100
Db 238 AACTTCTACACCGGAGCGGTTCCTGAGCGCGCTCAAGGCGGTACCCAGGCTTCGCCCAT 297
Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaPheAlaHisAlaThrHis 120
Db 298 GGCGGGTACAGGTGACGGGCAAGCGCGAGATTGCCGCTTCTTCGGCGCATGTCAACGCAC 357
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAenLysSerAsnAlaTyrCysAspPro 140
Db 358 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCCCTACTGCGACCCG 417
Qy 141 ThrLysArgGlnTrrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 418 ACCAAGAGCGAGTGGCGTGGCGCGCGGCGGAGAGTACTACGGCGCGCGCGCGCTGCGAG 477
Qy 161 IleSerTrrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 161 IleSerTrrAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180

478 ATCTCGTGGAACTACAACTAGCGGCGCGGGAGGGCCATCGGCTTCGACGGGCTCGGG 537
181 AspProGlyArgValAlaIleArgAspAlaValAlaPheLysAlaAlaLeuTrrPheTrrP 200
538 GACCCCGGCGAGGTGGCGCGGACGCGTGGTGGCGTTCAAGGCGCGCTCTGGTTCTGG 597
201 MetAenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAen 220
598 ATGAACAACGTCACCGTGTGATGCCGAGGCGTTCGGCGCCACCATCAGGCGCATCAAC 657
221 GlyAlaLeuGluCysAenGlyAsnGlyAsnProAlaGlnMetAenAlaArgValGlyTyr 240
658 GCGCCCTCGAGTCCGACGAGGAAACACCCGCCCGATGATGAACGCGCGGTGCGGTACTAC 717
241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAenAenLeuTrrCys 257
718 AGCGAGTACTGCGCGCAGCTCGGCGTCCAGCCAGGCGCCCAACCTCACTTGC 768

RESULT 10
US-10-389-432B-45
; Sequence 45, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 48949200300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: 4N1/80_F8 nucleic acid
US-10-389-432B-45

Alignment Scores:
Pred. No.: 3,86e-158 Length: 771
Score: 1382.00 Matches: 241
Percent Similarity: 97.28% Conservative: 9
Best Local Similarity: 93.77% Mismatches: 7
Query Match: 95.18% Indels: 0
DB: 18 Gaps: 0

US-10-692-367-12 (1-257) x US-10-389-432B-45 (1-771)
Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGTGCAGCCAACTTCTGCTGCAGCAAGTTTGGCTACTGCGGC 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGCTACTGCGGCGACGGGTGCCAGTCCGCGCGCTCGCGCGCGGTTCGCCCAT 120
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGT 180
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTACCCGACGCTTCTTCAACGGCATCAAGAACCCAGCGCGGAGCGGTGCGAGGGCAG 240
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleGlyPheAspGlyLeuGly 100
Db 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleGlyPheAspGlyLeuGly 100
```

Db 241 AACTTCTACACCCGGAGCGGTTCTGAGCCCGTCAAGGGGTACCCAGGCTTCGCCCAT 300  
Qy 101 GlySerGluValGluArgGlyArgGluLeuAlaPheAlaHisAlaThrHis 120  
Db 301 GCGGGTGCAGGTGCAGGGCAAGCGGAGATCGCGCTTCTTCGGCGCACCGCACGCAC 360  
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
Db 361 GAGACCGGGCATTTCTGTACTATCAGCGAGATCAACAGAGCAACGCCCTACTCGACCCG 420  
Qy 141 ThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
Db 421 ACCAAGAGCGAGTGGCGCTGCGCGCGGAGGAGTACTACGGGCGCGCGCGCTGCGAG 480  
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
Db 481 ATCTCGTGGAACTACAATACAGGGCGCGCGGGAGGGCCATCGGCTTTGACGGGCTCGGG 540  
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 541 GACCCCAACAGGTGGCGCGGAGCGCGTGTGGGTTCAGAGGGCGGCTCTGGTCTGG 600  
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
Db 601 ATGAACAGCGTGCAGCGGGTGTGCGCGAGGGTTCGGCGCGCACCCAGGGCCATCAAC 660  
Qy 221 GlyAlaLeuGlyCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240  
Db 661 GCGCGCTTCGAGTGCACGGGAACAACCCCGCCAGATGAACGCGCGGTGCGGTACTAC 720  
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257  
Db 721 AAGCAGTACTGCGCCAGCTCGGCGTGCACCCAGGGCCCACTTGC 771

## RESULT 11

US-10-692-367-45  
; Sequence 45, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 54916200320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; NAME/KEY: CDS  
; LOCATION: (1)...(774)  
US-10-692-367-45  
Alignment Scores: 3,876-158 Length: 774  
Pred. No.: 1382.00 Matches: 241  
Score: 97.28% Conservative: 9  
Percent similarity: 97.28%

Best Local Similarity: 93.77% Mismatches: 7  
Query Match: 95.18% Indels: 0  
DB: 19 Gaps: 0

US-10-692-367-12 (1-257) x US-10-692-367-45 (1-774)

Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
Db 1 TCGATGCAGAACTGCGGTCGCCAGCAAACTGATGTCAGCGGTTTCGGCTACTCGCGGC 60  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACCAGCCAGAGTACTCGGCGCAGCGGTGCGGCGCGCTGCCCTCGCGCGCGCGGT 120  
Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60  
Db 121 GCGGT 180  
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80  
Db 181 GTCACCGAGCGGTTCTTCAACGGCATCAAGAACCCAGCGCGGAGCGGTGCGAGGCAAG 240  
Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaTyrProGlyPheAlaHis 100  
Db 241 AACTTCTACACCCGAGCGGTTCTGAGCGCGGTCAAGCGCGTCAAGCGGCTTCGCCCAT 300  
Qy 101 GlyGlySerGluValGluArgLysArgGluLeuAlaAlaPheAlaHisAlaThrHis 120  
Db 301 GCGGGTGCAGGTGCGAGGCAAGCGCGAGATCGCGCGCTTCTTCGCGCGCACCGCAC 360  
Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro 140  
Db 361 GAGACCGGGCATTTCTGTACTATCAGCGAGATCAACAGAGCAACGCCCTACTCGACCCG 420  
Qy 141 ThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160  
Db 421 ACCAAGAGCGAGTGGCGCTGCGCGCGGCGGAGTACTACGGGCGCGCGCGCTGCGAG 480  
Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180  
Db 481 ATCTCGTGGAACTACAATACGGGCGCGCGGGAGGGCCATCGGCTTTGACGGGCTCGGG 540  
Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200  
Db 541 GACCCCAACAGGTGGCGCGGAGCGCGTGTGGGTTCAGAGGGCGGCTCTGGTCTGG 600  
Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220  
Db 601 ATGAACAGCGTGCAGCGGGTGTGCGCGAGGGTTCGGCGCGCACCCAGGGCCATCAAC 660  
Qy 221 GlyAlaLeuGlyCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240  
Db 661 GCGCGCTTCGAGTGCACGGGAACAACCCCGCCAGATGAACGCGCGGTGCGGTACTAC 720  
Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257  
Db 721 AAGCAGTACTGCGCCAGCTCGGCGTGCACCCAGGGCCCACTTGC 771

## RESULT 12

US-10-389-432B-65  
; Sequence 65, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; TITLE OF INVENTION: ACTIVITY  
; FILE REFERENCE: 48949200300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029

```
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: 4N1/35_G5 nucleic acid
US-10-389-432B-65

Alignment Scores:
Pred. No.: 1,57e-157 Length: 771
Score: 1377.00 Matches: 240
Percent Similarity: 96.50% Conservative: 8
Best Local Similarity: 93.39% Mismatches: 9
Query Match: 94.83% Indels: 0
DB: 18 Gaps: 0

US-10-692-367-12 (1-257) x US-10-389-432B-65 (1-771)

Qy 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGGTGCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db 61 ACAGCCGACGAGTACTGCGCGGACGGGTGCGAGTGCAGTCCGCCCGCGGTGGCGGT 120

Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Qy 61 ValThrAspAlaPhePheAsnGlyTyrLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTCCCGACTCTCTTTCACGGCATCAAGCAACCGCGCGCGCGCGCGCGCGCGCGCG 240

Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAla 100
Db 241 AACTTCTACACCCGAGCGCGTCTCTGAGCGCGGTCAAGGGGTACCCAGGCTTCGCC 300

Qy 101 GlySerGluValGluArgLysArgGluLeuAlaPheAlaPheAlaHisAlaThrHis 120
Db 301 GCGCGGTTCGAGGTGCAGGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360

Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAsp 140
Db 361 GAGACCGGGCATTTCTGTACTATCATCAGCGAGATCAACAGAGCAACGCGCTACTG 420

Qy 141 ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGCGAGTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTGTGTGAATACTACACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTyrPheTyr 200
Db 541 GACCCCAACAGGTGGCGCAGGACGCCGTGTGGGTTCAGAGCGCGCGCGCTCTGGTCT 600

Qy 201 MetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 601 ATGAACAACGTGCACCGGTGATCGCGCAGGGCTTCGGCGCGCACCATCAGGGCCAT 660

Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyr 240
Db 661 GCGCGCTTCGAGTGCAGGCGGGAACAACCCCGCCAGATGAACGCGCGCGCTCGGTACT 720

Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnLeuThrCys 257
Db 721 AAGCAGTACTCCCGCAGCTCGCGGTGCAGCCAGGGGCCAACCTCACTTGC 771
```

```
RESULT 13
US-10-692-367-65
; Sequence 65, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(774)
US-10-692-367-65

Alignment Scores:
Pred. No.: 1,57e-157 Length: 774
Score: 1377.00 Matches: 240
Percent Similarity: 96.50% Conservative: 8
Best Local Similarity: 93.39% Mismatches: 9
Query Match: 94.83% Indels: 0
DB: 19 Gaps: 0

US-10-692-367-12 (1-257) x US-10-692-367-65 (1-774)

Qy 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGGTGCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db 61 ACAGCCGACGAGTACTGCGCGGACGGGTGCGAGTGCAGTCCGCCCGCGGTGGCGGT 120

Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 121 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Qy 61 ValThrAspAlaPhePheAsnGlyTyrLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 181 GTCCCGACTCTCTTTCACGGCATCAAGCAACCGCGCGCGCGCGCGCGCGCGCGCG 240

Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAla 100
Db 241 AACTTCTACACCCGAGCGCGTCTCTGAGCGCGGTCAAGGGGTACCCAGGCTTCGCC 300

Qy 101 GlySerGluValGluArgLysArgGluLeuAlaPheAlaPheAlaHisAlaThrHis 120
Db 301 GCGCGGTTCGAGGTGCAGGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360

Qy 121 GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAsp 140
Db 361 GAGACCGGGCATTTCTGTACTATCATCAGCGAGATCAACAGAGCAACGCGCTACTG 420
```

```
Qy 141 ThrlyArgGlnTyrProCysAlaAlaGlyGlnlystYrGlyArgGlyProLeuGln 160
Db 421 ACCAAGAGGCGAGTGGCGGTGCGCGGGGAGAGTACTACGGGGCGTGGCCCTGCGAG 480

Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 481 ATCTCGTGAACACTACACTAGCGGCGCGGGAGGGCCATCGCTTCGACGGGCTCGCC 540

Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaLeuTrpPheTrp 200
Db 541 GACCCCAACAGGCTGGCGCAGCAGCCCGTGGTGGCTTCAAGGGCGGCGCTGGTGGTTC 600

Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 601 ATGAACAACAGTGCACCGTGTATCGCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 660

Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
Db 661 GCGGCCCTCGAGTGGCGCGGAGACACACCCCGCCAGATGAACGCGCGGCTCGGCTACTAC 720

Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 721 AAGCAGTACTGCGCGCAGCTGGGGTGCAGCCAGGGCCCAACCTCACTTGC 771

RESULT 14
US-10-389-432B-61
; Sequence 61, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Naseer
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 48949200300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: 4N1/11_B11 nucleic acid
US-10-389-432B-61

Alignment Scores:
Pred. No.: 4.15e-157 Length: 768
Score: 1373.50 Matches: 242
Percent Similarity: 97.28% Conservative: 8
Best local Similarity: 94.16% Mismatches: 6
Query Match: 94.59% Indels: 1
DB: 18 Gaps: 1

US-10-692-367-12 (1-257) x US-10-389-432B-61 (1-768)

Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTGCGGGTGCAGCAACAGTATCTGCAGCAAGTTCGGCTACTGCGGCG 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGAGTACTGCGGGCGAGCGGTGCAGTGTGGCGCCCGTGGCGCGC 117

Qy 41 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
Db 118 GCGCGCGGTGGCGGGCGAGCGCGGAGGCGAGTGGCGGTGCGAACTGCTAGCGTGC 177
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```
Qy 61 ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys 80
Db 178 GTACCGCGCTCTTCTTCAACGCATCAGAGCCGCGGAGCGGGTGGAGGGCAAG 237

Qy 81 AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaIleAlaIleAlaIle 100
Db 238 AACCTTCTACACCGGAGCGGTTCCTGAGCGCGGTCAAGGGGTACCCAGGCTTCGCCCAT 297

Qy 101 GlyGlySerGluValGluArgLysArgGluIleAlaIleAlaPhePheAlaIleAlaIle 120
Db 298 GCGCGCTCCGAGGTGCGAGCGCAAGCGCGAGATTTCGCGCTTCTTCGCGGCAAGCGCAC 357

Qy 121 GlnThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaIleAlaIleAla 140
Db 358 GAGACCGGGCATTTCTCTATCATCAGCATCAACAAGAGCAACGCTACTGCGACCCG 417

Qy 141 ThrLysArgGlnTrpProCysAlaAlaGlyGlnlystYrGlyArgGlyProLeuGln 160
Db 418 ACCAAGAGGCGAGTGGCGGTGCGCGCGGCGAGAGTACTACGGCGCGCGCTGCAG 477

Qy 161 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly 180
Db 478 ATCTCGTGAACACTACAACTACGGCGCGCGGAGGGCCATCGGCTTCGACGGGCTCGCC 537

Qy 181 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 200
Db 538 GACCCCGCAGGGTGGCGCGGAGCGCGCTGGTGGCTTCAAGGGCGGCTCTGGTTCGG 597

Qy 201 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 220
Db 598 ATGAACAACAGTGCACCGTGTATCGCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 657

Qy 221 GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr 240
Db 658 GCGCGCTCGAGTGCAGCGGAGCAACCCCGCCAGATGAACGCGCGGCTCGGCTACTAC 717

Qy 241 ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys 257
Db 718 AAGCAGTACTGCGCGCAGCTGGGGTGCAGCCAGGGCCCAACCTCACTTGC 768

RESULT 15
US-10-692-367-61
; Sequence 61, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Naseer
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE:
; NAME/KEY: CDS
```

i LOCATION: (1)...(771)  
US-10-692-367-61

## Alignment Scores:

Pred. No.:	4.17e-157	Length:	771
Score:	1373.50	Matches:	242
Percent Similarity:	97.28%	Conservative:	8
Best Local Similarity:	94.16%	Mismatches:	6
Query Match:	94.59%	Indels:	1
DB:	19	Gaps:	1

US-10-692-367-12 (1-257) x US-10-692-367-61 (1-771)

Qy	1	SerMetGlnAsnGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly	20
Db	1	TCGATGCAAGAACTCGCGGTGCGAGCAAACTATGCTGCAGCAAGTTCTGGCTACTGGCGC	60
Qy	21	ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly	40
Db	61	ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCCGTGCGCCCG---GGCGGC	117
Qy	41	Gly	60
Db	118	GGCGCGGTGCGCGCGCGGAGCGCGGCGGAGTGGCGTGGCGACGTCGCTAGCGTC	177
Qy	61	ValThrAspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLys	80
Db	178	GTACCGCGCTCTTCTTCAACGGCATCAAGAGCCAGCGCGGAGCGGTGCGAGGGCAAG	237
Qy	81	AsnPheTyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHis	100
Db	238	AACTTCTACACCGGAGCGGCTTCTTGAGCCCGTCAAGGCGTACCCAGGCTTCGCCAT	297
Qy	101	GlyGlySerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHis	120
Db	298	GGCGGCTCCGAGGTCCGAGCGAAGCGGAGATTGCGCGCTTCTTCCGCGACGCCACGCAC	357
Qy	121	GluThrGlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspPro	140
Db	358	GAGACCGGGCAATTCTGTCTACATCAACGAGATCAACAGAGCAACGCTACTGCGACCCG	417
Qy	141	ThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln	160
Db	418	ACCAAGAGGCAAGTGGCCGTGCGCGCGGGGCGAAGTACTACGGGCGGCGCGCTGCGAG	477
Qy	161	IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGly	180
Db	478	ATCTCGTGAACACTACAACCTACGGCGCCCGCGGAGGGCCATCGGCTTCGACGGGCTCGCC	537
Qy	181	AspProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTrp	200
Db	538	GACCCCGCAGGTGGCGCGGACCGCGTGGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGG	597
Qy	201	MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn	220
Db	598	ATGAACACAGTGCACCGTGTATGCCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAAC	657
Qy	221	GlyAlaLeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyr	240
Db	658	GGCGCGTCTGAGTGGCAGCGGCAACACCCCGCCAGATGACGCGCGCTCGGCTACTAC	717
Qy	241	ArgGlnTyrCysArgGlnLeuGlyValAspProGlyAsnAsnLeuThrCys	257
Db	718	AAGCAGTACTGCCCGCAGCTCGCGGTGACCCAGGCGCCCACTCACTTGC	768

Search completed: May 23, 2005, 22:41:51  
Job time : 419.647 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 17:04:03 ; Search time 2300.33 Seconds  
(without alignments)  
4252.663 Million cell updates/sec

Title: US-10-692-367-12

Perfect score: 1452

Sequence: 1 SMQCGQPNVCCSKFYCG.....GYRQYRQLGVDPGNLTC 257

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0			0.5
Ygapop 6.0			7.0
Deiop 6.0			7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2 1/USPTO spooll/US10692367/runat 20052005 172255 20018/app query.fasta\_1.846  
-DB=EST -QWTF=fastap -SUPPLX=rest -MINMATCH=0.1 -LOECL=0 -LOEEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10692367.CGN 1 1 3556 @runat 20052005 172255 20018 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6  
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*

	1:	gb_est1.*
2:	gb_est2.*	
3:	gb_hc.*	
4:	gb_est3.*	
5:	gb_est4.*	
6:	gb_est5.*	
7:	gb_est6.*	
8:	gb_gsl1.*	
9:	gb_gsl2.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1333	91.8	1179	3	AY103546 Zea mays
2	1184	81.5	958	4	BG837479 Zea mays
3	1183.5	81.5	855	4	BG837663 Zea mays
4	1135.5	78.2	737	6	CD435649 Zea mays
5	1110.5	76.5	767	7	C0524416 Zea mays
6	1096	75.5	837	7	CN133023 Zea mays
7	1047	72.1	710	6	CD43492 Zea mays
8	1032	71.1	978	9	C0328450 Zea mays
9	1024	70.5	716	7	C0520138 Zea mays

10	1020.5	70.3	647	6	CA197556	SCBPA106
11	990	68.2	628	4	BM736454	BM736454
12	989	68.1	625	5	BM736454	BM736454
13	980.5	67.5	786	6	CA270202	CA270202
14	977.5	67.3	801	7	CN151443	CN151443
15	957.5	65.9	856	6	CB981065	CB981065
16	957.5	65.9	870	6	CB982079	CB982079
17	957.5	65.9	895	6	CB981562	CB981562
18	956.5	65.9	887	6	CB981996	CB981996
19	956.5	65.9	893	6	CB980773	CB980773
20	956.5	65.9	904	6	CB981568	CB981568
21	956.5	65.9	920	6	CB981043	CB981043
22	956	65.8	741	6	CD994869	CD994869
23	955.5	65.8	861	6	CB980332	CB980332
24	955.5	65.8	889	6	CB982059	CB982059
25	954.5	65.7	895	6	CB980998	CB980998
26	954	65.7	880	7	CD994156	CD994156
27	953.5	65.7	880	7	CF200723	CF200723
28	953	65.6	688	6	CA281399	CA281399
29	952	65.6	753	6	CD994885	CD994885
30	951.5	65.5	850	6	CB980173	CB980173
31	951.5	65.5	874	7	CF200575	CF200575
32	951	65.5	820	6	CD995497	CD995497
33	950	65.4	812	7	CN132942	CN132942
34	949.5	65.4	851	6	CB980181	CB980181
35	946	65.3	575	6	CD994132	CD994132
36	946	65.2	578	6	CD994454	CD994454
37	943.5	65.0	845	6	CB981100	CB981100
38	943.5	65.0	855	6	CB980750	CB980750
39	940.5	64.8	680	6	CA100718	CA100718
40	935.5	64.4	873	7	CF202886	CF202886
41	933.5	64.3	818	7	CF201611	CF201611
42	933	64.3	618	2	BE918591	BE918591
43	926	63.8	636	4	BG840312	BG840312
44	925	63.7	754	6	CD995176	CD995176
45	916.5	63.1	637	4	B1478959	B1478959

#### ALIGNMENTS

RESULT 1

LOCUS AY103546

DEFINITION Zea mays PCOL55066 mRNA sequence.

ACCESSION AY103546

VERSION AY103546.1

KEYWORDS HTc.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 1179)

AUTHORS Hainey, C.P., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,

Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

Maize Mapping Project/DuPont Consensus Sequences for Design of

Overgo Probes

JOURNAL Unpublished (2002)

REFERENCE 2 (bases 1 to 1179)

AUTHORS Coe, E.H.

TITLE Direct Submission

JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones,

these are publicly available from ZmDB and may be found by BLAST

searching at MSI, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,

www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat

Schnable, Iowa State, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.

FEATURES Location/Qualifiers

source 1..1179

/organism="Zea mays"

linear HTC 16-OCT-2002







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Db      217  GCCAGATGACGGCGGTGGCTACTACAGGAGTACTGCCGCCAGCTCGGCGTGCAC 158
Qy      251  ProGlyAenAenLeuThrCys 257
Db      157  CCGGGGCCCAACCTCACCTGC 137

RESULT 4
CD435649
LOCUS      CD435649
DEFINITION EL01N0364B04.b Endosperm_3 Zea mays cDNA, mRNA linear EST 03-JUN-2003
ACCESSION  CD435649
VERSION     CD435649.1 GI:31351292
KEYWORDS    EST.
SOURCE      Zea mays
ORGANISM    Zea mays
            Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 737)
AUTHORS     Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.P.,
            Larkins, B., Beecraft, P. and Messing, J.
TITLE       Characterization of the maize endosperm transcriptome and its
            comparison to the rice genome
JOURNAL     Genome Res. 14 (10), 1932-1937 (2004)
COMMENT     Contact: Lai, Jinheng
            Dr. Joachim Messing's lab
            Waksman Institute, Rutgers University
            190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
            Tel: 732-445-3801
            Fax: 732-445-5735
            Email: jlai@waksman.rutgers.edu
            Seq primer: T3
            Location/Qualifiers
            1..737
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FEATURES             source
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            XhoI"

ORIGIN
Alignment Scores:
Pred. No.:      7,67e-102      Length:      737
Score:          1135.50      Matches:    203
Percent Similarity: 91.74%      Conservative: 8
Best Local Similarity: 88.26%      Mismatches: 7
Query Match:    78.20%      Indels:     12
Db:             6             Gaps:      1

US-10-692-367-12 (1-257) x CD435649 (1-737)

Qy      3  GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrcysGlyThrThr 22
Db      83  CAGAACTCGGCTGCCACCAACCTCTGTCAGCAAGTTCGGCTACTCGGCGACGACC 142
Qy      23  AspGlnTyrcysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42
Db      143  GACGAGTACTCGGGACGGGTGCGCAGTCGGGCCCGTCCGCTCGGGCGGGCGGC--- 199
Qy      43  GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62
Db      200  -----GGTGTGCGAAGCTGGCTAGCGTCTGTCACC 229
Qy      63  AspalApeAenAenGlyLeuAenGlnAlaGlySerGlyCysGlnGlyLeuAenPhe 82
Db      230  GGCTCTTCTTCACGGGATCAGAACCGCGGGAGCGGGTGCAGGGCAAGACTTC 289
Qy      83  TyrThrArgSerAlaPheLeuGlnAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAla 102
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Db      290  TACACCGGAGCGCGTTCCTGAGCGCGGTCAAGCGGTACCCAGGCTTCGCCCATGGCGG 349
Qy      103  SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122
Db      350  TCGCAGGTGACGGCAAGCGGAGATCGCCGCTTCTTCGGCGACCGCACGACGAGACC 409
Qy      123  GlyHisPheCysTyrlleSerGluValAsnLysSerAsnAlaTyrcysAspProThrLys 142
Db      410  GGGCATTTCTGTACATCAGCGAGATCAACAGANGCAACGCTACTTCGGACCCGACCAAG 469
Qy      143  ArgGlnTrpProCysAlaAlaGlyGlnLysTyrcysGlyArgGlyProLeuGlnIleSer 162
Db      470  AGCAGTGGCGGTGCGCGCGGCGGAGTACTACGGGCGGCGCGCTCGCAGATCTCG 529
Qy      163  TrpAsnTyrcysTyrcysGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182
Db      530  TGGAACTACAACTACGGCGCGCGGAGCGGAGGCCATCGCTTCGACGGGCTCGGGGACCCC 589
Qy      183  GlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn 202
Db      590  GGCAGGGTGGCGGGGACGCGGTGTGCGTTCAGGGCGGGCTCTGTTCTGGATGAAC 649
Qy      203  AsnValHis-ArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAl 222
Db      650  AGCGTGCACGGGGTGTGCGCGGAGGGGTTCGGCGCCACCACCGGGCCATCAACGGCGC 709
Qy      222  aLeuGluCysAsnGlyAsnAenProAla 231
Db      710  CCTCGAGTGGCGGGCGGGAACACCCCGCC 737

RESULT 5
CD524416
LOCUS      CD524416
DEFINITION 3530.1.161.1_E12.Y.1 3530 - Full length cDNA library created by
            Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION  CD524416
VERSION     CD524416.1 GI:50329290
KEYWORDS    EST.
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 767)
AUTHORS     Walbot, V.
TITLE       Maize ESTs from various cDNA libraries sequenced at Stanford
            University
            Unpublished (1999)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 3530.1.161.1 row: E column: 12.
            Location/Qualifiers
            1..767
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            /cultivar="B73"
            /db_xref="taxon:4577"
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            /dev_stage="varies by tissue"
            /lab_host="DH10B"
            /clone_lib="3530 - Full length cDNA library created by
            Invitrogen from multiple tissues"
            /note="Organ: silks, husks, ears, pollen, shoot tips,
            leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
            6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
            Project contracted with Invitrogen to produce a
            normalized, full length library in a pSPORT vector. This
            is a Gateway compatible vector, permitting clone movement

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to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,38e-99 Length: 767  
 Score: 1110.50 Matches: 196  
 Percent Similarity: 93.18% Conservative: 9  
 Best Local Similarity: 89.09% Mismatches: 8  
 Query Match: 76.48% Indels: 7  
 DB: 7 Gaps: 1

US-10-692-367-12 (1-257) x C0524416 (1-767)

Qy 3 GlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyCysGlyThrThr 22  
 Db 127 CAGAACTCGCGTCTGCGAGCAAGCATGCTGCGAGCAAGTTTGGCTACTGCGGCGACGACC 186  
 Qy 23 AspGluTyCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGly 42  
 Db 187 GACGAGTACTCGCGGACGGTGCAGTGCAGGCGCGTGCCTCGCGGCGCGGCGGCGAGC 246  
 Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr 62  
 Db 247 AGTGGCGC-----GGTGGTGGACGTTGGCTAGCTGTCTACC 285  
 Qy 63 AspAlaPheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPhe 82  
 Db 286 GGCCTCTTCTCAACGGCATCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 345  
 Qy 83 TyThrArgSerAlaPheLeuGluAlaIleAlaAlaPhePheAlaHisAlaThrHisGluThr 102  
 Db 346 TACACCGGAGCGGTCTCTGAGCGCGCTCAAGCGGTACCCAGCGCTTTCGCCCATATGGCGGG 405  
 Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr 122  
 Db 406 TCGCAGGTGCGAGGCGGAGATGCCGCTTCTTCGCGAGCGGCGGCGGCGGCGGCGGCGG 465  
 Qy 123 GlyHisPheCysTyrlleSerGluValAsnLysSerAenAlaTyCysAspProThrLys 142  
 Db 466 GGGCATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCGCTACTGCGAGCCCGGACCAAG 525  
 Qy 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyTyTyGlyArgGlyProLeuGlnIleSer 162  
 Db 526 AGGAGTGTGCGTGTGCGCGGCGGAGAGTACTACGCGCGCGCGCGCTGCAATCTCG 585  
 Qy 163 TrpAenTyAenTyGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182  
 Db 586 TGGAACTACAACTACGCGGCGGCGGAGGCCATTCGGCTTCGACGGGCTCGGGGACCCC 645

Qy 183 GlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn 202  
 Db 646 GGCAGGGTGGCGCGGAGCGCGTGGTTCAGGCGGCGCTCTGGTTCTGGATGAAC 705  
 Qy 203 AsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla 222  
 Db 706 AGCGTGACGCGGGTGGTGGCGGCGGTTGGCGGCCACACCGAGGGCCATCAAGCGGCC 765

RESULT 6  
 CNI133023  
 LOCUS CNI133023 837 bp mRNA linear EST 01-APR-2004  
 DEFINITION OX1\_9\_D11.g1\_A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA clone OX1\_9\_D11\_A002 5', mRNA sequence.  
 ACCESSION CNI133023  
 VERSION CNI13023.1 GI:45963543  
 KEYWORDS EST.  
 SOURCE Sorghum bicolor (sorghum)  
 ORGANISM Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
 REFERENCE 1 (bases 1 to 837)  
 AUTHORS Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.  
 TITLE An EST database from Sorghum: oxidatively stressed leaves and roots  
 JOURNAL Unpublished (2003)  
 COMMENT Other ESTs: OX1\_9\_D11.b1\_A002  
 Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpratt@uga.edu  
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).

## FEATURES

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 /cultivar="BTx623"  
 /db\_xref="taxon:4558"  
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 /lab\_host="DH10B-T1 phage-resistant E. coli"  
 /clone\_11b="Oxidatively-stressed leaves and roots"  
 /note="Organ: Leaf and Root; Vector: pME18S-FL3; Site: 1: XhoI; Site\_2: XhoI; The library was prepared from polyA+ RNA from oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were misted with 10 uM methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

## ORIGIN

Alignment Scores:  
 Pred. No.: 7.21e-98 Length: 837  
 Score: 1096.00 Matches: 199  
 Percent Similarity: 84.15% Conservative: 8  
 Best Local Similarity: 80.89% Mismatches: 27  
 Query Match: 75.48% Indels: 12

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US-10-692-367-12 (1-257) x CN133023 (1-837)			
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Db	134	CAGAACTACGGCTCCAGGACAGGTTACTGCTGCAGCAAGTTCCGTTACTCGCGCACGACC	193
QY	23	AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly	42
Db	194	GACGAGTACTCGCGCGACGGTGCAGTCGGGCGCGCTGCGCTCGCGCGGCGAGCAGT	253
QY	43	GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAsnValAlaAsnValValThr	62
Db	254	GGAGGTGG-----AACGTGGCTGGGTTGTTCACC	283
QY	63	AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGlyGlyLysAsnPhe	82
Db	284	GACGCATTCTCAACAGCATCAAGAACACAGCGCGGAACGGTTCGAGGGGCAAGAACTTC	343
QY	83	TyrThrArgSerAlaPheLeuGluAlaIleAlaIleAlaTyrProGlyPheAlaHisGlyGly	102
Db	344	TACACCGGAGCGGTTCTCGAGCGCGCCGACGCTACAAAGGCTTC-----GGTGGC	397
QY	103	SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr	122
Db	398	AGTCTGGTGCAGGCAAGCGGAGATCGCCGCTTCTTCGCCCAACATCACGACGACGACC	457
QY	123	GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys	142
Db	458	GGACATTCTCTACATCAGCGAGATCAACAAGAACAGCGCTACTGCGACTCGAGCAAC	517
QY	143	ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer	162
Db	518	AGGCACTGTCGCGTGTGCGCGGGTTCAGAACTACTACGCGCGCGCGCTGCAAACTTCG	577
QY	163	TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro	182
Db	578	TGGAACTACACTACGGGCTTCGCGGGAGGACATCGGCTTCGACGGGCTTCGGAACCG	637
QY	183	GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn	202
Db	638	GACAGGTGGCGCAAGACCGCGTGTGCGTTCAGACGCGCTCTGCTTCGACCAAC	697
QY	203	AsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla	222
Db	698	AACGTGCAAGGGTGTATGTCAGGGGTTTCGGCGCCACCATCAGGGCCCATCAACGGCGCC	757
QY	223	LeuGluCysAsnGlyAsnAsnProAlaGlnMetAsnAlaArgValGlyTyrTyrArgGln	242
Db	758	CTGAGTGCACCGGCAAGATACTGCCAGATGAACGGCGGGTGGGTACTACTACAGGCAG	817
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DEFINITION	EL01N0427B11.b EndospERM_4 Zea mays cDNA, mRNA sequence.		
ACCESSION	CD443492		
VERSION	CD443492.1	GI:31359135	
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 710)		
AUTHORS	Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Bercraft, P. and Messing, J.		
TITLE	Characterization of the maize endospERM transcriptome and its comparison to the rice genome		
JOURNAL	Genome Res. 14 (10), 1932-1937 (2004)		
COMMENT	Contact: Lai, Jinsheng Dr. Joachim Messing's lab Waksman Institute, Rutgers University 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801 Fax: 732-445-5735 Email: jlai@waksman.rutgers.edu Seq primer: T3		
FEATURES	Location/Qualifiers		
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Pred. No.:	1047.00	Matches:	183
Score:	94.53%	Conservative:	7
Percent Similarity:	91.04%	Mismatches:	5
Best Local Similarity:	72.11%	Indels:	6
Query Match:	6	Gaps:	1
DB:			
US-10-692-367-12 (1-257) x CD443492 (1-710)			
QY	3	GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr	22
Db	126	CAGAACTGCGGCTGCCAGCCAAACGCTGCTGCAGCAAGTTCCGTTACTCGCGCACGACC	185
QY	23	AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly	42
Db	186	GACGAGTACTGTCGCGACGCGTGCAGTCGGGCGCGCTCGCGCGCGCGCGCGGC	245
QY	43	GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAlaAsnValAlaAsnValValThr	62
Db	246	GGCAGTGGTGGC-----GGTGGTGGCAACGTGGTCTAGCTCGTCAAC	287
QY	63	AspAlaPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGlyLysAsnPhe	82
Db	288	AGTCTCTCTTCAACGGCATCAGAACACAGCGCGGAGCGGTCGAGGGGCAAGAACTTC	347
QY	83	TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly	102
Db	348	TACACCGGAGCGGTTCTCTGAGCGCGCTCAAGGCGTACCAGGCTTCGCCCATGGCGGG	407
QY	103	SerGluValGluArgLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThr	122
Db	408	TCGAGGTGCAGGGCAAGCGGAGATCGCGCTTCTTCGGCACGCGCACGACGAGACC	467
QY	123	GlyHisPheCysTyrIleSerGluValAsnLysSerAsnAlaTyrCysAspProThrLys	142
Db	468	GGGCATTTCTGTACATCAGCGAGATCAACAGAGCAACGCTACTCGACCCGACCAAG	527
QY	143	ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer	162
Db	528	AGGCACTGCGCGTTCGCGCGGCGGAGTACTACGCGCGCGCGCTCGAGTCTCG	587
QY	163	TrpAsnTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro	182
Db	588	TGGAACTACAACTACGGGCGCGCGGAGGCGCATCGCTTCGACGGGCTCGGGAGACCCC	647
QY	183	GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsn	202
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QY	203	Asn	203
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Db		708 AGC 710
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	ACCESSION	CG328450
	VERSION	CG328450.1 GI:34245716
	KEYWORDS	GSS.
	SOURCE	Zea mays
	ORGANISM	Zea mays
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
	REFERENCE	1 (bases 1 to 978)
	AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
	TITLE	Consortium for Maize Genomics
	JOURNAL	Unpublished (2002)
	COMMENT	Other GSSs: OG3CW08TH Contact: Cathy Whitelaw
	TIGR	Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TF Class: sheared ends.
	FEATURES	Location/Qualifiers
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		/mol_type="genomic DNA"
		/strain="B73"
		/db_xref="taxon:4577"
		/clone="ZMMBma0778B15"
		/clone_lib="ZM_0.7_1.5 KB"
		/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"
	ORIGIN	
	Alignment Scores:	
	Pred. No.:	Length: 978
	Score:	1032.00 Matches: 197
	Percent Similarity:	Conservative: 9
	Best Local Similarity:	Mismatches: 15
	Query Match:	Indels: 37
	DB:	Gaps: 1
	US-10-692-367-12 (1-257) x CG328450 (1-978)	
Qy	37 SerGlycylglycylglycylglycylglycylglycylglycylglycylglycylglycylalan	56
Db	976 TCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG	917
Qy	57 ValAlaAsnValThrAspAlaPheAsnGlyIleLeuAsnGlnAlaGlySerGly	76
Db	916 GTGGCTAATGT-GTCAACGAGCGGTTCCTCAACGGCATCAAGAACCCGCGGGCGGG	858
Qy	77 CysGluGlyLysAsnPheTyrrArg-SerAlaPheLeuGluAlaIleAlaAlaTyrrPr	96
Db	857 TGCAGGGCAAGAATTCTACACCGGAGCGGTTCCTGAGCGCGGTCAACGCCGTACCC	798
Qy	96 OGIYPheAlaHisGlyGlySerGluValGluArgLysArgGluIleAlaAlaPhePhal	116
Db	797 GGGCTTCGCCCATYGGGGGAACGAGGTGGAGGCAAGCGGAGATCGCGGCTTCCTGCG	738
Qy	116 aHISAlaThrHisGluThrGly-----	123
Db	737 GCACGTCAACGACGACGACGACGTAAGTTATTAAACACTTAACCAACACGGAACTA	678
Qy	123 -----	123



is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20x to 80x reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day old seedlings; 10. 10 day whole seed; 11. 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the unique clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,72e-91 Length: 716  
 Score: 1024.00 Matches: 180  
 Percent Similarity: 93.50% Conservative: 7  
 Best Local Similarity: 90.00% Mismatches: 13  
 Query Match: 70.52% Indels: 1  
 DB: 7 Gaps: 0

US-10-692-367-12 (1-257) x C0520138 (1-716)

Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerIysPheGlyTyrCysGlyThrThr 22  
 Db 117 CAGAACTCGCGTGCAGCCAACTTCTGCTGCAGCAAGTTTCGGCTATCTGGCGCAGCACC 176  
 Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
 Db 177 GACGCTACTGCGGCGAGCGGTGCAGTCGGCCCGCTCGGCGCGCGCGCGCG 236  
 Qy 43 GlyGlyGlyGlyGlyGlyGlyGlySerGlyGlyAlaAenValAlaAenValThr 62  
 Db 237 GCGCGCGCGCGAGCGCGGAGCGAGTGGCGGTGCGAACGTGGCTTAATGTGTGTCACC 296  
 Qy 63 AspAlaPheAenGlyIleAysAenGlnAlaGlySerGlyCysGluGlyIysAenPhe 82  
 Db 297 GACGCGTTCTTTCACGCGCATCAAGAACAGCGCGGAGCGGTGCGAGGGGCAAGAACTTC 356  
 Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
 Db 357 TACACCGGAGCGGCTTCTGAGCGCGCTCAACGCGTACCCGGGCTTCGCCATCGCGCGG 416  
 Qy 103 SerGluValGluArgGlyAlaAlaPheAlaHisAlaThrHisGluThr 122  
 Db 417 ACGGAGGTGGAGGCGAGCGGAGATCGCGCTTCTTCGCGCAGCTCACGCGCAGAGACC 476  
 Qy 123 GlyHisPheCysTyrIleSerGluValAenIysSerAenAlaTyrCysAspProThrIys 142  
 Db 477 GGACATTTCTGTACATCAGCGAGATCAACAGAGCAACCGCTTACTGCGAGCGCGCAAC 536  
 Qy 143 ArgGlnTyrProCysAlaAlaGlyGlnIysTyrTyrGlyArgGlyProLeuGlnIleSer 162  
 Db 537 AGCGAGTGGCGGCGCGGCGGAGAGTACTACGCGCGCGCGCGCGCTCGAGATCTCG 596  
 Qy 163 TrpAenTyrAsnTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182

Db 597 TGGAACTACAACTACGCGCGCGCC-GGGAGGGACATCGGCTTCACGGGCTCGCGGACCCC 655  
 Qy 183 GlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsn 202  
 Db 656 AACAGGGTGGCGAGGACGCGGTGATCGGTTCAAGACGCGCTCTGGTTCTGGATGAAC 715  
 RESULT 10  
 CAI97556 647 bp mRNA linear EST 25-SEP-2003  
 LOCUS SCBFAD1067A11.g AD1 Saccharum officinarum cDNA clone SCBFAD1067A11  
 DEFINITION 5', mRNA sequence.  
 ACCESSION CAI97556  
 VERSION CAI97556.1 GI:35227930  
 KEYWORDS EST.  
 SOURCE Saccharum officinarum  
 ORGANISM Saccharum officinarum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.  
 REFERENCE 1 (bases 1 to 647)  
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
 TITLE The libraries that made SUCEST  
 JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br  
 Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bccceniter.fcav.unesp.br>  
 Plate: 067 row: A column: 11  
 Seq primer: T7 Promoter Primer.  
 Location/Qualifiers  
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 /db\_xref="taxon:4547"  
 /clone="SCBFAD1067A11"  
 /lab\_host="DH10B"  
 /clone\_lib="AD1"  
 /note="Organ: seedlings inoculated with Gluconacetobacter diazotrophicus; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with Gluconacetobacter diazotrophicus]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.51e-90 Length: 647  
 Score: 1020.50 Matches: 185  
 Percent Similarity: 88.29% Conservative: 11  
 Best Local Similarity: 83.33% Mismatches: 19  
 Query Match: 70.28% Indels: 7  
 DB: 6 Gaps: 2  
 US-10-692-367-12 (1-257) x CAI97556 (1-647)  
 Qy 31 GlnSerGlyProCysArgSerGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 50  
 Db 3 CAGTCGGCGCGTCCGCTCGGCGCGGAGCCAGCGGTGGCAGCAGTGGTGGG 62  
 Qy 51 GlySerGlyGlyAlaAenValAlaAenValThrAspAlaPheAsnGlyIleIys 70



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Db 63 -----AACGTGGCTAGCGTTGTCTACCGACGATCTTCTCAACGGCATCAAG 107
Qy 71 AsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeuGlu 90
Db 108 AACCAAGCGCGGAAACGGGTGCGAGGCAAGAACTTCTACACCGGAGTGGCTTCTTGAGC 167
Qy 91 AlaIleAlaAlaTyrProGlyPheAlaHisGlyGlySerGluValGluArgLysArgGlu 110
Db 168 GCCGCCGACTCGTACAAGGGCTTC-----GGTGGCGGGTCCGGTGGAGGGCAACGGCGAG 221
Qy 111 IleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGlu 130
Db 222 ATCCCGCGCTTCTTCGGCAGCTCAGCAGACGAGACGACATTTCTGTACATCAGCGAA 281
Qy 131 ValAsnLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAlaGly 150
Db 282 ATCAACAAGAACCAACGCTACTGCGACTCGAGCAACAGGCGAGTGGCGCGCGGGA 341
Qy 151 GlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAla 170
Db 342 CAGAAGTACTACGGCGCGCGCCGCTGCAGATCTCGTGAACACTACAACACTACGGGCGCTGCC 401
Qy 171 GlyArgAlaIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAspAlaVal 190
Db 402 GGCAGGACATCGGCTTCAACGGGCTCGGGACCCCAACAGGGTGGCGAGGACCGCGTG 461
Qy 191 ValAlaPheLysAlaAlaLeuTyrPheTrpMetAsnAsnValHisArgValMetProGln 210
Db 462 ATCGCGTTCAAGACGGCGCTCTGCTTCTGGACGAAACAGCTGCACCGCGGTGATGTCGCG 521
Qy 211 GlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAsnGlyAsnAsnPro 230
Db 522 GGGTTCGGAGCACCATCAGGGCTATCAACGGAGCCCTCGAGTGCACCGGAACAACCC 581
Qy 231 AlaGlnMetAsnAlaArgValGlyTyrTyrArgGlnTyrCysArgGlnLeuGlyValAsp 250
Db 582 GCCCAGATGAACGGCGGGTGGGTACTACAAAGCAGTACTGTGACGAGCTCGGCGTGCAC 641
Qy 251 ProGly 252
Db 642 CCGGGC 647

RESULT 11
BM736454
LOCUS
DEFINITION 952051A06.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.
ACCESSION BM736454
VERSION BM736454.1 GI:19057787
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
Zealot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Contact: Walbot V
Unpublished (1999)
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952051 row: A column: 06.
location/Qualifiers
FEATURES
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1. .628
/organism="Zea mays"
/moltype="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
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phases"
/lab_host="DH10B"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced
rRNA)"
/notes="Vector: pUC19, Site 1: EcoRI; Site 2: EcoRI; The
library was prepared by George Rudenko using poly (A)
selected RNA and Universal Riboclone cDNA Synthesis System
(Promega). cDNA was synthesized using both random and
oligo(dT) primers in separate reactions and equipped with
EcoRI adaptors. Library was size-fractionated on agarose
gels (for insert size >400bp) and non-directionally cloned
into EcoRI-digested pUC19 vector. Blue/white selection on
carbenicillin-containing plates was used to recover
positive clones."

ORIGIN
Alignment Scores: 1.5e-87 Length: 628
Pred. No.: 990.00 Matches: 180
Score: 92.68% Conservative: 10
Percent Similarity: 87.80% Mismatches: 15
Best Local Similarity: 68.18% Indels: 1
Query Match: 4 Gaps: 0
DB:

US-10-692-367-12 (1-257) x BM736454 (1-628)
Qy 53 GlyAlaAlaValAlaAlaValValThrAsnAlaPheAsnGlyIleLysAsnGln 72
Db 3 GGGCGGCGCAACGGGTGCTTAACGTGGC-AGCGACGCTTCTTCAACGGCATCAAGACCGAG 61
Qy 73 AlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeuGluAlaIle 92
Db 62 GCCGGAGCGGTGCGAGGGCAAGAACTTCTACACCGGAGCGGTTCTCTGAGCGCGTC 121
Qy 93 AlaAlaTyrProGlyPheAlaHisGlyGlySerGluValGluArgLysArgGluAlaIle 112
Db 122 AACAAAGTACCGCGGCTTCGCCCATGCGCGGACGAGGAGGCGCAAGCGCGAGATCGCC 181
Qy 113 AlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluValAsn 132
Db 182 GCCTTCTTCGGCAGCTGTCGACGACGAGACCGGACATTTCTGTACATCAGCGAGATCAAC 241
Qy 133 LysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAlaGlyGlnLys 152
Db 242 AAGAGCAACGCTTACTCGACGCAAGCAACAGGCGAGTGGCGGTGGCGGGCGGAGAG 301
Qy 153 TyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArg 172
Db 302 TACTACGGCGCGCGCTGCGAGATCTCGTGGAACTTACAACTACGCGCGCGCGGAGG 361
Qy 173 AlaIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAspAlaValAla 192
Db 362 GACATCGGCTTCAACGGGCTCGCGGACCCCAACAGGGTGGCGGAGCGCGGTGATCGG 421
Qy 193 PheLysAlaAlaLeuTyrPheTrpMetAsnAsnValHisArgValMetProGlnGlyPhe 212
Db 422 TTCAAGACGGGCTCTGTGTTCTGGATGAACAACTGCGACCGTGTGTATGCCGCGGCTTC 481
Qy 213 GlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAsnGlyAsnAsnProAlaGln 232
Db 482 GGGCGCCACCATCAGGGCCATCAACGGCGCTCTCGAGTGAACAGGGAACAACCCCGCCAG 541
Qy 233 MetAsnAlaArgValGlyTyrTyrArgGlnTyrCysArgGlnLeuGlyValAspProGly 252
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Db 602 CCCAACCTCACTTGC 616
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RESULT 12
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LOCUS
DEFINITION 625 bp mRNA linear EST 11-MAR-2002
mays cDNA, mRNA sequence.
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VERSION BM895383.1 GI:19350851
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 625)
Walbot V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952073 row: H column: 05.
FEATURES
source
location/Qualifiers
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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
phases"
/lab_host="DH10B"
/clone_lib="952" - BMS tissue from Walbot Lab (reduced
rRNA)"
/note="Vector: pUC19, Site 1: EcoRI; Site 2: EcoRI; The
library was prepared by George Rudenko using poly (A)
selected RNA and Universal Riboclone cDNA Synthesis System
(Promega). cDNA was synthesized using both random and
oligo(dT) primers in separate reactions and equipped with
EcoRI adaptors. Library was size-fractionated on agarose
gels (for insert size >400bp) and non-directionally cloned
into EcoRI-digested pUC19 vector. Blue/white selection on
carbenicillin-containing plates was used to recover
positive clones."
ORIGIN
Alignment Scores:
Fred. No.: 1.87e-87 Length: 625
Score: 989.00 Matches: 179
Percent Similarity: 93.60% Conservative: 11
Best Local Similarity: 88.18% Mismatches: 13
Query Match: 68.11% Indels: 1
DB: 5 Gaps: 0
US-10-692-367-12 (1-257) x BM895383 (1-625)
Qy 50 GlyGlySerGlyGlyAlaAsnValAlaAsnValThrAspAlaPheAsnGlyIle 69
Db 13 GGAGGCAGTGGCGGTGGGAAGTGGCTAACCGG-GTCAGCGACGGGTCTTCAACGGCATC 71
Qy 70 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheThrArgSerAlaPheLeu 89
Db 72 AAGAACACGAGCCGGAGCGGTGGCGAGGCAAGAACTTCTACCCGAGCGCGTTCCTG 131
Qy 90 GluAlaIleAlaAlaTyProGlyPheAlaHisGlySerGluValGluArgIleArg 109
Db 132 AGCCCGGTCACAAAGTACCCGGCTTCGCCCATGGCGGACGGAGGTGGAGGGCAAGGC 191
Qy 110 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrlleSer 129

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192 GAGATCGCCGCTCTTCGCGCACGTCACACGAGACCGGACATTTCTGTACATCAGC 251
130 GluValAsnLysSerAsnAlaTyCysAspProThrLysArgGlnTTPProCysAlaAla 149
252 GAGATCAACAAAGAGCAACGCTTACTGCGACGCAAGCAAGGAGTGGCGTGGCGGCG 311
150 GlyGlnLysTyTyGlyArgGlyProLeuGlnIleSerTrpAsnTyArgnTyGlyPro 169
312 GGGCAGAAGTACTACGGGCGCGCGCTCGAGATCTCGTGGAACTACAACTACGGGCCC 371
170 AlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla 189
372 GCGGGAGGAGACATCGGCTTCAACGGGCTCGCGACCCCAACAGGGTGGCGGAGAGCGCC 431
190 ValValAlaPheLysAlaAlaLeuTTPPheTTPMetAsnValHisArgValMetPro 209
432 GTATCGCGTTCAAGACGGCGCTCTGGTTCTGGATGAAACAGCTGCACCGCTCTGATCGCG 491
210 GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAsnGlyAsnAsn 229
492 CAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGGCGCCCTCGAGTCAACGGGAAACAAC 551
230 ProAlaGlnMetAsnAlaArgValGlyTyTyArgGlnTyrCysArgGlnLeuGlyVal 249
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250 AspProGly 252
612 GACCCAGGG 620
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SCQSLB2051F10.g LB2 Saccharum officinarum cDNA clone SCQSLB2051F10
5', mRNA sequence.
ACCESSION
VERSION CA270202
KEYWORDS CA270202.1 GI:35976513
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE
1 (bases 1 to 786)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCESr
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 051 row: F column: 10
Seq primer: T7 promoter Primer.
FEATURES
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location/Qualifiers
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/clone="SCQSLB2051F10"
/lab_host="DH10B"
/clone_lib="LB2"
/note="Organ: Lateral buds from plants adult plants
growing in greenhouse; Vector: pSport1; Site_1: SalI;
Site_2: NotI; An unidirectional cDNA library generated
from [lateral buds from plants adult plants growing in

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greenhouse]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-column and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>.

## ORIGIN

Alignment Scores:  
Pred. No.: 1.73e-86 Length: 786  
Score: 980.50 Matches: 183  
Percent Similarity: 84.48% Conservative: 13  
Best Local Similarity: 78.88% Mismatches: 25  
Query Match: 67.53% Indels: 11  
DB: 6 Gaps: 2

US-10-692-367-12 (1-257) x CA270202 (1-786)

Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 117 CAAACTCGCGCTGCCAGCAAACTACTGCTGCAGCAAGTTCTGGGTACTCGGCGCAGACC 176

Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 177 GACGACTACTGTGGCGAGGGTGCAGTTCGGCCGCTGCGGCGGCGGCGGCGGCGGCA 236

Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62  
Db 237 GCGGCTGCGCAGCAGTGGTGGTGGG-----AACGTGGCTAGCGTTGTCTCACC 281

Qy 63 AspAlaPhePheAenGlyIleGlyAenGlnAlaGlySerGlyCysGlyGlyGlyAenPhe 82  
Db 282 GACGCAATTCATCAACGGGATCAAAACAGCGCCGGGAACGGGTGCGAGGGCAAGACTTC 341

Qy 83 TyrThrArgSerAlaPheLeuGluAlaIleAlaAlaTyrProGlyPheAlaHisGlyGly 102  
Db 342 TACACCGGAGTGGTCTCTGAGCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 395

Qy 103 SerGluValGluArgLysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThr 122  
Db 396 GGGTCGGTGGAGGCAAGCGCGAGATCGCCGCTTCTTCGGCGCAGCTCAGCAGCAGACC 455

Qy 123 GlyHisPheCysTyrIleSerGluValAenLysSerAenAlaTyrCysAspProThrLys 142  
Db 456 GGACATTTCTCTACATCAGCGGAATCAACAGAACCAACCGCTACTCGACTCGAGCAAC 515

Qy 143 ArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSer 162  
Db 516 AGGAGTGGCGTGGCGCGGACAGAGTACTACGGCGCGCGCGCGCGCGCGCGCGCGCG 575

Qy 163 TrpAenTyrAenTyrGlyProAlaGlyArgAlaIleGlyPheAspGlyLeuGlyAspPro 182  
Db 576 TGGAACTACAACTACGGGCTCGCGGAGGAGCATCGGCTTCAACGGGCTCGGGAACCCC 635

Qy 183 GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAen 202  
Db 636 GACAGTGGCGCGAGGACCGCGTTCGAGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCT 695

Qy 203 AenValHisArgVal-MetProGlnGlyPheGlyAlaThr-IleArgAlaIle-AenGly 221  
Db 696 AACTTGACCGGGTGAATGTCNAGGGGTTCGGACCCACCCATTCAGGCTATTAAACGGA 755

Qy 222 Ala-LeuGluCysAenGlyAenAenPro 230  
Db 756 ACCCGCTCGAGTCAAGGAAAGCAACACC 783

## RESULT 14

CN151443  
LOCUS  
DEFINITION WOUND1\_75\_B02.g1 A002 Wounded leaves Sorghum bicolor cDNA clone  
WOUND1\_75\_B02\_A002 5', mRNA sequence.  
CN151443  
ACCESSION

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CN151443.1 GI:45994576  
Sorghum bicolor (sorghum)  
Sorghum bicolor

REFERENCE  
AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 801)  
Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Brady,J., Eastman,A., Miller,V., Gonzalez,M., Anfuso,C., Chhabra,D., Johnson,H., Kamran,D. and Pratt,L.H.  
A Sorghum EST database: mechanically damaged and methyl  
jasmonate-treated leaves  
Unpublished (2003)  
Other ESTs: WOUND1\_75\_B02.b1\_A002  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

## TITLE

JOURNAL  
COMMENTFEATURES  
source

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).  
Location/Qualifiers  
1..801  
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/mol\_type="mRNA"  
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/db\_xref="taxon:4558"  
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/clone\_lib="Wounded leaves"  
/note="Organ: Leaf; Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI. The library was prepared from polyA+ RNA harvested from 8-day-old hydroponically grown, BTx623 sorghum seedlings. For some plants, one-half of the second leaf was crushed without damaging the midvein. For others, methyl jasmonate was added to the growth medium to a final concentration of 100 uM. Leaves were harvested 3 and 27 hr after treatment and pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGG, 3-prime DraIII site is CACCATGTG). XhoI excises the insert."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.5e-86 Length: 801  
Score: 977.50 Matches: 176  
Percent Similarity: 83.70% Conservative: 14  
Best Local Similarity: 77.53% Mismatches: 29  
Query Match: 67.32% Indels: 8  
DB: 7 Gaps: 2

US-10-692-367-12 (1-257) x CN151443 (1-801)

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Db 138 CAGAACTCGCGCTGCCAGCCAGACTTCTGCTGCAGCCAGTATGGCTACTCGGCGCAGACC 197

Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 42  
Db 198 AGCGAGTACTGTGCGACCGCGGTGCGGTGCGGCGCCCTGCACA-----GGG 242

Qy 43 GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 62





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:14:26 ; Search time 2450.33 Seconds  
(without alignments)  
14890.544 Million cell updates/sec

Title: US-10-692-367-69  
Perfect score: 753  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	715.6	95.0	1094	6 AR321624	AR321624 Sequence
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3	638.2	84.8	843	8 MZECHITA	M84164 Zea mays ch
4	582.6	77.4	1121	8 AY532735	AY532735 Zea mays
5	578.6	76.8	1127	8 AY532723	AY532723 Zea mays
6	574.8	76.3	1080	8 AY532739	AY532739 Zea diplo
7	573.8	76.2	1081	8 AY532737	AY532737 Zea diplo
8	573.8	76.2	1081	8 AY532738	AY532738 Zea diplo
9	573.8	76.2	1081	8 AY532742	AY532742 Zea diplo
10	572.4	76.0	1114	8 AY532725	AY532725 Zea mays
11	570.4	75.8	1134	8 AY532734	AY532734 Zea mays
12	570.2	75.7	1123	8 AY532729	AY532729 Zea mays
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19	560.2	74.4	1123	8 AY532726	AY532726 Zea mays

20	559.6	74.3	1127	8 AY532730	AY532730 Zea mays
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24	549	72.9	1104	8 AY532782	AY532782 Zea diplo
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26	548.8	72.9	1140	8 AY532731	AY532731 Zea mays
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36	543	72.1	1110	8 AY532787	AY532787 Zea diplo
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43	532.6	70.7	1131	8 AY532780	AY532780 Zea mays
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ALIGNMENTS

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LOCUS AR321624 1094 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1 from patent US 6563020.  
ACCESSION AR321624  
VERSION AR321624.1 GI:33706864  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1094)  
AUTHORS Simmons,C.R. and Yalpani,N.  
TITLE Maize chitinases and their use in enhancing disease resistance in crop plants  
JOURNAL Patent: US 6563020-A 1 13-MAY-2003;  
FEATURES Location/Qualifiers  
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Qy	66 CGACGAGTACTGCGGCGCACGGTGCCAGTCCGCGCCGTCGGCTCGGGCGGGGGCGAG 125
Db	209 CGACGAGTACTGCGGCGCACGGTGCCAGTCCGCGCCGTCGGCTCGGGCGGGGGCGAG 268
Qy	126 CAGTGGGCGGGTGCTGCGAACGTTAGCGTCCGCTCAGCGGCTCTTCTTCAACGGCAT 185
Db	269 CAGTGGGCGGGTGCTGCGAACGTTAGCGTCCGCTCAGCGGCTCTTCTTCAACGGCAT 328
Qy	186 CAAGAACCCAGCGCGGAGCGGGTGCAGGGGCAAGAACTTCTTACACCGGAGCGGGTTCCCT 245
Db	329 CAAGAGCCAGCGCGGAGCGGGTGCAGGGGCAAGAACTTCTTACACCGGAGCGGGTTCCCT 388
Qy	246 GAGCGCGCTCAGCGGCTACCCAGGCTTCGCCCTTGGCGGGTGCACAGGTGCAGGGCGAGCG 305



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Db      389  GAGCGCGCTCAAGGCGTACCCAGGCTTCGCCCATGGCGGTGCGAGGTGCGAGGGCAAGCG 448
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Qy      366  CGAGATCAGCAAGAGCAACGCTACTCGGACCCCGACCAAGAGGAGTGCGCGTGCAGCGC 425
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Qy      426  GGGGAGAGATCTACGGGCGCGCCCGCTGCGAGATCTGTGGAATCTACAATACGGGCC 485
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Qy      486  CGCGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGGAGGAGTGCGCGGAGCG 545
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Qy      546  CGTGTGCGCTTCAAGCGCGCGCTCTGGTCTTGATGAACAAAGTGCACCGCTGTGATGCC 605
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Qy      606  GCAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCAGCGGAAACA 665
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Qy      666  CCGCGCCAGATGAACGGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTCGGGT 725
Db      809  CCGCGCCAGATGAACGGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTCGGGT 868
Qy      726  GCAGCCAGGCGCCCAACCTCACTTGT 751
Db      869  GCAGCCAGGCGCCCAACCTCACTTGT 894
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LOCUS      Zea mays chitinase B (seed chitinase) gene, 3'end.
DEFINITION M84165
ACCESSION M84165.1 GI:168442
VERSION    1
KEYWORDS   chitinase B.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            Huynh,Q.K., Hironaka,C.M., Levine,E.B., Smith,C.E., Borgmeyer,J.R.
            and Shah,D.M.
            Antifungal proteins from plants. Purification, molecular cloning,
            and antifungal properties of chitinases from maize seed
            J. Biol. Chem. 267 (10), 6635-6640 (1992)
            1551872
COMMENT    Original source text: Zea mays (library: Lamda GT 10 corn seed
            (imbibed)) seed DNA.
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Best Local Similarity 95.9%; Pred. No. 1.1e-82;
Matches 718; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

Qy      6   GCAGAACTGCGGCTGCAGGCCAAACGATATCTGTCAGCAAGTTTCGGCTACTGCGGCACAAAC 65
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Qy      66   CGACAGTACTGCGGCGACAGGGTGCAGTGGGGCCCGTCCGCTCGGGC---GGGGCGG 122
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Qy      183   CATCAAGAACCCAGGCCCGGAGCGGGTGCAGGGCAAGAACTTTCTACCCCGGAGCGGTT 242
Db      240   CATCAAGAACCCAGGCCCGGAGCGGGTGCAGGGCAAGAACTTTCTACCCCGGAGCGGTT 299
Qy      243   CTTGAGCGCGCTCAAGGGTACCCAGGCTTTCGCCCATGCGGGGTCAAGGTGCGAGGCAA 302
Db      300   CTTGAGCGCGCTCAAGGGTACCCAGGCTTTCGCCCATGCGGGGTTCGAGGTGCGAGGCAA 359
Qy      303   GCGGAGATCGCGCTTCTTCGCGCAGCGCCACGACGAGACCGGGCATTTCTGTATCAT 362
Db      360   GCGGAGATCGCGCTTCTTCGCGCAGCGCCACGACGAGACCGGGCATTTCTGTATCAT 419
Qy      363   CAGCGAGATCAGCAAGAGCAACGCTACTGCGACCCCGACCAAGAGGAGTGGCGTGGCG 422
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Qy      423   GCGGGCGAGAGTACTACGGGCGGGCGCGCTCGAGTCTCGTGGAACTACAACTACGG 482
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Db      720   CAACCGCGCCAGATGAACGGCGCGCTCGGCTACTTACAGGAGTACTGCCGCCAGCTCGG 779
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Db      780   CGTCAAGCCAGGGGCCCAACCTCACTTGT 808
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RESULT 3
MZECHITA
LOCUS      Zea mays chitinase A (seed chitinase) gene, complete cds.
DEFINITION M84164
ACCESSION M84164.1 GI:168440
VERSION    1
KEYWORDS   chitinase A.
SOURCE     Zea mays
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Query Match      77.4%; Score 582.6; DB 8; Length 1121;
Best Local Similarity 83.3%; Pred. No. 1.3e-68;
Matches 727; Conservative 0; Mismatches 19; Indels 123; Gaps 1;

Qy 6 GCAGAACTGCGGCTGCCAGCCAAACGATGCTGCGCAAGTTGCGCTACTGCGGCAAC 65
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Qy 66 CGACAGTACTGCGGCAAGCGGTCCAGTGGGCGCGCTGCCGCTCGGCGCGGCGGCGAG 125
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Qy 246 GAGCGCGGTCAAGCGGTACCCAGGCTTCCGCTCGGCGGCGGTGCGAGGCGCAAGCG 305
Db 346 GAGCGCGGTCAAGCGGTACCCAGGCTTCCGCTCGGCGGCGGTGCGAGGCGCAAGCG 405

Qy 306 CGAGATCGCGGCTTCTTCCGCGCAGCGCAGCAGCGAGACCGGCG----- 349
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Qy 350 ----- 349
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Qy 350 -----ATTTCTGTTACAT 362
Db 526 TATTATTTTGAAATTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585

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Db 586 CAGCGAGATCAGCAAGAGCAACGCTTACTCGGACCCGACCAAGAGGCGAGTGGCGGTGCGC 645

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Qy 543 CGCGGTGCTGCGGCTTCAAGCGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
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Qy 603 CGCGCAGGCTTGGCGCGCACATCAGGCGCATCAACCGGCGCGCTGAGTGGCGAGCGGAA 662
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Qy 723 CGTGACCCAGGCGCGCAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 751
Db 946 CGTGACCCAGGCGCGCAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
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RESULT 5
AY532723
LOCUS
DEFINITION Zea mays subsp. parviglumis isolate p2 chitinase (chib) gene,
complete cds.
ACCESSION AY532723
VERSION AY532723.1 GI:48093227
KEYWORDS
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Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1127)
AUTHORS Tiffin,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
zeae and family poaceae
JOURNAL Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE 2 (bases 1 to 1127)
AUTHORS Tiffin,P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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mRNA
CDS
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Best Local Similarity 83.3%; Pred. No. 4.3e-68;
Matches 727; Conservative 0; Mismatches 19; Indels 127; Gaps 1;
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Db 106 GCAGAACTGCGGCTGCCAGCCAAACGATGCTGCGCAAGTTGCGCTACTGCGGCAAC 165
Qy 66 CGACAGTACTGCGGCAAGCGGTCCAGTGGGCGCGCTGCCGCTCGGCGCGGCGGCGAG 125
Db 166 CGACAGTACTGCGGCAAGCGGTCCAGTGGGCGCGCTGCCGCTCGGCGCGGCGGCGAG 225
Qy 126 CAGTGGCGGCGGTGCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
Db 226 CAGTGGCGGCGGTGCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285
Qy 186 CAAGAAACAGGCGCGGCGGTGCGAGGCGCAAGAACTTCTACACCGCGAGCGGTTCTCT 245
Db 286 CAAGAAACAGGCGCGGCGGTGCGAGGCGCAAGAACTTCTACACCGCGAGCGGTTCTCT 345
Qy 246 GAGCGCGGTCAAGCGGTACCCAGGCTTCCGCTCGGCGGCGGTGCGAGGCGCAAGCG 305
Db 346 GAGCGCGGTCAAGCGGTACCCAGGCTTCCGCTCGGCGGCGGTGCGAGGCGCAAGCG 405
Qy 306 CGAGATCGCGGCTTCTTCCGCGCAGCGCAGCAGCGAGACCGGCG----- 349
Db 406 CGAGATCGCGGCTTCTTCCGCGCAGCGCAGCAGCGAGACCGGCGGTAAGTTGGCTCTATC 465
Qy 350 ----- 349
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Db 766 GGGACGCGCTGTGCGCTTCAAGGCGCGCTCTGTTCTGATGAACAACTGCACCGTG 825  
Qy 599 TGATGCGCGCAGGGCTTTCGGCGCCACCATCAGGGCCATCAAGCGCGCGCTCGAGTGCAGC 658  
Db 826 TGGTGCGCGCAGGGTTTCGGCGCCACCATCAGGGCCATCAAGCGCGCTCGAGTGCAGC 885  
Qy 659 GGAACAACCCCGCGCGAGTGAACGGCGCATCGGCTACTACAAGCAGTACTGCGCGCAGC 718  
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RESULT 6  
AY532739  
LOCUS AY532739 1080 bp DNA linear PLN 29-JUL-2004  
DEFINITION Zea diploperennis isolate d5 chitinase (chIB) gene, complete cds.  
ACCESSION AY532739  
VERSION AY532739.1 GI:48093259  
KEYWORDS  
SOURCE Zea diploperennis  
ORGANISM Zea diploperennis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 1080)  
Tiffin, P.  
Comparative evolutionary histories of chitinase genes in the genus  
zea and family poaceae  
Genetics 167 (3), 1331-1340 (2004)  
15280246  
2 (bases 1 to 1080)  
Tiffin, P.  
Direct Submission  
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
Location/Qualifiers  
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ORIGIN  
Query Match 76.3%; Score 574.8; DB 8; Length 1080;  
Best Local Similarity 84.2%; Pred. No. 1.4e-67;  
Matches 721; Conservative 0; Mismatches 22; Indels 113; Gaps 2;  
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Qy 66 CGACAGTACTGCGGCGACGGGTGCGAGTGGGCGCGCTCGGCTCGGGCGGGCGGCGAG 125  
Db 166 CGACAGTACTGCGGCGACGGGTGCGAGTGGGCGCGCTCGGCTCGGGCGGGCGAG 222  
Qy 126 CAGTGGCGGGCTGCTGCGAAAGTGGCTAGCGTCTGTCACCGGCTCTTCTTCAACGGCAT 185  
Db 223 CAGTGGCGGGCTGCTGCGAAAGTGGCTAGCGTCTGTCACCGGCTCTTCTTCAACGGCAT 282  
Qy 186 CAAGAAACAGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCGCGAGCGGTTCTCT 245  
Db 283 CAAGAAACAGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCGCGAGCGGTTCTCT 342  
Qy 246 GAGCGCGCTCAAGCGTACTCCAGGCTTTCGCCCATGCGGGGTCAAGTGCAGGGCAAGCG 305  
Db 343 GAGCGCGCTCAAGCGTACTCCAGGCTTTCGCCCATGCGGGGTGCGAGGTGCGAGGGCAAGCG 402  
Qy 306 CGAGATCGCGCGCTTCTTCGCGCACCGCACGAGAGCGGGC----- 349  
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Db 583 AAGAGCAACGCTACTTCGACACCGACCAAGAGGCGAGTGGCGCGCGCGGGCGAGAG 642  
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Db 823 GGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCAGCGGGAACAACCCCGCCGAG 882  
Qy 676 ATGAACGGCGCGCTCGGCTACTACAAGCACTATGCGCGCAGCTCGGCGTGCAGCCAGGG 735  
Db 883 ATGAACGGCGCGCTCGGCTACTACAAGCACTATGCGCGCAGCTCGGCGTGCAGCCCGGG 942  
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[illegible]









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Qy	666	CCCGGCCAGATGAACCGCGCCATCGGCTACTACAAGCAGTACTCGCCGACCTCGGGT	725
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RESULT 11	
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DEFINITION	Zea mays subsp. parviglumis isolate pl3 chitinase (chiB) gene, complete cds.
ACCESSION	AY532734
VERSION	AY532734.1 GI:48093249
KEYWORDS	
SOURCE	Zea mays subsp. parviglumis
ORGANISM	Zea mays subsp. parviglumis
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 1134)
AUTHORS	Tiffin,P.
TITLE	Comparative evolutionary histories of chitinase genes in the genus Zea and family poaceae
JOURNAL	Genetics 167 (3), 1331-1340 (2004)
PUBMED	15280246
REFERENCE	2 (bases 1 to 1134)
AUTHORS	Tiffin,P.
TITLE	Direct Submission
JOURNAL	Submitted (23-JAN-2004) Plant Biology, University of Minnesota, 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
FEATURES	Location/Qualifiers
	1..1134

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Query Match	75.8%; Score 570.4; DB 8; Length 1134;
Best Local Similarity	83.5%; Pred. No. 5.3e-67;
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DB	
QY	123 CAGCAGTGGCGGCGGTGTCGGAACGTGGCTACGGTCGTACACGGCTCTCTTCTTCAACGG 182
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QY	183 CATCAAGAACAGCGCGGAGCGGTCGAGGGCAAGAACTTCTPACACCCGGAGCGGCTT 242
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QY	243 CCTGAGCGCGCTCAAGCGCTACCCAGGCTTCGCCCATGCGCGGCTCAAGGTGCAAGGGCAA 302
DB	
QY	358 CCTGAGCGCGCTCAAGCGCTACCCAGGCTTCGCCCATGCGCGGCTCGAGGTGCAAGGGCAA 417
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QY	303 GCGCGAGATCGCGCGCTTCTTGGGCAAGCGCAAGACGACGAGACCGGGC----- 349
DB	
QY	418 GCGCGAGATCGCGCGCTTCTTTCGCGCACGCGCACGACGAGACCGGGCGTAAAGTTGGCTCC 477
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QY	350 ----- 349
DB	
QY	478 GGCGTTCCGCGCGCGAGGTTCTTTGATTTTAAATTTGACCCCATCANGCTGATCATTTT 537
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QY	350 -----ATTTCTGTTACATC 363
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QY	598 AGCGAGATCAACAGAGCAAAGCTTACTGCGAACCCGAGCAAGAGGAGTGGCCGTGCGCC 657
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QY	484 CCGCGGGGAGGACATCGGCTTTCGACGGGCTCGGGGACCCCGGCAAGGTGGCGCGGGAC 543
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QY	544 GCGGTGTGCGTTCAGAGCGCGGCTCTGGTCTTGAGTGAACACGTGACCGTGTGATG 603
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QY	604 CCGCAGGCTTCGGCGCCACATCAGGGCCATCAACGGCGGCTCGAGTGCAGCGGAAC 663
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QY	664 AACCCGCCAGATGAACGCGCGCATCGGCTACTCAAGCAGTACTGCCCGCAGCTCGGC 723
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QY	898 AACCCGCCAGATGAACGCGCGCTCGGCTACTACAGGAGTACTGCCCGCAGCTCGGC 957
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QY	724 GTCGACCCAGGGGCCAACCTCACTTGCT 751
DB	
QY	958 GTCGACCCGGGGCCCAACCTCACTGCT 985
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## ORIGIN

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KEYWORDS
SOURCE
ORGANISM
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 1123)
AUTHORS
Tiffin,P.
TITLE
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
JOURNAL
Genetics 167 (3), 1331-1340 (2004)
PUBMED
15280246
REFERENCE
2 (bases 1 to 1123)
AUTHORS
Tiffin,P.
TITLE
Direct Submission
JOURNAL
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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Best Local Similarity 83.4%; Pred. No. 5.7e-67;
Matches 728; Conservative 0; Mismatches 18; Indels 127; Gaps 2;
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Db 109 GCAGAACTGCGGCTGCCAGCCAAACGCTGCTGCAGCAAGTTCGGCTACTCGCGCAACGAC 168
Qy 66 GCAGAGTACTGCGGCGACAGGCTGCAGTTCGGGCGCGTGCCTGCGGCGCGCGCGCGCGCG 122
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659 GGAACAACCCCGCCAGATGAACGCGCGCATCGGCTACTACAGCAGTACTTGCAGCGCGCAGC 718
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LOCUS
DEFINITION
Zea mays subsp. parviglumis isolate p12 chitinase (chiB) gene,
complete cds.
ACCESSION
AY532733
VERSION
AY532733.1 GI:48093247
KEYWORDS
SOURCE
ORGANISM
Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 1127)
AUTHORS
Tiffin,P.
TITLE
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
JOURNAL
Genetics 167 (3), 1331-1340 (2004)
PUBMED
15280246
REFERENCE
2 (bases 1 to 1127)
AUTHORS
Tiffin,P.
TITLE
Direct Submission
JOURNAL
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
LOCATION/Qualifiers
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DEFINITION	AY532741	
ACCESSION	AY532741.1	GI:48093263
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
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TITLE		
JOURNAL		
PUBMED		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
source		
gene		
mRNA		
CDS		
ORIGIN		
Query Match	75.4%; Score 567.6; DB 8; Length 1111;	
Best Local Similarity	83.4%; Pred. No. 1.3e-66;	
Matches	724; Conservative 0; Mismatches 19; Indels 125; Gaps 2;	
Qy	6 GCAGAACTGCGGCTGCAGCCAGGTCAGTATGCTGCGAGCAAGTTCCGCTACTCGGCGCACAC 65	
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Qy	66 GCAGAGTACTGCGGCGACCGGTCAGTATGCTGCGGCGCGCTGCGGCGCGCGGCGAG 125	
Db	166 GCAGAGTACTGCGGCGACCGGTCAGTATGCTGCGGCGCGCTGCGGCGCGCGGCGAG 222	
Qy	126 CAGTGGCGCGGTCGGTGCAGACGTGGCTAGCGTCTGTCACCGGCTCTTTCTTCAACGGCAT 185	
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Qy 306 CGAGATCGCCGCCCTTCTTCGCGCACCGCACCGACGAGACCGGGC----- 349
Db 403 CGAGATCGCCGCCCTTCTTCGCGCACCGCACCGACGAGACCGGGCTAAGTTGGCACGGTC 462
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DEFINITION Zea diploperennis isolate d1 chitinase (chiB) gene, complete cds.
ACCESSION AY532736
VERSION AY532736.1 GI:48093253
KEYWORDS
SOURCE Zea diploperennis
ORGANISM Zea diploperennis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1122)
Tiffin,P.
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE 2 (bases 1 to 1122)
Tiffin,P.
AUTHORS Direct Submission
TITLE Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
JOURNAL 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
LOCATION/Qualifiers
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FTGRAPLSAVKAYPGFAHGSQVQGRREIAFAFAHATHETGHFCTISEINKNAYCD
PTQRWPCAGQKYGRGLQISWNTYNGPAGRAIGFDGLGDFRVARDAVAFKAL
WFMWNSVHGVVPGFGATTATRAINGALECGGNPAQMNARVGYTRYQRCQLGVDPGPNL
TC"

ORIGIN
Query Match 74.7%; Score 562.6; DB 8; Length 1122;
Best Local Similarity 82.9%; Pred. No. 5.9e-66;
Matches 724; Conservative 0; Mismatches 19; Indels 130; Gaps 2;

Qy 6 GCAGACTCGGCTGCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTCGGCACAAC 65
Db 106 GCAGAACTCGGCTGCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTCGGCACAAC 165
Qy 66 CGACAGTACTCGCGGCGACCGGTCGACAGTCCGCGCGCGCGCGCGCGCGCGAG 125
Db 166 CGACAGTACTCGCGGCGACCGGTCGACAGTCCGCGCGCGCGCGCGCGCGCG--G 222
Qy 126 CAGTGGCGCGGCTGTCGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
Db 223 CAGTGGCGCGGCTGTCGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 282
Qy 186 CAGAAACCGCGCGGAGCGGTCGAGGCGCAAGAACTTCTACACCGGAGCGGTTCTCT 245
Db 283 CAGAGCCAGCGCGGAGCGGTCGAGGCGCAAGAACTTCTACACCGGAGCGGTTCTCT 342
Qy 246 GAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGCGGGTTCACAGTGCAGGCGAAGCG 305
Db 343 GAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGCGGGTTCGAGTGCAGGCGAAGCG 402
Qy 306 CGAGATCGCGCGCTTCTTCGCGCACCGCACCGACGAGACCGGGC----- 349
Db 403 CGAGATCGCGCGCTTCTTTCGCGCACCGCACCGACGAGACCGGGCGTAAGCTGGCTTATC 462
Qy 350 ----- 349
Db 463 TATTAACCTCGCTTTCAGCGCGCGCGAGGTTCTTTGATTTTGAACCATCATCTGATC 522
Qy 350 -----ATTTCGTGT 358
Db 523 AATTTTTCGGAATAATTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
Qy 359 ACATCAGCGAGATCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCG 418
Db 583 ACATCAGCGAGATCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCG 642
Qy 419 GCGCGCGCGGCGAGAGTACTACGGGCGCGCGCGCTGCGAGATCTCGTGAACCTACAACT 478
Db 643 GCGCGCGCGGCGAGAGTACTACGGGCGCGCGCGCTGCGAGATCTCGTGAACCTACAACT 702
Qy 479 ACGGCGCGCGCGGAGGAGATTCGGCTTCGACGGGCTCGGGGACCCCGGAGGGTGGCG 538
Db 703 ACGGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 762
Qy 539 GGGACCGCGTGGTGGCGGTTCAAGCGCGGCTCTGGTTCTGGATGAACCAACGTCACCGTG 598
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Db 763 GGGACGCGTGGTGGCGTTCAAGGGCGGCTCTGGTTCTGGATGAACAGCGTGCACGGGG 822  
Qy 599 TGATCCCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCAGCG 658  
Db 823 TGGTGGCGCAGGGGTTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCAGCG 882  
Qy 659 GGAACAACCCCGCCAGATGAACCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGC 718  
Db 883 GGAACAACCCCGCCAGATGAACCGCGCGTGGCTACTACAGGAGTACTGCCGCCAGC 942  
Qy 719 TCGGCGTCGACCCAGGGCCCAACCTCACTTGCT 751  
Db 943 TCGGCGTCGACCCCGGGCCCAACCTCACCTGCT 975

Search completed: May 23, 2005, 14:20:15  
Job time : 2457.33 sec

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:11:31 ; Search time 351.104 Seconds  
(without alignments)  
12695.850 Million cell updates/sec

Title: US-10-692-367-69  
Perfect score: 753  
Sequence: 1 tcgatgcagactcggctg.....ggcccaacctcactgtctga 753

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003cs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004as.\*  
13: Geneseq2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	753	13	ADS92685
2	732.2	97.2	753	13	ADS92667
3	725.8	96.4	753	13	ADS92671
4	722.6	96.0	753	13	ADS92693
5	719.4	95.5	753	13	ADS92697
6	717.8	95.3	753	13	ADS92651
7	716.2	95.1	753	13	ADS92659
8	715.6	95.0	1094	3	AAA96222 cDNA enco
9	714.6	94.9	753	13	ADS92637
10	711.8	94.5	753	13	ADS92683
11	711.4	94.5	753	13	ADS92669
12	711.4	94.5	753	13	ADS92665
13	708.2	94.1	750	13	ADS92695
14	701.8	93.2	753	13	ADS92673
15	701.8	93.2	753	13	ADS92647
16	697.8	92.7	771	13	ADS92663
17	696.4	92.5	774	13	ADS92687
18	693	92.0	771	13	ADS92689
19	689.8	91.6	771	13	ADS92677
20	689	91.5	753	13	ADS92643

21	686.6	91.2	771	13	ADS92699	Ads92699 Chitinase
22	685	91.0	771	13	ADS92675	Ads92675 Chitinase
23	683.6	90.8	774	13	ADS92681	Ads92681 Chitinase
24	675.6	89.7	774	13	ADS92679	Ads92679 Chitinase
25	672.4	89.3	774	13	ADS92661	Ads92661 Chitinase
26	671.2	89.1	780	13	ADS92655	Ads92655 Chitinase
27	671.2	89.1	780	13	ADS92691	Ads92691 Chitinase
28	667.6	88.7	774	13	ADS92653	Ads92653 Chitinase
29	664.4	88.2	774	13	ADS92649	Ads92649 Chitinase
30	662.8	88.0	774	13	ADS92645	Ads92645 Chitinase
31	659.6	87.6	774	13	ADS92639	Ads92639 Chitinase
32	659.4	87.6	771	13	ADS92657	Ads92657 Chitinase
33	653.2	86.7	774	13	ADS92627	Ads92627 Chitinase
34	650.4	86.4	756	13	ADS92621	Ads92621 Chitinase
35	648.8	86.2	756	13	ADS92629	Ads92629 Chitinase
36	647.2	85.9	756	13	ADS92625	Ads92625 Chitinase
37	642	85.3	840	11	ADJ12126	Adj12126 Maize cDN
38	640.4	85.0	774	13	ADS92623	Ads92623 Chitinase
39	631.8	83.9	777	13	ADS92619	Ads92619 Chitinase
40	628.6	83.5	765	13	ADS92641	Ads92641 Chitinase
41	625.8	83.1	777	13	ADS92631	Ads92631 Chitinase
42	442	58.7	636	12	ADA49298	Ada49298 Maize gen
43	442	58.7	636	12	ADJ44871	Adj44871 Plant cDN
44	418.2	55.5	843	8	ADA70140	Ada70140 Rice gene
45	418.2	55.5	843	11	ADJ11575	Adj11575 Rice DNA

ALIGNMENTS

RESULT 1

ADS92685  
ID ADS92685 standard; DNA; 753 BP.

XX AC ADS92685;

XX DT 02-DEC-2004 (first entry)

XX DB Chitinase variant polynucleotide #32.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX OS Synthetic.

XX PN WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-PSDB; ADS92686.

XX New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 69; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The



CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

XX  
SQ Sequence 753 BP; 141 A; 245 C; 261 G; 106 T; 0 U; 0 Other;  
Query Match 100.0%; Score 753; DB 13; Length 753;  
Best Local Similarity 100.0%; Pred. No. 1.9e-132;  
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCGATGCAGAACTGGCGTGCAGCCAAAGTATGCTGTCAGCAAGTTTCGGTACTGCGGC 60  
Db 1 TCGATGCAGAACTGGCGTGCAGCCAAAGTATGCTGTCAGCAAGTTTCGGTACTGCGGC 60  
Qy 61 ACAACCGAGAGTACTGCGGCGAGCGGTGTCAGTGCAGTCCGCGTCCGCGTCCGCGCGGC 120  
Db 61 ACAACCGAGAGTACTGCGGCGAGCGGTGTCAGTGCAGTCCGCGTCCGCGTCCGCGCGGC 120  
Qy 121 GGCAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 180  
Db 121 GGCAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 180  
Qy 181 GGCATCAAGAACACGCGCGGAGCGGTGTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 240  
Db 181 GGCATCAAGAACACGCGCGGAGCGGTGTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 240  
Qy 241 TTCCTGAGCGCGTCAAGCGGTGTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 300  
Db 241 TTCCTGAGCGCGTCAAGCGGTGTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 300  
Qy 301 AAGCGCAGATGCGCGCTTCTTCGCGACGCGGCTGCGAGCGGCTGCGAGCGGCTGCGAGCGG 360  
Db 301 AAGCGCAGATGCGCGCTTCTTCGCGACGCGGCTGCGAGCGGCTGCGAGCGGCTGCGAGCGG 360  
Qy 361 ATCAGCAGATCAGCAAGACGCGCTTCTTCGCGACGCGGCTGCGAGCGGCTGCGAGCGGCTGCG 420  
Db 361 ATCAGCAGATCAGCAAGACGCGCTTCTTCGCGACGCGGCTGCGAGCGGCTGCGAGCGGCTGCG 420  
Qy 421 GCGCGCGGCGAGAGTACTAGCGCGCGCGCGCTGCGAGTCTGCTGAACTACACTAC 480  
Db 421 GCGCGCGGCGAGAGTACTAGCGCGCGCGCGCTGCGAGTCTGCTGAACTACACTAC 480  
Qy 481 GCGCGCGGCGAGAGTACTAGCGCGCGCGCGCTGCGAGTCTGCTGAACTACACTAC 540  
Db 481 GCGCGCGGCGAGAGTACTAGCGCGCGCGCGCTGCGAGTCTGCTGAACTACACTAC 540  
Qy 541 GACGCGGTGGTGGCGTTCAAGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 541 GACGCGGTGGTGGCGTTCAAGCGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Qy 601 ATGCGCGAGGCTTTCGGCGCCACCATCAGGCGGCTGCGAGTCTGCTGAACTACACTAC 660  
Db 601 ATGCGCGAGGCTTTCGGCGCCACCATCAGGCGGCTGCGAGTCTGCTGAACTACACTAC 660  
Qy 661 AACAAACCCCGCCAGATGAAAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Db 661 AACAAACCCCGCCAGATGAAAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Qy 721 GCGGTGCGACCCAGGCGCCAACTCACTTGTCTGA 753  
Db 721 GCGGTGCGACCCAGGCGCCAACTCACTTGTCTGA 753

RESULT 2  
ADS92667  
ID ADS92667 standard; DNA; 753 BP.  
XX  
AC ADS92667;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #23.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; *Fusarium*;  
KW *Heterodera*.  
XX Synthetic.  
OS  
XX WO2004037194-A2.  
XX 06-MAY-2004.  
XX 22-OCT-2003; 2003WO-US033588.  
XX 22-OCT-2002; 2002US-0420666P.  
XX 06-NOV-2002; 2002US-00290086.  
XX 14-MAR-2003; 2003US-00389432.  
XX (VERD-) VERDIA INC.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX Muller ML, True T, Simmons CR, Yalpani N;  
XX WPI; 2004-365417/34.  
XX P-PSDB; ADS92668.  
XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX Claim 4; SEQ ID NO 51; 197pp; English.  
XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus *Fusarium*. The nematode is from the genus  
XX *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
XX plant resistance to a fungus or nematode. This sequence represents a  
XX chitinase variant polynucleotide of the invention.

SQ Sequence 753 BP; 135 A; 245 C; 265 G; 108 T; 0 U; 0 Other;

Query Match 97.2%; Score 732.2; DB 13; Length 753;  
Best Local Similarity 98.3%; Pred. No. 1.5e-128;  
Matches 740; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
Qy 1 TCGATGCAGAACTGGCGTGCAGCCAAAGTATGCTGTCAGCAAGTTTCGGTACTGCGGC 60  
Db 1 TCGATGCAGAACTGGCGTGCAGCCAAAGTATGCTGTCAGCAAGTTTCGGTACTGCGGC 60  
Qy 61 ACAACCGAGAGTACTGCGGCGAGCGGTGTCAGTGCAGTCCGCGTCCGCGTCCGCGCGGC 120  
Db 61 ACAACCGAGAGTACTGCGGCGAGCGGTGTCAGTGCAGTCCGCGTCCGCGTCCGCGCGGC 120  
Qy 121 GGCAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 180  
Db 121 GGCAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 180  
Qy 181 GGCATCAAGAACACGCGCGGAGCGGTGTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 240  
Db 181 GGCATCAAGAACACGCGCGGAGCGGTGTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 240  
Qy 241 TTCCTGAGCGCGTCAAGCGGTGTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 300  
Db 241 TTCCTGAGCGCGTCAAGCGGTGTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 300  
Qy 301 AAGCGCAGATGCGCGCTTCTTCGCGACGCGGCTGCGAGCGGCTGCGAGCGGCTGCGAGCGG 360  
Db 301 AAGCGCAGATGCGCGCTTCTTCGCGACGCGGCTGCGAGCGGCTGCGAGCGGCTGCGAGCGG 360  
Qy 361 ATCAGCAGATCAGCAAGACGCGCTTCTTCGCGACGCGGCTGCGAGCGGCTGCGAGCGGCTGCG 420  
Db 361 ATCAGCAGATCAGCAAGACGCGCTTCTTCGCGACGCGGCTGCGAGCGGCTGCGAGCGGCTGCG 420

Qy	421	GC	CGCGGGCGAGACTACTACGGGGCGCGCGCGCTCGTGGAACTCAACTAC	480
Db	421	GC	CGCGGGCGAGAGTACTACGGGGCGCGCGCGCTCGTGGAACTCAACTAC	480
Qy	481	GG	CCCCCGCGGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCGGGACGGGTGGCGCG	540
Db	481	GG	CCCCCGCGGGGAGGAGCCATCGGCTTCGACGGGCTCGGGGACCCGGGACGGGTGGCGCG	540
Qy	541	GAC	CGCGTGTGGCGTTCAAGCGCGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTG	600
Db	541	GAC	CGCGTGTGGCGTTCAAGCGCGCGCTCTGGTTCTGGATGAACAACGTGCACCGTGTG	600
Qy	601	ATG	CGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCACCGG	660
Db	601	ATG	CGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCACCGG	660
Qy	661	AACA	CCCCCGCCAGATGAACCGCGCCTACGGCTACTACAAGCAGTACTCCGCCAGCTC	720
Db	661	AA	CAACCCCGCCAGATGAACCGCGCTCGGTACTACAGGCAGTACTCCGCCAGCTC	720
Qy	721	GGCGT	CGACCCAGGGCCCAACTCACTTGTCTGA	753
Db	721	GGCGT	CGACCCAGGGCCCAACCTCACTTGTCTGA	753

### RESULT 3

RESOL 3  
AD592671  
ID AD592671 standard; DNA; 753 BP.

AC ADS92671;

DT 02-DEC-2004 (first entry)

DE Chitinase variant polynucleotide #25.

KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium; Heterodera.

OS Synthetic.

PN WO2004037194-A2.

PD 06-MAY-2004.

PF 22-OCT-2003; 2003WO-US033588.

PR 22-OCT-2002; 2002US-0420666P.

PR 14-MAR-2003: 2003US-00389432.

PA (VERD-) VERDIA INC.

[illegible][illegible]

DR P-PSDB: ADS92672.

**PT** New chitinase polynu

XX  
XX

XX  
 2-1

CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

Seq	Sequence	753 BP; 144 A; 245 C; 255 G; 109 T; 0 U; 0 Other;
Query Match	96.4%;	Score 725.8; DB 13; Length 753;
Best Local Similarity	97.7%;	Pred. No. 2.4e-127;
Matches	736; Conservative	0; Mismatches 17; Indels 0; Gaps 0;
Qy	1	TCGNTGCAGAACTCGCGCTGCCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTCGCGC 60
Db	1	TCGATGCAGAACTCGCGCTGCCAGCCAAACGTATGCTGCAGCAAGTTTGCTACTTCGCGC 60
Qy	61	ACAACCACGAGTACTTCGCGCGACGGGTGCAGTCGGGCGCCGTGCGCCTCGGGCGGCGGC 120
Db	61	ACAACCACGAGTACTTCGCGCGACGGGTGCCAGTCGGGCGCCGTGCGCACTCGGGCGGCGGT 120
Qy	121	GGCAGCAGTGGCGCGGTGTGTGCGAAGCTGGCTAGCGTGTGCTCACCAGGCTCCTTCTTCAAC 180
Db	121	GGCGCGGTGGCGCGGTGTGTGCGAAGCTGGCTAGCGTGTGCTCACCAGGCTCCTTCTTCAAC 180
Qy	181	GGCATCAAGAACACAGGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCCCGAGGCGCG 240
Db	181	GGCATCAAGAACACAGGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCCCGAGGCGCG 240
Qy	241	TTCTGTAGCGCCGTCAAGGGGTGTAACCAAGGCTTCGCCCATGCGCGGTGCACAGGTGCAGGGC 300
Db	241	TTCTGTAGCGCCGTCAAGGGGTGTAACCAAGGCTTCGCCCATGCGCGGTGCACAGGTGCAGGGC 300
Qy	301	AAGGCGCAGATCGCGCGCTTCTTCGCGCACGCCACGCAACGAGACCGGGCANTTCTGTCTAC 360
Db	301	AAGGCGCAGATCGCGCGCTTCTTCGCGCATGTCAACGCAACGAGACCGGGCANTTCTGTCTAC 360
Qy	361	ATCAGCGAGATCAGCAAGAGCAACGCCCTACTTCGGACCCGACCAAGAGCGAGTGGCCGTGC 420
Db	361	ATCAGCGAGATCAACAGAGCAACGCCCTACTTCGGACCCGACCAAGAGCGAGTGGCCGTGC 420
Qy	421	GCGCGGGGCGAAGTACTAAGGGCGCGGCCCGCTGCAGATCTGCTGGAACTACAATCTAC 480
Db	421	GCGCGGGGCGAAGTACTAAGGGCGCGGCCCGCTGCAGATCTGCTGGAACTACAATCTAC 480
Qy	481	GGGCGCGCGGGAGGGACATCGGCTTCGACGGGCTCGGGACCCCGGCAAGGTGGCGCGG 540
Db	481	GGGCGCGCGGGAGGGACATCGGCTTCACGGGCTCGCGACCCCGCAACAGGTGGCGCGAG 540
Qy	541	GAGCCGTGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGGATGAACAAACGTCGACCGGTGTG 600
Db	541	GAGCCGTGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGGATGAACAAACGTCGACCGGTGTG 600
Qy	601	ATGCGCGAGGGCTTCGCGGCCACCATCAGGGCCCATCAACGGCGGCTTCGAGTGGCAGGG 660
Db	601	ATGCGCGAGGGCTTCGCGGCCACCATCAGGGCCCATCAACGGCGGCTTCGAGTGGCGGGG 660
Qy	661	AACAAACCCCGCCAGATGAACGGCGCATCGGCTACTTACAAGCAGTACTGCCCGCAGCTC 720
Db	661	AACAAACCCCGCCAGATGAACGGCGCATCGGCTACTTACAAGCAGTACTGCCCGCAGCTC 720
Qy	721	GGCGTGCACCGAGGGCCAAACCTCACTTGCTGA 753
Db	721	GGCGTGCACCGAGGGCCAAACCTCACTTGCTGA 753

## RESULT 4

RESOLU 4  
ADS92693  
ID ADS92693 standard; DNA; 753 BP.

AC ADS92693;

DT 02-DEC-2004 (first entry)

DE Chitinase variant polynucleotide #36.

Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium; Heterodera.

OS Synthetic.

```
XX WO2004037194-A2.
XX
XX PD 06-MAY-2004.
XX
XX PF 22-OCT-2003; 2003WO-US033588.
XX
XX PR 22-OCT-2002; 2002US-0420666P.
XX
XX PR 06-NOV-2002; 2002US-00290086.
XX
XX PR 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Muller ML, True T, Simmons CR, Yalpani N;
XX
XX WPI; 2004-365417/34.
XX
XX DR P-PSDB; ADS92694.
XX
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
XX PS Claim 4; SEQ ID NO 77; 197pp; English.
XX
XX CC The invention relates to chitinase polypeptides and the polynucleotides
XX encoding them. A method of enhancing plant resistance to a fungus or
XX nematode comprises introducing into a plant a recombinant expression
XX cassette comprising a promoter operably linked to a chitinase
XX polynucleotide of the invention. The plant is maize or soybean. The
XX fungus is from the genus Fusarium. The nematode is from the genus
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX plant resistance to a fungus or nematode. This sequence represents a
XX chitinase variant polynucleotide of the invention.
XX
XX SQ Sequence 753 BP; 142 A; 244 C; 262 G; 105 T; 0 U; 0 Other;

Query Match          96.0%; Score 722.6; DB 13; Length 753;
Best Local Similarity 97.5%; Pred. No. 9,7e-127;
Matches 734; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 TCGATGCGAAGTGGCGGTGCGAGCCAAAGTATGCTGCAGCAAGTTGCGGTACTGCGGC 60
DB 1 TCGATGCGAAGTGGCGGTGCGAGCCAAAGTATGCTGCAGCAAGTTGCGGTACTGCGGC 60
QY 61 ACAACCGACGAGTACTGCGGCGACGGGTGCGAGTGGCGCCGCTGCGGCGGCGGC 120
DB 61 AGCAGCGAGAGTACTGCGGCGACGGGTGCGAGTGGCGCCGCTGCGGCGGCGGC 120
QY 121 GGCAGCAGTGGCGGCGGTGGTGCAGAACGTGGCTAGCGTCCGCGCTCTTCTTCAAC 180
DB 121 GGCAGCAGTGGCGGCGGTGGTGCAGAACGTGGCTAGCGTCCGCGCTCTTCTTCAAC 180
QY 181 GGCATCAGAACCGCGGCGGAGCGGTGCGAGGGCAGAACTTACACCGGAGCGGC 240
DB 181 GGCATCAGAACCGCGGCGGAGCGGTGCGAGGGCAGAACTTACACCGGAGCGGC 240
QY 241 TTCCTGAGCGCGTCAAGCGGTACCGAGCTTTCGCCCATGGCGGTACAGGTGCGAGGC 300
DB 241 TTCCTGAGCGCGTCAAGCGGTACCGAGCTTTCGCCCATGGCGGTACAGGTGCGAGGC 300
QY 301 AAGCGCGAGATGCGCGCTTCTTCGCGCAGCGCAGCAGCGAGCGGCAATTTCTGTTCAC 360
DB 301 AAGCGCGAGATGCGCGCTTCTTCGCGCAGCGCAGCAGCGGCAATTTCTGTTCAC 360
QY 361 ATCAGCGAGATCAGAACGCAACCGCTTCTGCGACCGCGCAGCGAGCGAGTGGCGGTC 420
DB 361 ATCAGCGAGATCAGAACGCAACCGCTTCTGCGACCGCGCAGCGAGCGAGTGGCGGTC 420
QY 421 GCGCGGCGGCGAGAGTACTACGGGCGCGCGCGCTGCGAGATCTCGTGGAACTTACAATAC 480
DB 421 GCGCGGCGGCGAGAGTACTACGGGCGCGCGCGCTGCGAGATCTCGTGGAACTTACAATAC 480
QY 481 GGGCCCCGGGGGAGGAGACATCGGCTTTCGACGGGCTTCGGGGACCCCGCGAGGGTGGCGGC 540
```

```
DB 481 GGGCCCGCGGCGAGGCGCATCGGCTTCGAGCGGCTCGGGGACCCCAACAGGGTGGCGGC 540
QY 541 GAGCCCGTGGTGGCGTTCAAGGGCGCGCTCTGGTTCTTGGATGAACAACGTGCACCGTGTG 600
DB 541 GAGCCCGTGGTGGCGTTCAAGGGCGCGCTCTGGTTCTTGGATGAACAACGTGCACCGTGTG 600
QY 601 ATGCGCGCAGGGCTTTCGGCGGCACCATCAGGGGCCATCAACGCGCGGCTCGAGTGCAGCGG 660
DB 601 ATGCGCGCAGGGCTTTCGGCGGCACCATCAGGGGCCATCAACGCGCGGCTCGAGTGCAGCGG 660
QY 661 AACAAACCCCGCCAGATGAACGCGCGCATCGGCTTACTACAAGCAGTACTGCGCGCAGTTC 720
DB 661 AACAAACCCCGCCAGATGAACGCGCGCATCGGCTTACTACAAGCAGTACTGCGCGCAGTTC 720
QY 721 GGGCTGCGACCGCGGCGCCAACTCCTTGTGTA 753
DB 721 GGGCTGCGACCGCGGCGCCAACTCCTTGTGTA 753
```

## RESULT 5

ADS92697  
ID ADS92697 standard; DNA; 753 BP.XX AC  
XX ADS92697;

DT 02-DEC-2004 (first entry)

DE Chitinase variant polynucleotide #38.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

XX Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

XX 06-NOV-2002; 2002US-00290086.

XX 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

XX (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX P-PSDB; ADS92698.

XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 81; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing  
XX plant resistance to a fungus or nematode. This sequence represents a  
XX chitinase variant polynucleotide of the invention.

XX SQ Sequence 753 BP; 140 A; 240 C; 263 G; 110 T; 0 U; 0 Other;

Query Match 95.5%; Score 719.4; DB 13; Length 753;

Best Local Similarity 97.2%; Pred. No. 3.9e-126;

Matches 732; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
QY 1 TCGATGCGAGAACTGGCGGTGCGAGCAAAAGTATGCTGCGAGCAAGTTGGGCTACTGGCGC 60
Db 1 TCGATGCGAGAACTGGCGGTGCGAGCAAAAGTATGCTGCGAGCAAGTTGGGCTACTGGCGC 60
QY 61 ACAACCGAGAGTACTGGCGGCGAGCGGTGCGAGTGGCGGCGGCTGGCGGCGGCGC 120
Db 61 AGCAGCGAGAGTACTGGCGGCGAGCGGTGCGAGTGGCGGCGGCTGGCGGCGGCGC 120
QY 121 GCGACAGTGGCGGCGGTGCGAGCGGTGCGAGTGGCGGCGGCTGGCGGCGGCGC 180
Db 121 GCGACAGTGGCGGCGGTGCGAGCGGTGCGAGTGGCGGCGGCTGGCGGCGGCGC 180
QY 181 GGCATCAGAGAACCGCGGCGAGCGGTGCGAGCGGTGCGAGTGGCGGCGGCGC 240
Db 181 GGCATCAGAGAACCGCGGCGAGCGGTGCGAGCGGTGCGAGTGGCGGCGGCGC 240
QY 241 TTCCTGAGCGCGTCAAGCGGTACCGAGCTTTCGCGGCGGCTGGCGGCGGCGC 300
Db 241 TTCCTGAGCGCGTCAAGCGGTACCGAGCTTTCGCGGCGGCTGGCGGCGGCGC 300
QY 301 AAGCGCGAGATCGCGGCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 360
Db 301 AAGCGCGAGATCGCGGCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 360
QY 361 ATCAGCGAGATCAGCAAGAGCAACCGCTTTCGCGGCGGCGGCGGCGGCGGCGC 420
Db 361 ATCAGCGAGATCAGCAAGAGCAACCGCTTTCGCGGCGGCGGCGGCGGCGGCGC 420
QY 421 GCGCGCGGCGGAGAGTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 480
Db 421 GCGCGCGGCGGAGAGTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 480
QY 481 GCGCGCGGCGGAGAGTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 540
Db 481 GCGCGCGGCGGAGAGTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 540
QY 541 GAGCGCGTGGTGGCGGCTTCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGC 600
Db 541 GAGCGCGTGGTGGCGGCTTCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGC 600
QY 601 ATGCGCGAGGCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 660
Db 601 ATGCGCGAGGCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 660
QY 661 AACAAACCGCGCGAGATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 720
Db 661 AACAAACCGCGCGAGATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 720
QY 721 GCGGTGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 753
Db 721 GCGGTGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 753
```

## RESULT 6

ADS92651

ID ADS92651 standard; DNA; 753 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

22-OCT-2003; 2003WO-US033588.

22-OCT-2002; 2002US-0420666P.

06-NOV-2002; 2002US-00290086.

14-MAR-2003; 2003US-00389432.

(VERD-) VERDIA INC.

(PION-) PIONEER HI-BRED INT INC.

Muller ML, True T, Simmons CR, Valpani N;

WPI; 2004-365417/34.

P-PSDB; ADS92652.

New chitinase polynucleotides and polypeptides, useful in producing

plants with enhanced resistance against a fungus or a nematode.

Claim 4; SEQ ID NO 35; 197pp; English.

The invention relates to chitinase polypeptides and the polynucleotides

encoding them. A method of enhancing plant resistance to a fungus or

nematode comprises introducing into a plant a recombinant expression

cassette comprising a promoter operably linked to a chitinase

polynucleotide of the invention. The plant is maize or soybean. The

fungus is from the genus Fusarium. The nematode is from the genus

Heterodera. The polynucleotides and polypeptides are useful in enhancing

plant resistance to a fungus or nematode. This sequence represents a

chitinase variant polynucleotide of the invention.

Sequence 753 BP; 140 A; 247 C; 260 G; 106 T; 0 U; 0 Other;

Query Match 95.3%; Score 717.8; DB 13; Length 753;

Best Local Similarity 97.1%; Pred. No. 7.7e-126;

Matches 731; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCGATGCGAGAACTGGCGGTGCGAGCAAAAGTATGCTGCGAGCAAGTTGGGCTACTGGCGC 60

Db 1 TCGATGCGAGAACTGGCGGTGCGAGCAAAAGTATGCTGCGAGCAAGTTGGGCTACTGGCGC 60

QY 61 ACAACCGAGAGTACTGGCGGCGAGCGGTGCGAGTGGCGGCGGCTGGCGGCGGCGC 120

Db 61 AGCAGCGAGAGTACTGGCGGCGAGCGGTGCGAGTGGCGGCGGCTGGCGGCGGCGC 120

QY 121 GCGACAGTGGCGGCGGTGCGAGCGGTGCGAGTGGCGGCGGCTGGCGGCGGCGC 180

Db 121 GCGACAGTGGCGGCGGTGCGAGCGGTGCGAGTGGCGGCGGCTGGCGGCGGCGC 180

QY 181 GGCATCAGAGAACCGCGGCGAGCGGTGCGAGCGGTGCGAGTGGCGGCGGCGC 240

Db 181 GGCATCAGAGAACCGCGGCGAGCGGTGCGAGCGGTGCGAGTGGCGGCGGCGC 240

QY 241 TTCCTGAGCGCGTCAAGCGGTACCGAGCTTTCGCGGCGGCTGGCGGCGGCGC 300

Db 241 TTCCTGAGCGCGTCAAGCGGTACCGAGCTTTCGCGGCGGCTGGCGGCGGCGC 300

QY 301 AAGCGCGAGATCGCGGCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 360

Db 301 AAGCGCGAGATCGCGGCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 360

QY 361 ATCAGCGAGATCAGCAAGAGCAACCGCTTTCGCGGCGGCGGCGGCGGCGGCGC 420

Db 361 ATCAGCGAGATCAGCAAGAGCAACCGCTTTCGCGGCGGCGGCGGCGGCGGCGC 420

QY 421 GCGCGCGGCGGAGAGTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 480

Db 421 GCGCGCGGCGGAGAGTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 480

QY 481 GCGCGCGGCGGAGAGTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 540

Db 481 GCGCGCGGCGGAGAGTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 540

QY 541 GAGCGCGTGGTGGCGGCTTCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGC 600

Db 541 GAGCGCGTGGTGGCGGCTTCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGC 600

QY 601 ATGCGCGAGGCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 660

Db 601 ATGCGCGAGGCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 660

QY 661 AACAAACCGCGCGAGATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 720

Db 661 AACAAACCGCGCGAGATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 720

QY 721 GCGGTGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 753

Db 721 GCGGTGCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGC 753

## RESULT 6

ADS92651

ID ADS92651 standard; DNA; 753 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

WO2004037194-A2.

06-MAY-2004.

Chitinase variant polynucleotide #15.

Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

Heterodera.

Synthetic.

Db 541 GACGCCGTGGTGGCTTCAAGGGCGCGCTCTGGTTCTGGATGAACAAGTGCACCGGTG 600  
 Qy 601 ATGCCGAGGGCTTTCGGCGCCACCATCAAGGCCATCAACGGCGCGCTCGAGTGCAGCGG 660  
 Db 601 ATGCCGAGGGCTTTCGGCGCCACCATCAAGGCCATCAACGGCGCGCTCGAGTGCAGCGG 660  
 Qy 661 AACAAACCCGCCAGATGAAACGGCGCATCGGCTACTACAAAGCAGTACTGCGCGCAGCTC 720  
 Db 661 AACAAACCCGCCAGATGAAACGGCGCATCGGCTACTACAAAGCAGTACTGCGCGCAGCTC 720  
 Qy 721 GGCGTCGACCCAGGCGCCAACTCACTTGTGA 753  
 Db 721 GGCGTCGACCCAGGCGCCAACTCACTTGTGA 753

## RESULT 7

ADS92659

ID ADS92659 standard; DNA; 753 BP.

XX

AC ADS92659;

XX

DT 02-DEC-2004 (first entry)

XX

DE Chitinase variant polynucleotide #19.

XX

KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

XX

KW Heterodera.

XX

OS Synthetic.

XX

XX WO2004037194-A2.

XX

XX 06-MAY-2004.

XX

XX 22-OCT-2003; 2003WO-US033588.

XX

XX 22-OCT-2002; 2002US-0420666P.

XX

XX 06-NOV-2002; 2002US-00290086.

XX

XX 14-MAR-2003; 2003US-00389432.

XX

XX (VERD-) VERDIA INC.

XX

XX (PION-) PIONEER HI-BRED INT INC.

XX

XX Muller ML, True T, Simmons CR, Yalpani N;

XX

XX WPI; 2004-365417/34.

XX

XX P-PSDB; ADS92660.

XX

XX New chitinase polynucleotides and polypeptides, useful in producing

XX

XX plants with enhanced resistance against a fungus or a nematode.

XX

XX Claim 4; SEQ ID NO 43; 197pp; English.

XX

XX The invention relates to chitinase polypeptides and the polynucleotides  
 encoding them. A method of enhancing plant resistance to a fungus or  
 nematode comprises introducing into a plant a recombinant expression  
 cassette comprising a promoter operably linked to a chitinase  
 polynucleotide of the invention. The plant is maize or soybean. The  
 fungus is from the genus *Fusarium*. The nematode is from the genus  
*Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 plant resistance to a fungus or nematode. This sequence represents a  
 chitinase variant polynucleotide of the invention.

XX

SQ Sequence 753 BP; 139 A; 243 C; 262 G; 109 T; 0 U; 0 Other;

XX

Query Match 95.1%; Score 716.2; DB 13; Length 753;

XX

Best Local Similarity 96.9%; Pred. No. 1.5e-125;

XX

Matches 730; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

XX

Qy 1 TCGATGCAGAACTGGCGTGCAGCAACGATATGCTCGAGCAAGTTGGCTACTGCGGC 60

Db

1 TCGATGCAGAACTGGCGTGCAGCAACGATATGCTCGAGCAAGTTGGCTACTGCGGC 60

Qy 61 ACAACCGACAGTACTCGCGCGACGGGTGCACTCGGGCCCCGTGCGCTCGGGCGGCGGC 120  
 Db 61 ACACCGACAGTACTCGCGCGACGGGTGCACTCGGGCCCCGTGCGCTCGGGCGGCGGC 120  
 Qy 121 GGACGAGTGGCGCGGTGCGAAGCTGGCTAGGGTGGTCAACGGCTCTCTTCTTCAAC 180  
 Db 121 GGACGAGTGGCGCGGTGCGAAGCTGGCTAAATGTGGTCAACGGCTCTCTTCTTCAAC 180  
 Qy 181 GGATCAAGAACCAAGCGCGGTGCGAGGGCAAGAACTTCTACACCGGAGCGCG 240  
 Db 181 GGATCAAGAACCAAGCGCGGTGCGAGGGCAAGAACTTCTACACCGGAGCGCG 240  
 Qy 241 TTCTGAGCGCGCTCAAGCGGTATCCAGGCTTCCCATGCGCGCTCCGAGGTCGAGCGC 300  
 Db 241 TTCTGAGCGCGCTCAAGCGGTATCCAGGCTTCCCATGCGCGCTCCGAGGTCGAGCGC 300  
 Qy 301 AAGCGGAGATCGCGCGCTTCTTCGGCGCACCGACGACGAGACCGGGCAATTTCTGTAC 360  
 Db 301 AAGCGGAGATCGCGCGCTTCTTCGGCGCATGTCAACGAGACCGGGCAATTTCTGTAC 360  
 Qy 361 ATCAGCGAGATCAAGAGCAACGCTTCTGCGACCCGACCAAGAGGCGAGTGGCGTGC 420  
 Db 361 ATCAGCGAGATCAAGAGCAACGCTTCTGCGACCCGACCAAGAGGCGAGTGGCGTGC 420  
 Qy 421 GCGCGGGCGAGAGTACTACGGCGCGCGCTGCGATCTGTTGGAATCAACAATAC 480  
 Db 421 GCGCGGGCGAGAGTACTACGGCGCGCGCTGCGATCTGTTGGAATCAACAATAC 480  
 Qy 481 GGGCGCGGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGGAGGTTGGCGGG 540  
 Db 481 GGGCGCGGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGGAGGTTGGCGGG 540  
 Qy 541 GAGCGGTGTGGCGTTCAAGGGCGGCTCTGTTCTGGATGAACAACGTCACCGTGTG 600  
 Db 541 GAGCGGTGTGGCGTTCAAGGGCGGCTCTGTTCTGGATGAACAACGTCACCGTGTG 600  
 Qy 601 ATGCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCTCGAGTGCACGGG 660  
 Db 601 ATGCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCTCGAGTGCACGGG 660  
 Qy 661 AACACCCCGCCAGATGAACGGCGCATCGGCTACTACAGCAGTACTCGCGCAGCTC 720  
 Db 661 AACACCCCGCCAGATGAACGGCGCATCGGCTACTACAGCAGTACTCGCGCAGCTC 720  
 Qy 721 GGGTCGACCCAGGGCCCAACCTCACTTGTGA 753  
 Db 721 GGGTCGACCCAGGGCCCAACCTCACTTGTGA 753

## RESULT 8

AAA96222

ID AAA96222 standard; cDNA; 1094 BP.

XX

AC AAA96222;

XX

DT 08-FEB-2001 (first entry)

XX

DE cDNA encoding a maize chitinase polypeptide designated ZmCh2.

XX

XX Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase family 18;  
 pathogen control; disease resistance; molecular marker; ss.

XX

OS Zea mays.

XX

FH Key Location/Qualifiers

FT CDS 51..896

FT /\*tag= a

FT /product= "chitinase"

XX

PN WO200056908-A2.

XX

XX 28-SEP-2000.

XX

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PF 09-MAR-2000; 2000WO-US006121.
XX
PR 24-MAR-1999; 99US-0125915P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Simmons CR, Yalpani N;
XX
DR WPI; 2000-628269/60.
DR P-PSDB; AAB18894.
XX
PT New maize chitinase genes encoding seven chitinases of glucosyl hydrolase
PT family 19 are useful for enhancing disease resistance in crop plants by
PT modulating its expression in plants.
XX
PS Claim 1; Page 64-65; 96pp; English.
XX
CC The present sequence encodes a chitinase polypeptide. The specification
CC describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896,
CC AAB18899, and AAB18902-05), and glucosyl hydrolase family 18 chitinases
CC (AAB18895, AAB1897-98 and AAB18900-01). The level of chitinase in plants
CC can be modulated to enhance disease resistance in crop plants and for
CC control of pathogens. The chitinase polynucleotides are also useful as
CC molecular markers for genotype in a plant, and for sequence shuffling
XX
SQ Sequence 1094 BP; 226 A; 339 C; 368 G; 161 T; 0 U; 0 Other;

Query Match 95.0%; Score 715.6; DB 3; Length 1094;
Best Local Similarity 97.5%; Pred. No. 2e-125;
Matches 727; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 6 GCAGAACTGCGGTCGCCAGCAAGATGCTGCGAGCAAGTTCGGCTACTCGGCAAC 65
DB 149 GCAGAACTGCGGTCGCCAGCAAGATGCTGCGAGCAAGTTCGGCTACTCGGCAAC 208
QY 66 CGACGAGTACTGCGGCGAGCGGTGCGAGTCCAGTCCGCGCCGCTCGGCGCGCGCGGCGAG 125
DB 209 CGACGAGTACTGCGGCGAGCGGTGCGAGTCCAGTCCGCGCCGCTCGGCGCGCGCGGCGAG 268
QY 126 CAGTGGCGCGGTGCTGCGAAGTGGTCTAGCGTGTCTACCGCGCTCTTCTTCAACGGCAT 185
DB 269 CAGTGGCGCGGTGCTGCGAAGTGGTCTAGCGTGTCTACCGCGCTCTTCTTCAACGGCAT 328
QY 186 CAGAACCCAGCGCGGAGCGGTGCGAGGCGCAAGACTTCTACACCGGAGCGGTTCCT 245
DB 329 CAAGAGCCAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGGTTCCT 388
QY 246 GAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGCGCGGTTCACAGGTGCGAGGCAAGCG 305
DB 389 GAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGCGCGGTTCGCAGGTGCGAGGCAAGCG 448
QY 306 CGAGATCGCGCGCTTCTTTCGCGCAGCGCCACGCAAGAGACCGGGCATTTCTGTATCATCAG 365
DB 449 CGAGATCGCGCGCTTCTTTCGCGCAGCGCCACGCAAGAGACCGGGCATTTCTGTATCATCAG 508
QY 366 CGAGATCAGCAAGAGCAAGCTTCTGCGACCGCGCCGCAAGAGCGAGTGGCGCGCGCGC 425
DB 509 CGAGATCAACAGAGCAAGCGCTTCTGCGACCGCGCCGCAAGAGCGAGTGGCGCGCGCGC 568
QY 426 GCGGCGAGAGTACTACGCGCGCGCGCGCTGCAGATCTCGTGGAACTACAACACTACGCGCC 485
DB 569 GCGGCGAGAGTACTACGCGCGCGCGCGCGCTGCAGATCTCGTGGAACTACAACACTACGCGCC 628
QY 486 GCGGCGAGAGGACATTCGGCTTTCGACGCGGCTTCGGGACCCCGGCGAGGGTGGCGCGGACGC 545
DB 629 GCGGCGAGAGGACATTCGGCTTTCGACGCGGCTTCGGGACCCCGGCGAGGGTGGCGCGGACGC 688
QY 546 GTGTGTGGCTTCAAGCGCGCGCTCTGGTTCTGTGATGAACACGCTGCAACCGTGTATGCC 605
DB 689 GTGTGTGGCTTCAAGCGCGCGCTCTGGTTCTGTGATGAACACGCTGCAACCGGCTGTGTC 748
QY 606 GCAGGGCTTCGCGCGCACCATCAGGGCCCATCAACGCGCGCGCTTCGAGTGCAGCGGAAACA 665
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Db 749 GCAGGGGTTGGCGCCACCACCGGCATCAACGGCGCCCTCGAGTGGCGGGGAACA 808
QY 666 CCCGCCCAGATGAACCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGCGT 725
DB 809 CCCGCCCAGATGAACCGCGCATCGGCTACTACAAGCAGTACTGCCGCCAGCTCGGCGT 868
QY 726 CGACCCAGGGCCCAACCTCACTTGTCT 751
DB 869 CGACCCCGGGCCCAACCTCACTTGTCT 894

RESULT 9
ADS92637
ID ADS92637 standard; DNA; 753 BP.
XX
AC ADS92637;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polynucleotide #8.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
WPI; 2004-365417/34.
P-PSDB; ADS92638.
XX
PT New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 4; SEQ ID NO 21; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 132 A; 247 C; 269 G; 105 T; 0 U; 0 Other;

Query Match 94.9%; Score 714.6; DB 13; Length 753;
Best Local Similarity 96.8%; Pred. No. 3.1e-125;
Matches 729; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TCGATGCAGAACTCGGCTGCCAGCAAGATGCTGTCAGCAAGTTTCGGCTACTCGGCG 60
DB 1 TCGATGCAGAACTCGGCTGCCAGCAAGATGCTGTCAGCAAGTTTCGGCTACTCGGCG 60
QY 61 ACAACCGACGAGTACTCGGCGCGAGCGGTGCGAGTTCGGCGCCCGCTCGGCGCGCGC 120
DB 61 ACGACCGACGAGTACTCGGCGCGAGCGGTGCGAGTTCGGCGCCCGCTCGGCGCGCGC 120
|||||
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QY 121 GGCAGCAGTGGCGGGTGGTGGCAAGTGGCTAGCGTGGTACCGGCTCTTCTTCAAC 180  
DB |||||||  
121 GGCAGCAGTGGCGGGTGGTGGCAAGTGGCTAGCGTGGTACCGGCTCTTCTTCAAC 180  
QY 181 GGCATCAAGAACCAAGCGCGGAGCGGGTGGAGGGCAAGAACTTCTACACCGGAGCGG 240  
DB |||||||  
181 GGCATCAAGAACCAAGCGCGGAGCGGGTGGAGGGCAAGAACTTCTACACCGGAGCGG 240  
QY 241 TTCTGAGCGCGCTCAAGCGCTACCCAGGCTTGGCCCATGGCGGGTCAAGGTGCAAGGG 300  
DB |||||||  
241 TTCTGAGCGCGCTCAAGCGCTACCCAGGCTTGGCCCATGGCGGGTCAAGGTGCAAGGG 300  
QY 301 AAGCGGAGATGCGCGCTTCTCGCGACGCCACGACGACGAGCGGGCACTTCTGTTC 360  
DB |||||||  
301 AAGCGGAGATGCGCGCTTCTCGCGACGCCACGACGAGCGGGCACTTCTGTTC 360  
QY 361 ATCAGCGAGATCAGCAAGAGCAAGCCCTACTTGGACCCGACCAAGAGGCACTCAACTAC 420  
DB |||||||  
361 ATCAGCGAGATCAGCAAGAGCAAGCCCTACTTGGACCCGACCAAGAGGCACTCAACTAC 420  
QY 421 GCCGGGGGAGAGTACTACGGGGGGCGCGCTGCGAGATCTGTGGAATCAACTAC 480  
DB |||||||  
421 GCCGGGGGAGAGTACTACGGGGGGCGCGCTGCGAGATCTGTGGAATCAACTAC 480  
QY 481 GGGCGCGGGGAGGAGCATCGCTTTCAGCGGGCTCGGGGACCCCGGAGGGTGGCGGG 540  
DB |||||||  
481 GGGCGCGGGGAGGAGCATCGCTTTCAGCGGGCTCGGGGACCCCGGAGGGTGGCGGG 540  
QY 541 GACGCGGTGGTGGGTTCAAGGCGCGCTCTGGTTCTGGATGAACAACGTCACCGGTG 600  
DB |||||||  
541 GACGCGGTGGTGGGTTCAAGGCGCGCTCTGGTTCTGGATGAACAACGTCACCGGTG 600  
QY 601 ATGCGGAGGGCTTGGCGGCCACCATCAGGGGCGCTCGAGTGGAGCGGG 660  
DB |||||||  
601 ATGCGGAGGGCTTGGCGGCCACCATCAGGGGCGCTCGAGTGGAGCGGG 660  
QY 661 AACAAACCCCGCCAGATCAAGCGCGCATCGCTACTACAAGCAGTACTGCGCGCAGCTC 720  
DB |||||||  
661 AACAAACCCCGCCAGATCAAGCGCGCATCGCTACTACAAGCAGTACTGCGCGCAGCTC 720  
QY 721 GCGGTGCGACCCAGGCGCCCAACTCTCACTTGCTGA 753  
DB |||||||  
721 GCGGTGCGACCCAGGCGCCCAACTCTCACTTGCTGA 753

## RESULT 10

AD592683  
ID AD592683 standard; DNA; 765 BP.  
XX  
AC AD592683;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #31.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

Synthetic.

WO2004037194-A2.

06-MAY-2004.

22-OCT-2003; 2003WO-US033588.

22-OCT-2002; 2002US-0420666P.

PR 06-NOV-2002; 2002US-00290086.

PR 14-MAR-2003; 2003US-00389432.

(VERD-) VERDIA INC.

(PION-) PIONEER HI-BRED INT INC.

PI Muller ML, True T, Simmons CR, Yalpani N;  
XX WPI; 2004-365417/34.  
DR P-PSDB; ADS92684.  
XX  
PT New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 4; SEQ ID NO 67; 197pp; English.  
XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprising introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX  
SQ Sequence 765 BP; 144 A; 248 C; 267 G; 106 T; 0 U; 0 Other;

Query Match 94.5%; Score 711.8; DB 13; Length 765;  
Best Local Similarity 96.9%; Pred. No. 1e-124;  
Matches 741; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 1 TCGATGACAGAACTGCGGCTGCCAGCAAGCTAGCTGCAGCAAGTTTCGGCTACTCGGC 60  
DB |||||||  
1 TCGATGACAGAACTGCGGCTGCCAGCAAGCTAGCTGCAGCAAGTTTCGGCTACTCGGC 60  
QY 61 ACAACCCAGCAAGTACTGCGGCGACGGGTGCGAGTTCGGGCCCGCTCGCGCTCGGGCGGCG 120  
DB |||||||  
61 ACAACCCAGCAAGTACTGCGGCGACGGGTGCGAGTTCGGGCCCGCTCGCGCTCGGGCGGCG 120  
QY 121 GGCAGCAGTGGCGGC-----GGTGTGCGAACTGGTGGTACGCTGCTCACCAGC 168  
DB |||||||  
121 GGCAGCAGTGGCGGC-----GGTGTGCGAACTGGTGGTACGCTGCTCACCAGC 180  
QY 169 TCCTTCTTCAACGCATCAAGAACAGCGCGGAGCGGGTGCAGGGCAAGAACTTCTTAC 228  
DB |||||||  
181 TCCTTCTTCAACGCATCAAGAACAGCGCGGAGCGGGTGCAGGGCAAGAACTTCTTAC 240  
QY 229 ACCGCGAGCGGTTCTTGAAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATTCGGGGTCA 288  
DB |||||||  
241 ACCGCGAGCGGTTCTTGAAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATTCGGGGTCA 300  
QY 289 CAGGTGACAGGGCAAGCGGAGATCGCGCTTCTTCGGGCACGCGCAGCAGACCGGG 348  
DB |||||||  
301 CAGGTGACAGGGCAAGCGGAGATTCGCGCTTCTTCGGGCACGCGCAGCAGACCGGG 360  
QY 349 CATTTCTGTTACATCAGCGAGATCAGCAAGAGCAACGCTTACTCGACCCCGACCAAGAGG 408  
DB |||||||  
361 CATTTCTGTTACATCAGCGAGATCAAGAGCAACGCTTACTTCGACCCCGACCAAGAGG 420  
QY 409 CAGTGGCGGTCGCGCGGCGGAGAACTACTACGGGCGCGGCGCGCTGCGAGATCTCGTGG 468  
DB |||||||  
421 CAGTGGCGGTCGCGCGGCGGAGAACTACTACGGGCGCGGCGCGCTGCGAGATCTCGTGG 480  
QY 469 AACTACAACTACGGGCGCGGAGAGGAGCACTCGGCTTCGACGGGCTCGGGGACCGCGG 528  
DB |||||||  
481 AACTACAACTACGGGCGCGGAGAGGAGCACTCGGCTTCGACGGGCTCGGGGACCGCGG 540  
QY 529 AGGTGCGCGGAGCGCGGCTTCAAGCGCGGCTCTGTTCTGATGAACAAC 588  
DB |||||||  
541 AGGTGCGCGGAGCGCGGCTTCAAGCGCGGCTCTGTTCTGATGAACAAC 600  
QY 589 GTGCACCGTGTGATGCGCGGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTC 648  
DB |||||||  
601 GTGCACCGTGTGATGCGCGGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTC 660  
QY 649 GAGTGCAGCGGGAACAACCCCGCCAGATGAACCGCGGCATCGGCTACTACAAGCAGTAC 708  
DB |||||||  
661 GAGTGCAGCGGGAACAACCCCGCCAGATGAACCGCGGCATCGGCTACTACAAGCAGTAC 720



QY 709 TGCCGCGAGCTCGCGTGCAGACCCAGGGGCCCAACTCTCACTTCTGA 753  
 DB 721 TGCCGCGAGCTCGCGTGCAGACCCAGGGGCCCAACTCTCACTTCTGA 765

RESULT 11  
 ADS92669  
 ID ADS92669 standard; DNA; 753 BP.  
 XX AC ADS92669;  
 XX DT 02-DEC-2004 (first entry)  
 XX DE Chitinase variant polynucleotide #24.  
 XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 KW Heterodera.  
 XX OS Synthetic.  
 XX WO2004037194-A2.  
 XX PD 06-MAY-2004.  
 XX 22-OCT-2003; 2003WO-US033588.  
 XX 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 XX WPI; 2004-365417/34.  
 DR P-PSDB; ADS92670.  
 XX

New chitinase polynucleotides and polypeptides, useful in producing plants with enhanced resistance against a fungus or a nematode.

Claim 4; SEQ ID NO 53; 197pp; English.

The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus *Fusarium*. The nematode is from the genus *Heterodera*. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polynucleotide of the invention.

Query Match 94.5%; Score 711.4; DB 13; Length 753;  
 Best Local Similarity 96.5%; Pred. No. 1.2e-124;  
 Matches 727; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 TCGATGCGAAGTCTCGCGTGCAGCAACGTATGCTGCAGCAAGTTCCGCTACTCGGC 60  
 DB 1 TCGATGCGAAGTCTCGCGTGCAGCAACGTATGCTGCAGCAAGTTTGGCTACTCGGC 60  
 QY 61 ACAACCGACGAGTACTCGCGGACGGGTGCGAGTCGGCCGCTCGCGGCGCGGC 120  
 DB 61 ACGACCGACGAGTACTCGCGGCGCGGTGCGAGTCGGCCGCTCGCGGCGCGGC 120  
 QY 121 GCGAGCAGTGGCGGGTGGTGCAGCAAGTGGCTAGCGTGCACCGGCTCCTTCTCAAC 180  
 DB 121 GCGAGCAGTGGCGGGTGGTGCAGCAAGTGGCTAGCGTGCACCGGCTCCTTCTCAAC 180  
 QY 181 GGCATCAAGAACCGAGCGGGGAGCGGGTGCAGGGGCAAGAACTTCTTACACCCGAGCGCG 240

DB 181 GGCATCAAGAACCGAGCGGGGAGCGGGTGCAGGGCAAGAACTTCTTACACCCGAGCGCG 240  
 QY 241 TTCTGAGCGCGGTCAAGGGGTACCCAGGGTTCGCCCATCGCGGTCAACAGGTGCAGGGC 300  
 DB 241 TTCTGAGCGCGGTCAAGGGGTACCCAGGGTTCGCCCATCGCGGTGCAGGTGCAGGGC 300  
 QY 301 AAGCGGAGATCGCGGCTTCTTCGCGCAGCCACGCAAGAGACCCGGGCACTTCTGTTC 360  
 DB 301 AAGCGGAGATCGCGGCTTCTTCGCGCAGTGTTCGCGCATGTTCGCGACCCGGGCACTTCTGTTC 360  
 QY 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCCGCGGACCAAGAGAGCGAGTGCCTGC 420  
 DB 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCCGCGGACCAAGAGAGCGAGTGCCTGC 420  
 QY 421 GCGCGGGGAGAGTACTACGGGCGCGGCGCTGCAGATCTCTGGAACCTACAACCTAC 480  
 DB 421 GCGCGGGGAGAGTACTACGGGCGCGGCGCTGCAGATCTCTGGAACCTACAACCTAC 480  
 QY 481 GGGCCCGGGGAGAGATCGGCTTCGACGGGTCGGGGACCCCGGAGGGTGCCTGC 540  
 DB 481 GGGCCCGGGGAGAGATCGGCTTCGACGGGTCGGGGACCCCGGAGGGTGCCTGC 540  
 QY 541 GAGCGCGTGGTGGCTTCAAGGGCGGCGCTCTGGTTCTGGATGAACAACGTCACCGTGTG 600  
 DB 541 GAGCGCGTGGTGGCTTCAAGTTCGGGCGCTCTGGTTCTGGATGAACAACGTCACCGTGTG 600  
 QY 601 ATGCGCGAGGGCTTCGGGCGCACCATCAGGGGCCATCAACGGCGCTCGAGTGCAGCGG 660  
 DB 601 ATGCGCGAGGGCTTCGGGCGCACCATCAGGGGCCATCAACGGCGCTCGAGTGCAGCGG 660  
 QY 661 AACAAACCCCGCAGATGAACGGCGCTCGGCTACTACAGGCGAGTACTGCGCGCAGCTC 720  
 DB 661 AACAAACCCCGCAGATGAACGGCGCTCGGCTACTACAGGCGAGTACTGCGCGCAGCTC 720  
 QY 721 GCGTGCAGCCAGGGCCCAACTCACTTGTGA 753  
 DB 721 GCGTGCAGCCAGGGCCCAACTCACTTGTGA 753

RESULT 12  
 ADS92665  
 ID ADS92665 standard; DNA; 753 BP.  
 XX AC ADS92665;  
 XX DT 02-DEC-2004 (first entry)  
 XX DE Chitinase variant polynucleotide #22.  
 XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
 KW Heterodera.  
 XX OS Synthetic.  
 XX WO2004037194-A2.  
 XX PD 06-MAY-2004.  
 XX 22-OCT-2003; 2003WO-US033588.  
 XX 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 XX WPI; 2004-365417/34.  
 DR P-PSDB; ADS92666.  
 XX

PT New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
XX Claim 4; SEQ ID NO 49; 197pp; English.  
PS  
XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX  
SQ Sequence 753 BP; 138 A; 238 C; 270 G; 107 T; 0 U; 0 Other;  
  
Query Match 94.5%; Score 711.4; DB 13; Length 753;  
Best Local Similarity 96.5%; Pred. No. 1.2e-124;  
Matches 727; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
  
Qy 1 TCGATGACGAACTCGGGTGCAGCCAAACGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
Db 1 TCGATGACGAACTCGGGTGCAGCCAAACGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
  
Qy 61 ACAACCGACGAGTACTCGCGGACGGTGCAGTCCGCGCCGCTCGCGGCGCGGC 120  
Db 61 ACGACCGACGAGTACTCGCGGACGGTGCAGTCCGCGCCGCTCGCGGCGCGGC 120  
  
Qy 121 GGCAGCAGTGCAGGCGGTGTCGAAAGTGTGCTAGCGTGCACCGGCTCTCTTCAAC 180  
Db 121 GGCAGCAGTGCAGGCGGTGTCGAAAGTGTGCTAGCGTGCACCGGCTCTCTTCAAC 180  
  
Qy 181 GGCATCAAGAACCGAGCGCGGAGCGGTGCAGGGCAAGACTTCTACCCGAGCGCG 240  
Db 181 GGCATCAAGAACCGAGCGCGGAGCGGTGCAGGGCAAGACTTCTACCCGAGCGCG 240  
  
Qy 241 TTCCTGAGCGCGTCAAGCGGTACCGCGCTTCGCGCATGCGGTGCACAGTGCAGGC 300  
Db 241 TTCCTGAGCGCGTCAAGCGGTACCGCGCTTCGCGCATGCGGTGCAGAGTGCAGGC 300  
  
Qy 301 AAGCGCGAGATCGCGCGCTTCTTCGCGCATGCGGTGCAGAGCGCGGCAATTCGTATC 360  
Db 301 AAGCGCGAGATCGCGCGCTTCTTCGCGCATGCGGTGCAGAGCGCGGCAATTCGTATC 360  
  
Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGCATGCGGTGCAGAGCGCGGCTGC 420  
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGCATGCGGTGCAGAGCGCGGCTGC 420  
  
Qy 421 GCGCGCGGCGAGAGTACTACGGCGCGCGCGCTGCAGATCTCGTGAACCTACAACTAC 480  
Db 421 GCGCGCGGCGAGAGTACTACGGCGCGCGCGCTGCAGATCTCGTGAACCTACAACTAC 480  
  
Qy 481 GGGCGCGCGGAGAGGACATCGGCTTCGACCGGCTCGGGGACCCCGGAGGTTGCGCGG 540  
Db 481 GGGCGCGCGGAGGAGGACATCGGCTTCGACCGGCTCGGGGACCCCGGAGGTTGCGCGG 540  
  
Qy 541 GACGCGGTGTTGCGGTTCAAGCGCGCGCTCTGGTTCGGATGAAACAGTGCACCGGTG 600  
Db 541 GACGCGGTGTTGCGGTTCAAGCGCGCGCTCTGGTTCGGATGAAACAGTGCACCGGTG 600  
  
Qy 601 ATGCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCAGCGG 660  
Db 601 ATGCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTGCAGCGG 660  
  
Qy 661 AACAAACCCCGCAGATGAACCGCGCATCGGCTACTCAAGAGAGTACTCGCGCGAGCTC 720  
Db 661 AACAAACCCCGCAGATGAACCGCGCATCGGCTACTCAAGAGAGTACTCGCGCGAGCTC 720  
  
Qy 721 GCGCTCGACCCAGGCGCCCAACTCTTCTGA 753  
Db 721 GCGCTCGACCCAGGCGCCCAACTCTTCTGA 753

## RESULT 13

ADS92695 standard; DNA; 750 BP.

XX ADS92695;

XX AC (first entry)

DT 02-DEC-2004

XX Chitinase variant polynucleotide #37.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; *Fusarium*;KW *Heterodera*.

XX Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

PR 06-NOV-2002; 2002US-00290086.

PR 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

PA (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

DR P-PSDB; ADS92695.

XX New chitinase polynucleotides and polypeptides, useful in producing

PT plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 79; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

SQ Sequence 750 BP; 140 A; 247 C; 256 G; 107 T; 0 U; 0 Other;

Query Match 94.1%; Score 708.2; DB 13; Length 750;

Best Local Similarity 97.2%; Pred. No. 4.9e-124;

Matches 732; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

Qy 1 TCGATGACGAACTCGGGTGCAGCCAAACGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60

Db 1 TCGATGACGAACTCGGGTGCAGCCAAACGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60

Qy 61 ACAACCGACGAGTACTCGCGGACGGTGCAGTCCGCGCCGCTCGCGGCGCGGC 120

Db 61 ACGACCGACGAGTACTCGCGGACGGTGCAGTCCGCGCCGCTCGCGGCGCGGC 120

Qy 121 GGCAGCAGTGCAGGCGGTGTCGAAAGTGTGCTAGCGTGCACCGGCTCTCTTCAAC 180

Db 121 GGCAGCAGTGCAGGCGGTGTCGAAAGTGTGCTAGCGTGCACCGGCTCTCTTCAAC 180

Qy 181 GGCATCAAGAACCGAGCGCGGAGCGGTGCAGGGCAAGACTTCTACCCGAGCGCG 240

Db 181 GGCATCAAGAACCGAGCGCGGAGCGGTGCAGGGCAAGACTTCTACCCGAGCGCG 240

Qy 241 TTCCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATCGCGGTGCAGGTCAGGCG 300

Db 241 TTCCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATCGCGGTGCAGGTCAGGCG 300

Db 238 TTCCTGAGCGCGTCAAGCGGTACCCAGGCTTCCGCCATGCGGGTGCAGGTCCAGGGC 297  
Qy 301 AAGCGGAGATCGCGCGCTTCTTCGCGACGCCACGACGAGACCGGCAATTTCTGTAC 360  
Db 298 AAGCGGAGATCGCGCGCTTCTTCGCGCATGTACGACGAGACCGGCAATTTCTGTAC 357  
Qy 361 ATCAGCGAGATCAGCAGAGCAACGCTTACTGCGACCGGACCGGACCGGAGGCGAGTGCCTGC 420  
Db 358 ATCAGCGAGATCAACAGAGCAACGCTTACTGCGACCGGACCGGACCGGAGGCGAGTGCCTGC 417  
Qy 421 GCCCGCGGCGAGAAAGTACTACGGCGCGCGCGCTGCGAGATCTCGTGAACCTACAATAC 480  
Db 418 GCCCGCGGCGAGAAAGTACTACGGCGCGCGCGCTGCGAGATCTCGTGAACCTACAATAC 477  
Qy 481 GGGCGCGGCGGAGGAGCATCGGCTTTCGACGCGGCTCGGGGACCGCGGAGGCTGCGCGG 540  
Db 478 GGGCGCGGCGGAGGAGCATCGGCTTTCGACGCGGCTCGCGGACCGCGGAGGCTGCGCGG 537  
Qy 541 GACCGCTGTGTGGCGTTCAGGCGCGCGCTCTGCTTCTGGATGAACAACGTCGACCGGTG 600  
Db 538 GACCGCTGTGTGGCGTTCAGGCGCGCGCTCTGCTTCTGGATGAACAACGTCGACCGGTG 597  
Qy 601 ATGCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAACGCGCGCTCGAGTGCAGCGG 660  
Db 598 ATGCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAACGCGCGCTCGAGTGCAGCGG 657  
Qy 661 AACAAACCGCGCGAGATGAACGCGCGCATCGGCTTACTAAGCAGTACTGCGCGCAGTCT 720  
Db 658 AACAAACCGCGCGAGATGAACGCGCGCATCGGCTTACTAAGCAGTACTGCGCGCAGTCT 717  
Qy 721 GGCGTCGACCCAGGCGCGCAACCTCATTGCTGA 753  
Db 718 GGCGTCGACCCAGGCGCGCAACCTCATTGCTGA 750

## RESULT 14

ADS92673  
ID ADS92673 standard; DNA; 753 BP.

XX AC ADS92673;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #26.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
XX HW Heterodera.

XX OS Synthetic.

XX PN W02004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR WPI; 2004-365417/34.

XX DR P-PSDB; ADS92674.

XX FT New chitinase polynucleotides and polypeptides, useful in producing  
XX PT plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 4; SEQ ID NO 57; 197pp; English.

## RESULT 15

ADS92647

ID ADS92647 standard; DNA; 753 BP.

XX

CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

XX SQ Sequence 753 BP; 136 A; 250 C; 260 G; 107 T; 0 U; 0 Other;

Query Match 93.2%; Score 701.8; DB 13; Length 753;

Best Local Similarity 95.8%; Pred. No. 7.8e-123;

Matches 721; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 1 TCGATGCAAGTTCGGCTGCCAGCCAAAGTATGCTGCAGCAAGTTCGGCTACTGCGGC 60

Db 1 TCGATGCAAGTTCGGCTGCCAGCCAAAGTATGCTGCAGCAAGTTCGGCTACTGCGGC 60

Qy 61 ACAACCGACGAGTACTGCGCGGACGCGGTGCAAGTTCGGCTGCGCGCGCGCGGC 120

Db 61 ACAACCGACGAGTACTGCGCGGACGCGGTGCAAGTTCGGCTGCGCGCGCGCGGC 120

Qy 121 GGCAGCAGTGGCGCGGTGTCGAGAGTTCGGCTGCGCGCGCGCGGCCTCTTCTTCAAC 180

Db 121 GGCAGCAGTGGCGCGGTGTCGAGAGTTCGGCTGCGCGCGCGCGGCCTCTTCTTCAAC 180

Qy 181 GGCATCAAGAACCAAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGCG 240

Db 181 GGCATCAAGAACCAAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGCG 240

Qy 241 TTCCTGAGCGCGGTCAAGCGTACCCGCGTTCGCGCGCGCGCGGTTCAGAGTTCAGGGC 300

Db 241 TTCCTGAGCGCGGTCAAGCGTACCCGCGTTCGCGCGCGCGCGGTTCAGAGTTCAGGGC 300

Qy 301 AAGCGGAGATTCGCGCGGTTCGCGCGCGCGCGGTTCGCGCGCGCGCGGTTCGCGCGCG 360

Db 301 AAGCGGAGATTCGCGCGGTTCGCGCGCGCGCGGTTCGCGCGCGCGCGGTTCGCGCGCG 360

Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGCGCGCGCGGTTCGCGCGCGCGCGGT 420

Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGCGCGCGCGGTTCGCGCGCGCGCGGT 420

Qy 421 GCGCGGCGCAGAGTACTACGCGCGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCGGT 480

Db 421 GCGCGGCGCAGAGTACTACGCGCGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCGGT 480

Qy 481 GGGCGCGCGGAGGAGCATCGGCTTCGCGCGCGCGCGGTTCGCGCGCGCGCGGTTCGCGCG 540

Db 481 GGGCGCGCGGAGGAGCATCGGCTTCGCGCGCGCGCGGTTCGCGCGCGCGCGGTTCGCGCG 540

Qy 541 GAGCGCGTGTGCGGTTCAGGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCGGTTCGCGCG 600

Db 541 GAGCGCGTGTGCGGTTCAGGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCGGTTCGCGCG 600

Qy 601 ATGCGCGAGGCTTCGCGCGCGCATCAGGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCG 660

Db 601 ATGCGCGAGGCTTCGCGCGCGCATCAGGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCG 660

Qy 661 AACACCCCGCCAGATGAAGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCGGTTCGCGCG 720

Db 661 AACACCCCGCCAGATGAAGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCGGTTCGCGCG 720

Qy 721 GGGCTCGACCCAGGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCG 753

Db 721 GGGCTCGACCCAGGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCGGTTCGCGCGCGCG 753

## RESULT 15

ADS92647

ID ADS92647 standard; DNA; 753 BP.

XX

AC ADS92647;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #13.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Valpani N;  
XX  
XX WPI; 2004-365417/34.  
DR P-PSDB; ADS92648.  
DR  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
PT  
XX  
XX Claim 4; SEQ ID NO 31; 197pp; English.  
XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX  
SQ Sequence 753 BP; 136 A; 247 C; 259 G; 111 T; 0 U; 0 Other;

Query Match 93.2%; Score 701.8; DB 13; Length 753;  
Best Local Similarity 95.8%; Pred. No. 7.8e-123;  
Matches 721; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 TCGATGCAGAACTCGCGCTGCGCAGCAAACTATGCTGCGAGCAAGTTGCGGTACTGCGGC 60  
DB 1 TCGATGCAGAACTCGCGCTGCGCAGCAAACTTCTGCTGCGAGCAAGTTGCGGTACTGCGGC 60  
QY 61 ACAACCGACGAGTACTGCGCGACGGGTGCCAGTCCGAGTCCGCGCTCGGCGCGCGGC 120  
DB 61 ACGACCGACGAGTACTGCGCGCGCGGTGCCAGTCCGAGTCCGCGCTCGGCGCGCGGC 120  
QY 121 GCGAGCAGTGGCGCGGTGGTGGCAAGTGGCTAGCTGCTCAGCGGCTCTTCTTCAAC 180  
DB 121 GCGAGCAGTGGCGCGGTGGTGGCAAGTGGCTAGCTGCTCAGCGGCTCTTCTTCAAC 180  
QY 181 GGCATCAAGAACACAGCGCGGAGCGGGTGGAGGGCAAGAACTTCTACACCGGAGCGCG 240  
DB 181 GGCATCAAGAACACAGCGCGGAGCGGGTGGAGGGCAAGAACTTCTACACCGGAGCGCG 240  
QY 241 TTCTGTAGCGCGGTCAAGGCGTACCAGGCTTCGCGCCCATGCGGGTACAGGTGCGAGGCG 300  
DB 241 TTCTGTAGCGCGGTCAAGGCGTACCAGGCTTCGCGCCCATGCGGGTCCGAGGTGCGAGGCG 300  
QY 301 AAGCGCGAGATCGCGCGCTTCTTGGCGCAGCGCCAGCAGAGCGGGCATTTCTGTGTTAC 360  
DB 301 AAGCGCGAGATCGCGCGCTTCTTGGCGCAGCGCCAGCAGAGCGGGCATTTCTGTGTTAC 360

QY 361 ATCAGCGAGATCAGCAAGAGCAACGGCTACTGCGAACCCGACCAAGAGGCAAGTGGCCGTGC 420  
DB 361 ATCAGCGAGATCAGCAAGAGCAACGGCTACTGCGAACCCGACCAAGAGGCAAGTGGCCGTGC 420  
QY 421 GCGCGGGGCGAGAAAGTACTACGGGGCGCGCCCGCTGCGAGATCTCGTGGAACTACAATAC 480  
DB 421 GCGCGGGGCGAGAAAGTACTACGGGGCGCGCCCGCTGCGAGATCTCGTGGAACTACAATAC 480  
QY 481 GGGCCCGCGGGGAGGAGACATCGGCTTCGACGGGCTGGGGACCCCGGACGGGTGGCGCGG 540  
DB 481 GGGCCCGCGGGGAGGAGACATCGGCTTCGACGGGCTGGGGACCCCGGACGGGTGGCGCGG 540  
QY 541 GAGCGCGTGGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGAGTGAACAAACGTCGACCGGTGTG 600  
DB 541 GAGCGCGTGGTGGCGTTCAAGGGCGGCGCTCTGGTTCTGAGTGAACAAACGTCGACCGGTGTG 600  
QY 601 ATGCGCGAGGGCTTCGGCGCGCACCATCAGGGCCATCAACGGCGGCTCGAGTGGGACGGG 660  
DB 601 GTGCGCGAGGGCTTCGGCGCGCACCATCAGGGCCATCAACGGCGGCTCGAGTGGGACGGG 660  
QY 661 AACAAACCCCGCCAGATGAAACGGCGCGCTCGGCTACTTACAAGCAGTACTGCGCGCAGCTC 720  
DB 661 AACAAACCCCGCCAGATGAAACGGCGCGCTCGGCTACTTACAAGCAGTACTGCGCGCAGCTC 720  
QY 721 GGGCTCGACCCAGGGCGCCAACTCAGTTGCTGA 753  
DB 721 GGGCTCGACCCAGGGCGCCAACTCAGTTGCTGA 753

Search completed: May 23, 2005, 12:57:07  
Job time : 353.104 secs



449	CGAGATCGCGCCTTCTTCGGCGACGCCACGCA CGAGACCGGCGCATTTCTGCTCATCAG	508
366	CGAGATCAGCAAGAGCAACGCTTACTGCGA CCGGACCAAGAGGCAAGTGCCTGCGCGC	425
509	CGAGATCAACAGAGCAACGCTTACTGCGA CCGGACCAAGAGGCAAGTGCCTGCGCGC	568
426	GGGCGAGAAGTACTACGGGCGGGCCGCTG CAGATCTGTGGAATAAACTACGCGGC	485
569	GGGCGAGAACTACTACGGGCGGGCCGCTG CAGATCTGTGGAATAAACTACGCGGC	628
486	CGCGGGGAGGACATCGGCTTGCAGGGCTC GGGGACCCCGGACGGTGGCGGGACGC	545
629	CGCGGGGAGGGCCATCGGCTTGCAGGGCTC GGGGACCCCGGACGGTGGCGGGACGC	688
546	CGTGGTGGCGTTCAAGGGGGCGCTCTGGT TCTGGAATGAACAACGTGCACCGTGTGATGCC	605
689	CGTGGTGGCGTTCAAGGGGGCGCTCTGGT TCTGGAATGAACAACGTGCACCGGCGTGGTGGC	748
606	GCAGGGCTTCGGGGCCACATCAGGGCCATC AAGCGCGCTCGAGTGGCGACGGGAACA	665
749	GCAGGGTTCGGGGCCACATCAGGGCCATC AAGCGCGCTCGAGTGGCGGGGAGAACAA	808
666	CCCGGCCAGATGAACGGCGCGCATCGGCTT ACTCAAGCAGATACTGCGCGCAGCTCGGCGT	725
809	CCCGGCCAGATGAACGGCGCGCATCGGCTT ACTCAAGCAGATACTGCGCGCAGCTCGGCGT	868
726	CGACCCAGGGGCCAACCTCACTTGCT	751
869	CGACCCGGGGCCCAACCTCACTTGCT	894

## RESULT 2

US-09-522-714-21  
: Sequence 21. Application US/09522714

```

, Sequence no. of Application 05/09222/14
,
,
, GENERAL INFORMATION:
,
, APPLICANT: Simmons, Carl R.
, APPLICANT: Valpani, Nasser
, TITLE OF INVENTION: Maize Chitinases and Their Use in
, TITLE OF INVENTION: Enhancing Disease Resistance in Crop plants
, FILE REFERENCE: 1100
,

```

```

; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714

```

Query Match	Score 384.6;	DB 4;	Length 1048;
Best Local Similarity	51.1%;		
Matches 549;	72.5%;		
Conservative	Pred. No. 3.9e-72;		
	0;	Mismatches 184;	
		Indels 24;	Gaps 3;

186	QY	CAAGAA	CCAGCCGGGAGCGGTCGAGGGCAAGAACTTTACACCCGGAGCGCTTCT	245
281	DB	CCTCGCGCAGGCCCGGCTCTGTGCGAGGCCAAACGGCTTTACACCCGACGCGCTTCT	340	
246	QY	GAGCGCGTCAAGCGTACCAGGCTTCGCCCATCGCGGGTCACAGGTGCAGGGCAAGCG	305	
341	DB	CGCCGCGCGCGGCTACTACCCGGCGTTTCGGCCGACCCGGCAACCGTCGACGATCCNAGCG	400	
306	QY	CGAGATCGCCCGCTTTCTTCGGCGACGCCACGCAAGAGACCGGGCATTTCTGTTACATCAG	365	
401	DB	CGAGATCGCCCGCTTTCTTCGGCAAGGCCAACCAACGAGACCATTAAGTTCTGCTCATCAAA	460	
366	QY	CGAGAT---CAGCAAGAGCAACGCCCTACTGCGAACCCGACCCGACAGAGCGAGTGCCTGC	422	
461	DB	CGAGATCGACCGGGCGGACAGAGAACTACTGGACCGGAAACAACGACGATGGCCCGTGCCA	520	
423	QY	CGCGGGCAGAAGTACTACGCGCGGGCCGCTGCAGATCTGTCGAACTACAACTACCG	482	
521	DB	GGCGGGGAAGGGGTACTACGCGCGGGCCGCTGCAGATCTCTGGAACCTTCAACTACCG	580	
483	QY	GCCCGCGGGAGGGACATCGGCTTCGACGGGCTCGGGGACCCCGCAGGGTGGCGCGGA	542	
581	DB	GCCCGCGGGCAGAGCATCGGCTTCGACGGGTGGCGACCCCGCAGCGTGGCGCGCAG	640	
543	QY	CGCGTGTGTGGTTCAAGCGGGCGCTCTGGTTCTGGATGAAACAAGTGCAACGCTGTGAT	602	
641	DB	CGCGTGTGTGGTTTCGCTCCGGCTCTGGTACTGGATGAACAACGTCACCGGGCCAT	700	
603	QY	-----GCCGCAGGGCTTCGGGCCACCATCAGGGCCCATCAACGGCGGCTCGAGTGCGCA	656	
701	DB	CGTCTTCGGCGAGGGCTTCGGCGCCACCATCCGGGCCCATCAACGGCGGCGCTCGAGTGCGA	760	
657	QY	CGGGAACAACCCCGCCAGATGAACCGCGCATCGGCTACTACAAGACGATGCTGGCGCA	716	
761	DB	CGGCAAGAACCCCACTCCGTCNAACAACCGGCTCGCTACTACAAGACGATTCGCCAGGA	820	
717	QY	GCTCGGCGTCGACCGAGGGCCCAACTCACTGTCTGA	753	
821	DB	TTTTCGGCGTCGACCGGGCAACAACCTCACTGCTGA	857	

### RESULT 3

RESOL 3  
US-09-522-714-29  
: Sequence 29. Application IIS/09522714

```

, Sequence 29, Application US/09522114
, Patent No. 6563020
, GENERAL INFORMATION:
, APPLICANT: Simmons,
, APPLICANT: Yalpani, Nasser
, TITLE OF INVENTION: Maize Chitinases and Their Use in
, TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
, FILE REFERENCE: 1100

```

```

; FILE REFERENCE: I100
; CURRENT APPLICATION NUMBER: US/09/522,714

```

Query Match	46.2%	Score	348.2;	DB 4;	Length	881;			
Best Local Similarity	77.5%	Pred. NO.	1.8e-64;						
Matches	435;	Conservative	0;	Mismatches	123;	Indels	13;	Gaps	1;

Qy	254	TC	AAGCGGTAC	CCAGGCTTC	CGCCATCGCGGCT	CA	CAGGTG	CAGGCGCAAG	CCGCGAGATCG	313			
Db	61	TC	CGCGGTAT	CCCGGGCTTC	CGCATG	CGGCTCC	GAGGTCG	AGCGCGAGATTG	120				
Qy	314	CG	CGCTTCTTC	CGGCA	CGCAGCA	CGAGAC	CGGGCA	TTTCTGT	TACATCA	CGCGAGATCA	373		
Db	121	CG	CGCTTCTTC	CGCGATGT	CA	CGCA	CGAGAC	CGGGCA	TTTGTGT	TACATCA	CGAGGTGCG	180	
Qy	374	G	CAAGAGCA	ACGCTT	ACTG	CGAC	CCGAC	CCCA	GAGGCA	GTCGGCGCGCGCGGCAG	433		
Db	181	AC	TGGGGAGTA	CTG	CGACTG	GGAC	GTG	GAC	GTG	AGAC	GATGGCGCTG	240	
Qy	434	AG	TACTAC	GGCGGGCGG	CCGCTCG	CAGATCT	CGT	GGA	ACTT	ACA	ACTAC	CGGGCCCGCGGGGA	493
Db	241	GT	TACTAC	GGCGGGCGG	CCGCTCG	CAGCTGT	CGT	GGA	CTA	CA	ACTAC	GGGCCCGCGGGGA	300
Qy	494	GG	GACATCG	GCTTC	GAC	CGGGCTTC	GGGGA	CCCCGG	CAGGGTGG	CGCGGGGA	CGCCGTGTGTGG	553	
Db	301	GG	AGCTTCG	GCTTC	GAC	CGGGCTTC	GGGGA	CCCCGG	CAGGACTGG	CGCAGGAC	CCCGTGTGTGT	360	
Qy	554	CG	TTCAAGCGGCGCT	CTGGTTCT	GATG	GA	CA	ACGT	GCA	CGTGTG	ATGCCGCGAGGGCT	613	
Db	361	CG	TTCAAGCT	CGGCGCTCT	GTGTACT	GTGA	TGGAA	CATGC	ACCCAGCT	CA	TGCCCCAGGGGT	420	
Qy	614	TC	GGCGCCACCAT	CAGGSCCAT	CA	ACGGCGCGCT	CGAGTG	---	CG	ACGGGA	CAACCCCG	670	
Db	421	TC	GGCGCCACCAT	CAGGSCCAT	CA	ACGGCGCTTC	GA	CGAGTGT	CAC	GGCGGGGA	ACAACCG	480	
Qy	671	CC	CAGATGA	ACCGCGCAT	CGGCTACT	CA	AGCAGTA	CTG	CGCGCGCAGCT	TCGGCGCT	CGACC	730	
Db	481	CC	GAATGA	AAAGAC	CGGGTGC	GCTTCA	CTC	CGAGTACT	GC	CA	CACTCCG	540	
Qy	731	C	AGGGCCAA	ACCTCA	TTTGCT							751	
Db	541	C	GGGCTCG	ACCTCAG	TTTGCT							561	

## RESULT 4

```

US-09-522-714-31
; Sequence 31, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Carl R.
; APPLICANT: Silmonds,
; APPLICANT: Valpani, Naaser.
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 1116

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Query Match 40.9%; Score 308.2; DB 4; Length 1116;  
Best Local Similarity 66.7%; Pred. No. 4.9e-56;  
Matches 550; Conservative 0; Mismatches 103; Indels 92; Gaps 4;  
Qy 6 GCAGAACTGGCGTCCAGCCAAACGTATGCTGCAGCAAGTTCCGCTACTCGCGCACAC 65

116 CGAGAACTGCGGGTGGCGTTCGGGCTGTGCTGCAGCCGGTTCGGGTACTCGGGAGCGGG 176

66 CGACGAGTACTGCGCGGCGACGGGTGCACATCGGGGCCCCGTGCGCGTTCGGGCGGGCGGGCAG 125

176 CGAGGACTACTGCGCGCGCGGGTGCACATCGGGGCCCCGTGCGACGTGCGGAGACCAACAA 235

126 CAGTGGCGGGTGGTGGGAAGTGGCTTAGCGTGTGCTACCGGCTCTTCTTCAACGGCAT 185

236 C-----GGTCCGTGGCCAGCATCGTACGCCCGGCTTCTTCGACGCGCT 280

186 CAAGAACACGAGCCGGAGCGGGTGCAGGGGCAAGAACTTCTACACCCGAGGCGCGTTCCT 245

281 CCTCGCGAGGCGCGCGCTCTGTGCGAGGCCAAACGGCTTCTACACCGCGGACGCTTCT 340

246 GAGCGCGCTCAAGGGTACACAGGCTTCGCGCCAGGCGGGTCAAGGTGCAAGGCAAGCG 305

341 CGCGCGCGCGGTACTACCGCGGCTTCGGCGCGCACCGGCGACCGTGCAGCATCTCCAAGCG 400

306 CGAGATCGCGCGCTTCTTCGCGGACGCGCACGCAAGAGAC----- 344

401 CGAGATCGCGCGCTTCTTCGCGAACGCCAACACGAGAGCCATAAGTACGTGCGAACAAAC 460

345 -----CGGCGATTCTCT 357

461 CGAAGCTCGTCAAGCTCTAGCTGCTACTAATCAAGTTTCGACTGCTGCAGAGTTCGTC 520

358 TACATCAGCGAGAT---CAGCAAGAGCAACGCTACTGCGACCCGACCAAGAGGCGAGTGG 414

521 TACATCAACGAGATCGACGGGCGGAGCAAGAACTACTGCGACCCGGAACAAACGCGAGTGG 580

415 CCGTGGCGCGCGGGGCAAGTACTACGGGGCGCGGCCGCTGCGAGATCTCGTGGAACTAC 474

581 CCGTGCACGAGCGGGGAAGGGGTACTACGGCGCGCGGCCGCTGCGAGATCTCTCTGGAATTC 640

475 AACTACGGGCCCGCGGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGCGCAGGGTG 534

641 AACTACGGGCCCGCGGGGAGAGCATCGGCTTCGACGGGCTGCGGCGACCCCGACGCGGTG 700

535 GCGCGGACGCGGTGGTGGCGCTTCAAAGCGCGCGCTCTGGTTCGTGATGAACAAACGTGCAC 594

701 GCGCGCAGCGCGTCTCGCGTTCGCGTCCGCGCTCTGGTACTGGATGAACAAACGTGCAC 760

595 CGTGTGAT-----GCCGCGAGGCTTCGGCGCGCACCATCAGGGCCATCAAACGCGCGCTC 648

761 GGGGCCATCGTCTCGCGCAGGGCTTCGGCGCGCACCATCAGGGCCATCAAACGCGCGCTC 820

649 GAGTGCACGCGGACAAACCCCGCCAGNATGAACGGCGCATCGGTACTACAGCAGTAC 708

821 GAGTGCACGCGCAAGAACCCCAATTCGCTCAACACCGCGCTGCGCTACTACAAGCAGTTC 880

709 TGCCGCGCAGCTCGCGCTGCAGCCAGGGGCCAACCTCACTTGTCTGA 753

881 TGCAGGATTCGCGCTGCAGCCCGGGCAACAACTCACTGCTGA 925

RESULT 5

US-08-181-271A-37

; Sequence 37, Application US/08181271A

; Patent No. 5614395

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph





APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Robert  
APPLICANT: Harms, Jr., Frederick  
APPLICANT: Meins, Alice  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericea C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,315  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 800  
PRIORITY DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIORITY DATA:  
APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-449-315-37  
Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;  
QY 7 CAGAACTGCGCTGCCAGCCCAACGATATGCTGCAAGCAAGTTCGGCTACTGCGGCACACACC 66  
DB 93 CAAAACTGCGGTTCGCTCCAAACCTCTGTTGCAAGTTCAGTTCGGTTACTTGTGGTACCGAC 152  
QY 67 GACGAGTACTCGCGCAGCGGTGCGAGTCCGCGCCCGTCCGCTCGCGCGCGCGCGGAGC 126  
DB 153 GATGCATACCTCGCGGTGTTGATGCCGATCAGTCTTGTAGAGGTAGTGGNACCCCGACC 212  
QY 127 AGTGGCGCGGTGGTGGCAACGTGGGTAGCGTCCGCTCCGCTCCCTTCTTCAACGGGCATC 186  
DB 213 GGAGG-----GTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 260  
QY 187 AAGAACCGAGCGCGCGCGGTGCGAGGCGCAAGCACTTCTACACCGGAGCGGCTCTCTG 246  
DB 261 ATCAACCAAGCTGGTAATGTTGCGCGGGGAAAGATTCTACACCGGTGACTTCTTCGTT 320  
QY 247 AGCGCGTCAAGCGGTACCGAGGCTTCGCCCATGCGCGGTCACAGGTGCAGGGCAAGCGC 306  
DB 321 AACGCGCTAATACCTTTCGCCCACTTTCGCAATCTCTGTAC-----CAGAGGT 368  
QY 307 GAGATCGCGCTTCTTTCGCGCAGCGCAGCAGCAGCGCGGCACTTCTGTATCATCAGC 366  
DB 369 GAAATTGCTACCATGTTTGTCTCATTTCACTCAGCAGACCGGACATTTCTGCTACATAGAA 428  
QY 367 GAGAT----CAGCAAGACCAACGCTACTGCGACCGGCGGCGGCGGCGGCGGCGGCGG 423  
DB 429 GAGATTAAACGAGCAACACGTAATCTGTCAGAGCAGCAACACCAATACCCATGTGCA 488  
QY 424 GCGGGGCAAGTACTACGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 483  
DB 489 CCGGAAAAGGCTACTTTCGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 548  
QY 484 CCGCGGGGAGGACATCGGCTTCGACGGGCTCGGGGACCGCGGCGGCGGCGGCGGCGGCGG 543  
DB 549 GCGTGTGTCAAAGTCTCGGCTTCGACCTTCTACGCGCGCGGCGGCGGCGGCGGCGGCGG 608  
QY 544 GCGTGTGCGGTTCAAGCGCGGCGGCTCTGTTCTGGATGAACAACGTCGCGGCGGCGGCGG 603  
DB 609 CCAACTGTAGCTTTTCAGGTTCGGGTTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 668  
QY 604 CCGCAGGCTTCGCGCGCACCATCAGGCGCATCAACGCGCGGCTCGAGTGCAGCGGGAAC 663  
DB 669 AACCAAGGTTTGAGCCACCATTAGAGCTATTATGG---AATGGATGTAAACGGTGGT 725  
QY 664 AACCCCGCCAGATGAACGCGCGCATCGGCTACTCTAAGCAGTACTCCCGCCAGCTCGGC 723  
DB 726 AATTCGGTGCAGTCAACGCAAGGATTGGATGACTATAGAGACTATTGTGGACAGCTTGGT 785  
QY 724 GTGACCCAGGGGCCCAACCTCACTTGTCTGA 753

Db 786 GTGACCCCTGGTCTTAACCTTAGTTGCTAA 815

RESULT 7  
US-08-444-803-37  
Sequence 37, Application US/08444803  
Patent No. 5654414  
GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,803  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506

FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-444-803-37  
Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;  
Qy 7 CAGAACTGCGGTGCCAGCAAAACGATATGTCGAGCAAGTTTCGGTCTACTGCGGCACAAACC 66  
Db 93 CAAAACCTGCGGTTCGCTCCAAACCTCTGTTGCAGTCAGTTTCGGTCTACTGCGGTACCGAC 152  
Qy 67 GACGAGTACTGCGGCAGCGGTTCGAGTCGGGCCCGTCCGCTCGCGCGCGCGCGCGCGC 126  
Db 153 GATGCATACTGCGGTGTTGGATCCGATCAGGTCCTTTAGAGGTAGTGGAAACCCCGACC 212  
Qy 127 AGTGGCGCGGTGTCGAAACGTCGTCGTCGTCACCGCTCTCTTCTTCAACGGCATC 186  
Db 213 GGAGG-----GTGCGTTCGTCAGTTCGTCAGCAAGTTTCCTTAAACAATATT 260  
Qy 187 AAGAACCGCGCGGAGCGGTGCGAGGGCAAGAACTTCTTACACCGGAGCGGTTCCTG 246  
Db 261 ATCAACCAAGCTGTAATGTTGCGCGGGGAAAAGATTCTACACCCGCTGACTCTTTTCGTT 320  
Qy 247 AGCGCGTCAAGGGTACCCAGGCTTCGCCCATGGGGTTCACAGGTGCAGGGCAAGCGC 306  
Db 321 AACGCGCTAATACTTTTCCCAACTTTGCCAACTTCTGTTAC-----CAGACGT 368  
Qy 307 GAGATCGCGCTTCTTCGCGCACGCCACGACGAGACCGGGCATTTCTGTATCATCAGC 366  
Db 369 GAAATGCTACCATGTTGCTCATTTCACTCAAGACCGGACATTTCTGTACATAGAA 428  
Qy 367 GAGAT---CAGCAAGAACACGGCTACTGCGACCCGACCCGACGAGGAGTGGCGCGCGCC 423  
Db 429 GAGATTAAACGAGCAACACGTAATCTACTGTCAGAGCAGCAACACACATAATACCCATGTGCA 488  
Qy 424 GCGGGCAGAGTACTACGGCGCGCGCGCTCGAGATCTCGTGGAACTCAACTACGGG 483  
Db 489 CCGGGAAGAGGCTACTTCGGTTCGGTCCGATCCAACTATATGGAATCAACTACGGA 548  
Qy 484 CCGCGCGGAGGAGACATCGGCTTCGAGCGGTTCGGGACCCCGCAGGCGCGCGCGGAC 543  
Db 549 GCGTGTGTCAGAGTCTCGGTCTTGACTTCTACCGCCGCGCGGACTTGTGGGTAGCAAC 608  
Qy 544 GCGTGTGCGGTTCAGAGCGCGCGCTCTGTTCTGGATGAACACAGTGCACCGGTGTGATG 603

Db 609 CCAACTGTAGCTTTTCAGTCGGGTTTGTTGGTATGATAGCGTAAGCGCGTTCTG 668  
Qy 604 CCGCAGGCGCTTCGGCGCCACCATCAGGGCCCATCAACGGCGCGCTCGAGTGCAGCGGAAC 663  
Db 669 AACCAAGGGTTTGAGCCACCATTAGAGCTATTATGG--AATGGATGTAAACGGTGGT 725  
Qy 664 AACCCCGCCAGATGAAGCGCGCATCGGCTACTACAGCAGTACTGCGCGCCAGCTCGGC 723  
Db 726 AATTCGGTGTCAGTCAACGCAAGATTGGATCTATATAGAGACTATTGTGGACAGCTTGGT 785  
Qy 724 GTCGACCCAGGCGCCCAACCTCACTTGTCTGA 753  
Db 786 GTGACCTGTCTTAACCTTAGTTGCTAA 815

## RESULT 8

US-08-449-043-37  
; Sequence 37, Application US/08449043  
; Patent No. 5689044  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedman, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,043  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT 1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-449-043-37

Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;  
Qy 7 CAGNACTGCGCTGCCAGCCAAAGCTATGCTGCAGCAAGTTCCGGCTACTGCGGCACCAACC 66  
Db 93 CAAACTGCGGTTGCGCTCCAAACCTCTGTTCAGTCAAGTTCTGTTGTTACCGAC 152  
Qy 67 GACGAGTACTGCGGCGACGGTGCAGTCGCGGCCCGTCCGCTCGGCGCGCGGCGGACG 126  
Db 153 GATGCATACCTGCGGTGTGGATGCCGATCAGTCTCTGTAGAGGTAGTGGAAACCCGACC 212  
Qy 127 AGTGGCGGCGGTGGTGCAGACGTGGGTAGCGGTCTCACCGGCTCTCTTCTTCAACGGCATC 186  
Db 213 GGAGG-----GTGCGTGGTAGCATTTGTGACACAAGGTTTCTTTTAAACAATATT 260  
Qy 187 AAGNACCAGCGCGGAGCGGTGCGAGGCGAGCACTTCTACACCGGAGCGCGTCTCTG 246  
Db 261 ATCAACCAAGCTGGTAAATGGTTGCGCGGGGAAAGATTCTACACCGGTGACTCTTTGTT 320  
Qy 247 AGCGCGCTCAAGCGGTATCCAGGCTTCGCCATCGCGGCTCACAGGTGCAGGGCAAGCGC 306  
Db 321 AACGCCCTAATACTTTTCCCACTTTTGCCAACTTCTGTAC-----CAGAGCT 368  
Qy 307 GAGATCCCGCGCTTTCTTCGCGCAGCCGACGACGAGACCGGGGCAATTTCTGTATCATCAGC 366  
Db 369 GAATTCGTACCATGTTTGTCTCACTTCACTCAGCAGACCGGACATTTCTGTCTACATAGAA 428  
Qy 367 GAGAT---GAGCAAGACCAAGCGCTACTGCGACCCGACCAAGAGGAGTGCCTGCGGCC 423

Db 429 GAGATTAAAGGAGCAACACGTAACCTACTGCCAGAGCAGCAACACATAATCCCATGTGCA 488  
Qy 424 GCGGGGAGAGTACTAGGCGGCGCGCTGAGATCTCGTGAACACTCAACTACGGG 483  
Db 489 CCGGAAAGAGCTACTTCGGTGGTGGTCCGATCACTATCATGAACTCAACTACGGA 548  
Qy 484 CCGCGGGAGGAGCATCGGCTTCGAGCGGGCTCGGGACCCCGGACGGGTGGCGCGGAC 543  
Db 549 GCGTGTGTCGTAAGTCTCGCTTTCGCTTCTAGCCAGCCCGAATCTGTGGGTAGCAAC 608  
Qy 544 GCGTGTGTCGCTTCAAGGCGCGCTCTGGTTCGATGAACAAAGTGCACCGGTGATG 603  
Db 609 CCAACTGTAGCTTTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 668  
Qy 604 CCGAGGCTTCGGGCGGACCATCAGGCGCCATCAAGCGGCGCTCGAGTGCAGCGGAC 663  
Db 669 AACCAAGGTTTGGAGCCCACTTAGAGCTATTATG--AATGGAATGTAAACGGTGGT 725  
Qy 664 AACCCCGCCAGATGAACGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTCGG 723  
Db 726 AATTCGGTGCAGTCAACGCAAGATGGATGATGATGATGATGATGATGATGATGAT 785  
Qy 724 GTCAGCCAGGCGCAACCTCACTTGTGA 753  
Db 786 GTGACCCCTGGTCTCAACCTTAGTTGTAA 815

RESULT 9

US-08-456-265A-37  
; Sequence 37, Application US/08456265A  
; Patent No. 5767369  
; GENERAL INFORMATION:  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Ryals, John A.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Stinson, Jeffrey R.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/456,265A  
; FILING DATE: 31-MAY-95  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/181,271  
; FILING DATE: 13-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT 1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-456-265A-37  
  
Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;  
  
Qy 7 CAGAACTGCGGCTGCCAGCAAGCTATGCTGAGCAAGTTCTGGCTACTGCGGCACAAAC 66  
Db 93 CAAAACCTGCGGTTGCGCTCCAAACCTCTGTTGAGTCAGTTCTGGTTACTGTTGTTACCGAC 152  
Qy 67 GAGAGTACTGCGGAGCGGTGCCAGTCCGAGTCCGCTCGGCGCGCTCGGCGCGGCGGCGAGC 126  
Db 153 GATGCATACCTGCGGTGTTGATGCCGATCAGGTCCTTTGAGAGGTAGTGAACCCCGAC 212  
Qy 127 AGTGGCGCGGTGGTGGCAAGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186  
Db 213 GGAGG-----GTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 260  
Qy 187 AAGAACCAAGCGCGGAGCGGCTGCGAGGCAAGAACTTTCTACACCGGAGCGGCTTCTG 246  
Db 261 ATCAACCAAGCTGGTAATGTTGCGCGGGAAGAAATTTCTACACCGGAGCTCTTTCTGTT 320  
Qy 247 AGCGCGTCAAGCGGTACCCAGGTTCCCATGCGGCGGTCAAGGTGCAGGGGCAAGCGC 306  
Db 321 AAGCGCGCTAATATCTTTTCCCAACTTTGCGCAATTTCTGTTAC-----CAGACGT 368  
Qy 307 GAGATCGCGCTTCTTTCGCGCAGCCCAAGCAAGCGGCAATTTCTGTTTACATCAGC 366  
Db 369 GAATTTGCTACCATGTTTGTCTCATTTTCACTCAGGAGCGGACATTTCTGCTACATAGAA 428  
Qy 367 GAGAT---CAGCAAGCAAGCGCTACTGCGACCCGCAAGAGGAGTGGCGCGTGGCC 423

Db 429 GAGATTACGGAGCAACAGTAACTACTGCGAGCAGCAACACATATCCCATGTGCA 488  
Qy 424 CGGGGCGAGAGTACTACGGGCGGGCGCGCTGCGAGATCTCGTGGAACTACAACCTACGGG 483  
Db 489 CGGGGAAAGGCTACTTCGGTGGTCCGATCCAACTATCATGGAACCTACAACCTACGGA 548  
Qy 484 CCGGGGGGGAGGACATCGGCTTCACGGGCTCGGGGACCCGGGACGGGTGGCGGGGAC 543  
Db 549 GCGTGTGCTCAAAAGTCTCGGCTTGGACCTTCTACGCCAGCCCGAACTTTGTGGGTAGCAAC 608  
Qy 544 GCGGTGTGGGCTTCAAGCGGCGCTCTGGTTCGGATGAACAACGTCACCGTGTGTATG 603  
Db 609 CCAACTGTAGCTTTCAGTTCGGTGTGGTTTGGTTTGGATGATAGGTAAGCGCGGTCTG 668  
Qy 604 CGCAGGGCTTGGCGCCACCATCAGCGCCATCAACGGCGCGCTCGAGTGGGACGGGAAC 663  
Db 669 AACCAAGGGTTGGAGCCACCATTAGAGCTATTAATGG--AAATGAATGAACGGTGGT 725  
Qy 664 AACCCGCGCAGATGAACGCGCGCATCGGCTACTACAAGCAGTACTGCGGCCAGTGGC 723  
Db 726 AATTCGGTGCAGTCAACGCAAGGATTTGGATCTATAGAGACTATTGTGGACAGCTTGGT 785  
Qy 724 GTCCAGCCAGGCGCCCAACTCTACTTGTCTGA 753  
Db 786 GTGACCCCTGCTCTCACTTATGTTGCTAA 815

## RESULT 10

US-08-455-416-37  
Sequence 37, Application US/08455416  
Patent No. 577200

## GENERAL INFORMATION:

APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,416  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-455-416-37

Query Match 26.6%; Score 200.4; DB 1; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;

Qy 7 CAGAACTGCGGCTGCCAGCCAAACGATATGTCGAGCAAGTTCGCTACTCGGGCACAACC 66  
Db 93 CAAAACTGCGGTTTGGCTCCAAACCTCTGTTCAGTTCAGTTTCGTTTACCGGAC 152  
Qy 67 GACGAGTACTGCGGAGCGGTGCGAGTTCGCGGCCGCTCGGCGGGGGGCGG 126  
Db 153 GATGCATACCTGCGGTGTTGGATGCCGATCAGTTCCTTTGATAGAGTAGTGGNACCCCGACC 212  
Qy 127 AGTGGCGCGGTGGTGGCGAAGCTGGTGGCTGCTACCGGCTCTCTTCTCAACGGCATC 186  
Db 213 GGAGG-----GTCCGTCGGTAGCATTTGTGACACAAGGTTTCTTTTAAACAATTT 260  
Qy 187 AAGAACACAGCCCGGAGCGGCTGGGAGGGCAAGAACTTCTACACCCGAGCGGCTTCTGT 246

Db 261 ATCAACAGCTGTGTAATGTTGCGCGGGAAGAATTCACACCGTGACTCTTTGTT 320  
Qy 247 AGCCCGGTCAAGGCTACCCAGGCTTCGCCCATCGCGGTGACAGGTGCGAGGCAAGCGC 306  
Db 321 AACCCCGTAAATCTTTCCCAACTTTGCGCAATTTCTGTTAC-----CAGACGT 368  
Qy 307 GAGATCCCGCTTCTTCGGCAGCCGACGACGACGACGACGACGACGACGACGACGACGAC 366  
Db 369 GAAATGCTACCATGTTGCTCATTTCACTCACGAGACCGGACATTTCTGCTACATAGAA 428  
Qy 367 GAGAT---CAGCAAGAGCAACGCTACTTGCACGCCGACCCAGAGGCGAGTGCGCGGCC 423  
Db 429 GAGATTAACGAGCAACACGTAACCTACTTGCAGAGCAGCAACACACAATACCCATGTGCA 488  
Qy 424 CGCGGGCAGAGTACTACGCGCGCGCGCGCGCTGCGATCTCGTGAAGTCAACTACGCGG 483  
Db 489 CCGGGAAGGCTACTTTCGGTGGTTCGATCCCAACTATCATGGAACCTACAACTACGGA 548  
Qy 484 CCGCGGGGAGGACATCGGCTTCGAGGGCTCGCGGACCCCGGAGCGGCGCGGAC 543  
Db 549 GCGTGTGTTCAAGTCTCGGCTTGAACCTTCAAGCGCGGACCGGAACTTGTGGTAGCAAC 608  
Qy 544 GCGTGTGCGGTTCAAGCGCGGCTCTGTTCTGATGAACAAAGTGCACCGTGTGATG 603  
Db 609 CCAACTGTAGCTTTCAGTCCGGTGTGTTGTTGGATGAATAGCGTAAGCGCGTTCG 668  
Qy 604 CCGCAGGCTTCGGCGGCGGACCATCAGGCGGCGGCGGCGGCGGCGGCGGCGGAC 663  
Db 669 AACCAAGGGTTTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 725  
Qy 664 AACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 723  
Db 726 AATTCGGTGCAGTCAACGCGGAGGATGATGATGATGATGATGATGATGATGATGATG 785  
Qy 724 GTCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 753  
Db 786 GTGACCGCTGCTCAACCTTAGTTGCTAA 815

## RESULT 11

US-08-455-244-37  
Sequence 37, Application US/08455244

Patent No. 5789214

## GENERAL INFORMATION:

APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Steinson, Jeffrey R.  
APPLICANT: Ukenes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,244  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-455-244-37

Query Match 26.6%; Score 200.4; DB 1; Length 1079;

Best Local Similarity 58.5%; Pred. No. 2.5e-33;

Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;

Qy

7 CAGAACTGCGGCTGCCAGCAAAAGTATGTCGACGAAGTTTCGGCTACTCGCGGCAACCC 66









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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-456-262-37

Query Match      26.6%; Score 200.4; DB 2; Length 1079;
Best Local Similarity 58.5%; Pred. No. 2.5e-33;
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;

QY 7 CAGAACTGCGGCTCCAGCAAAAGTATGTCGACGAAAGTTGCGCTACTCGGGCACAACC 66
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 93 CAARACTGCGGTTGCGCTCCAAACTCTGTTGCACTGAGTTCGTTACTGTTGACCGAC 152
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 GACGAGTACTCGCGCAGCGGTGCGAGTCCAGTCCGGCCCGCTCGCGCTCGGGCGGGCGGCG 126
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 153 GATGCATACACTGCGGTGTTGGATCCGATCAGGTCTTTGTAGAGGTAGTGAACCCCGACC 212
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 127 AGTGGCGGCGGTGTCGGAAGTCGTAGCTGCTGCTCAGCGCTCTCTTCAACGGGCATC 186
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 213 GGAGG-----GTGCGTCTGAGCATGTTGACACAGGTTTCTTTAAACATATT 260-
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 187 AAGAACGAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGGTTCTCTG 246
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 261 ATCAACCAAGCTGTAATGTTGCGCGGGGAAAGATTCTACACCGTGACTCTTTGCTT 320
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 247 AGCGCGTCAAGGCTACCCAGGCTTCCCGCATCGCGGTCACAGTGCAGGGCAAGGC 306
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 321 AACCGCGTAACTACTTTCCCAACTTTGCCAAATTCTGTAC-----CAGACGT 368
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 307 GAGATCGCGCTTCTTCGCGCAGCCGACGACGAGACCGGGCATTCTGTTCATCAGC 366
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 369 GAAATGCTACATGTTTGCTCATTTCACTCAGAGACCGGACATTTCTGCTACATAGAA 428
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 367 GAGAT---CAGCAAGAGCAACCGCTACTTGGACCCGACCAAGAGCGAGTGCCTGGCC 423
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 429 GAGATTAACGAGCAACACGTAATCTACTGCGAGAGCAGCAACACATAATCCCATGTGCA 488
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 CGCGGCGGAGTACTACGGCGCGGCGCGCTGAGATCTGTTGAACTACACTACGGG 483
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 489 CCGGAAAGGCTACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 484 CCGCGGGGAGGACATCGGCTTCGAGGGCTCGGGGACCCCGGACCGGCGGCGGAC 543
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 549 CGGTGTGCTCAAGTCTCGCTTGTGACCTTCTAGCCGCGCGGAACTTGTGGGTAGCAAC 608
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 544 CCGGTGTGCGGTTCAAGCGCGCGCTCTGTTGATGAACAAACGTGCACCGGTGTGATG 603
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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## RESULT 15

US-08-456-240-37

; Sequence 37, Application US/08456240

; Patent No. 5856154

; GENERAL INFORMATION:

; APPLICANT: Rvals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/456,240

; FILING DATE: 31-MAY-1995

; CLASSIFICATION: 800

; APPLICATION NUMBER:

; FILING DATE: 13-JAN-94

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/042,847  
;; FILING DATE: 6-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/632,441  
;; FILING DATE: 21-DEC-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/425,504  
;; FILING DATE: 20-OCT-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/848,506  
;; FILING DATE: 6-MAR-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/768,122  
;; FILING DATE: 27-SEP-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/580,431  
;; FILING DATE: 7-SEP-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/368,672  
;; FILING DATE: 20-JUN-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/329,018  
;; FILING DATE: 24-MAR-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/045,957  
;; FILING DATE: 12-APR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Elmer, James Scott  
;; REGISTRATION NUMBER: 35,129  
;; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (919)541-8614  
;; TELEFAX: (919)541-8689  
;; INFORMATION FOR SEQ ID NO: 37:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1079 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
US-08-456-240-37

Query Match 26.6%; Score 200.4; DB 2; Length 1079;  
Best Local Similarity 58.5%; Pred. No. 2.5e-33;  
Matches 439; Conservative 0; Mismatches 281; Indels 30; Gaps 4;

Qy	7	CAGAACTGCGGCTGCCAGCCAAACGATATGCTGCAGCAAGTTGCGCTACTGCGGCACCAACC	66
Db	93	CAAAACTGCGGTTGCGCTCCAAACCTCTGTTGCAGTCAGTTGCGGTTACTGTGTACCGAC	152
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Db	153	GATGCATCTGCGGTTGGATGCCGATCAGGTCCTTTGTAGAGGTAGTGGNAACCCCGACC	212
Qy	127	AGTGGCGCGGTGTGTCGAAAGCTGGCTAGCGTGTCTCACCGGCTCTTTCTTCAACGGCATC	186
Db	213	GGAGG-----GTGCGTGGTAGCATTTGTGACACAAGGTTTCTTTAACAATATT	260
Qy	187	AAGAACCGAGCGCGGAGCGGTGCGAGGGCAAGAACTTCTACACCGGAGCGGTTCTTG	246
Db	261	ATCAACCAAGCTGGTAATGTTGCGCGGGGAAAGATTCTACACCGTGACTCTTTTCGTT	320
Qy	247	AGCGCCCTCAAGCGGTATACCCAGGCTTCGCCCATGCGCGGTCACAGGTGCAGGGCAAGCGC	306
Db	321	AACGCCGCTAATACTTTCCCACTTTTGCCAAATCTCTGTAC-----CAGACGT	368
Qy	307	GAGATCGCGCTTTCTTTCGCGCAACGCCAGCAACCGGCGCATTTCTGTTCATCAGC	366
Db	369	GAATTTGCTACCATGTTTGCTCAATTTCACTCACGAGACCGGACATTTCTGCTACATAGAA	428
Qy	367	GAGAT---CAGCAGAGCAAGCCCTACTTGGACCCGACCAAGGCGAGTGGCCGTGCGCC	423

Db	429	GAGATTAAAGGAGCAACACAGTAATACTACTGCCAGAGCAGCAACACACATATCCCATGTGCA	488
Qy	424	GCGGGCAGAAAGTACTACGGCGCGCGCCCGCTGCAGATCTCGTGGAACTACAACTACGGG	483
Db	489	CCGGGAAAAGGCTACTTCGGTCTGTTCCGATCCAACTATCATGGAACTACAACTACGGA	548
Qy	484	CCCGCGGGAGGACATCCGCTTCGACGGGCTCGGAGACCCCGCAGGCTGGCGCGGAC	543
Db	549	GCGTGTTGTCAAAAGTCTCGGTCTTGACCTTTCTAGCCAGCCCGAACTTTGTGGGTAGCAAC	608
Qy	544	GCCGTGTTGCGGTTCAAGGCGCGCTCTGCTCTCGATGAACAAACGTCACCGCTGTGATG	603
Db	609	CCACTGTAGCTTTCAAGTCGGGTTTGTGTTTGGATGATAGCGTAAGGCCGCTTCTG	668
Qy	604	CCGACGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCGAGTCGACGGGAAC	663
Db	669	AACCAAGGTTTGGAGCCACCATTAGAGCTATTAAATGG---AATGGAATGTAACGGTGGT	725
Qy	664	AACCCCGCCAGATGAACGGCGCATCGGCTACTACAGCAGTACTGCCCGCAGCTCGGC	723
Db	726	AATTCCGGTGCAGTCAACGCAAGGATTTGGATATCTATAGAGACTATTGTGGACAGCTTGGT	785
Qy	724	GTGACCCCGGCGCCCAACCTCACTTGTCTGA	753
Db	786	GTGACCCCTGCTCCTAACCTTAGTTGCTAA	815

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Job time : 120.87 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 14:20:22 ; Search time 386.609 Seconds  
(without alignments)  
11943.947 Million cell updates/sec

Title: US-10-692-367-69

Perfect score: 753

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IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
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- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	753	19	US-10-692-367-69
2	732.2	97.2	753	19	US-10-692-367-51
3	729.2	96.8	750	18	US-10-389-432B-51
4	725.8	96.4	753	19	US-10-692-367-55
5	722.8	96.0	750	18	US-10-389-432B-55
6	722.6	96.0	753	19	US-10-692-367-77
7	719.4	95.5	753	19	US-10-692-367-81
8	717.8	95.3	753	19	US-10-692-367-35
9	717.2	95.2	1037	17	US-10-425-114-19751
10	716.2	95.1	753	19	US-10-692-367-43
11	715.6	95.0	1094	15	US-10-304-928-1

12	714.8	94.9	750	18	US-10-389-432B-35	Sequence 35, Appl
13	714.6	94.9	753	19	US-10-692-367-21	Sequence 21, Appl
14	713.2	94.7	750	18	US-10-389-432B-43	Sequence 43, Appl
15	711.8	94.5	765	19	US-10-692-367-67	Sequence 67, Appl
16	711.6	94.5	750	18	US-10-389-432B-21	Sequence 21, Appl
17	711.4	94.5	753	19	US-10-692-367-49	Sequence 49, Appl
18	711.4	94.5	753	19	US-10-692-367-53	Sequence 53, Appl
19	708.4	94.1	750	18	US-10-389-432B-49	Sequence 49, Appl
20	708.4	94.1	750	18	US-10-389-432B-53	Sequence 53, Appl
21	708.2	94.1	750	19	US-10-692-367-79	Sequence 79, Appl
22	701.8	93.2	753	19	US-10-692-367-31	Sequence 31, Appl
23	701.8	93.2	753	19	US-10-692-367-57	Sequence 57, Appl
24	698.8	92.8	750	18	US-10-389-432B-31	Sequence 31, Appl
25	698.8	92.8	750	18	US-10-389-432B-57	Sequence 57, Appl
26	697.8	92.7	771	19	US-10-692-367-47	Sequence 47, Appl
27	696.4	92.5	774	19	US-10-692-367-71	Sequence 71, Appl
28	694.8	92.3	768	18	US-10-389-432B-47	Sequence 47, Appl
29	694.6	92.2	771	19	US-10-692-367-73	Sequence 73, Appl
30	689.8	91.6	771	19	US-10-692-367-61	Sequence 61, Appl
31	689	91.5	753	19	US-10-692-367-27	Sequence 27, Appl
32	686.8	91.2	768	18	US-10-389-432B-61	Sequence 61, Appl
33	686.6	91.2	771	19	US-10-692-367-83	Sequence 83, Appl
34	686	91.1	750	18	US-10-389-432B-27	Sequence 27, Appl
35	685	91.0	771	19	US-10-692-367-59	Sequence 59, Appl
36	683.6	90.8	774	19	US-10-692-367-65	Sequence 65, Appl
37	682	90.6	768	18	US-10-389-432B-59	Sequence 59, Appl
38	680.6	90.4	771	18	US-10-389-432B-65	Sequence 65, Appl
39	675.6	89.7	774	19	US-10-692-367-63	Sequence 63, Appl
40	674.2	89.5	1277	18	US-10-425-115-65712	Sequence 65712, A
41	672.6	89.3	771	18	US-10-389-432B-63	Sequence 63, Appl
42	672.4	89.3	774	19	US-10-692-367-45	Sequence 45, Appl
43	671.2	89.1	780	19	US-10-692-367-39	Sequence 39, Appl
44	671.2	89.1	780	19	US-10-692-367-75	Sequence 75, Appl
45	669.4	88.9	771	18	US-10-389-432B-45	Sequence 45, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-692-367-69  
; Sequence 69, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Valpari, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 54916200320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69  
; LENGTH: 753  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)....(753)  
US-10-692-367-69



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Query Match      100.0%; Score 753; DB 19; Length 753;
Best Local Similarity 100.0%; Pred. No. 7.9e-189; Indels 0; Gaps 0;
Matches 753; Conservative 0; Mismatches 0;

Qy 1 TCGATGACAGAACTCGCGCTGCGAGCCAAAGTATGCTGACAGCAAGTTTCGGCTACTGCGGC 60
Db 1 TCGATGACAGAACTCGCGCTGCGAGCCAAAGTATGCTGACAGCAAGTTTCGGCTACTGCGGC 60

Qy 61 ACAACGACAGAGTACTCGCGGCGACGGGTGCGAGTGCAGTTCGGGCGCGGCGGCG 120
Db 61 ACAACGACAGAGTACTCGCGGCGACGGGTGCGAGTGCAGTTCGGGCGCGGCGGCG 120

Qy 121 GGCAGCAGTTCGGGCGGCTGCGCAAGTGGCTAGCGTTCGACCGGCTCTCTTCTTCAAC 180
Db 121 GGCAGCAGTTCGGGCGGCTGCGCAAGTGGCTAGCGTTCGACCGGCTCTCTTCTTCAAC 180

Qy 181 GGCATCAAGAACACAGGCGGAGCGGCTGCGAGGCGCAAGAACTTCTACCCGAGCGCG 240
Db 181 GGCATCAAGAACACAGGCGGAGCGGCTGCGAGGCGCAAGAACTTCTACCCGAGCGCG 240

Qy 241 TTCTGAGCGCGTCAAGGCGTACCCAGGCTTGCAGGCTTGCAGGCTTCTGTAAGTCAACTAC 300
Db 241 TTCTGAGCGCGTCAAGGCGTACCCAGGCTTGCAGGCTTGCAGGCTTCTGTAAGTCAACTAC 300

Qy 301 AAGCGCGAGATCGCGGCTTCTTTCGCGCAGCCAGCGTGCAGTTCGCGGCTCTCTTCTTCAAC 360
Db 301 AAGCGCGAGATCGCGGCTTCTTTCGCGCAGCCAGCGTGCAGTTCGCGGCTCTCTTCTTCAAC 360

Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCGGCTGCGAGGCGAGTGCAGGCG 420
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCGGCTGCGAGGCGAGTGCAGGCG 420

Qy 421 GCGCGCGGCGAGAGTACTAGCGGCGGCGCGGCTGCGAGTCTCGTGGAACTACAACTAC 480
Db 421 GCGCGCGGCGAGAGTACTAGCGGCGGCGCGGCTGCGAGTCTCGTGGAACTACAACTAC 480

Qy 481 GGGCGCGCGGAGGAGCATCGGCTTTCGAGCGGCTCGGCGGACCCCGCGAGGCTGCGCGG 540
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Db 541 GACGCGGTGCGGCTTCAAGGCGGCGCTCTGCTTCTGATGAAACAGTGCACCGGTG 600

Qy 601 ATGCGCGAGGCTTTCGGGCGGCGGCTTTCGAGGCGGCTTTCGAGTGCAGCGG 660
Db 601 ATGCGCGAGGCTTTCGGGCGGCGGCTTTCGAGGCGGCTTTCGAGTGCAGCGG 660

Qy 661 AACAAACCGCGGCGGCGGCGGCTTTCGAGGCGGCTTTCGAGTGCAGCGGCTC 720
Db 661 AACAAACCGCGGCGGCGGCGGCTTTCGAGGCGGCTTTCGAGTGCAGCGGCTC 720

Qy 721 GGCCTGACCCAGGCGGCGGCGGCTTTCGAGTGCAGCGGCTC 753
Db 721 GGCCTGACCCAGGCGGCGGCGGCTTTCGAGTGCAGCGGCTC 753
```

## RESULT 2

```
US-10-692-367-51
; Sequence 51, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
```

```
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-51
```

```
Query Match      97.2%; Score 732.2; DB 19; Length 753;
Best Local Similarity 98.3%; Pred. No. 2.4e-183; Indels 0; Gaps 0;
Matches 740; Conservative 0; Mismatches 13;

Qy 1 TCGATGACAGAACTCGCGCTGCGAGCCAAAGTATGCTGACAGCAAGTTTCGGCTACTGCGGC 60
Db 1 TCGATGACAGAACTCGCGCTGCGAGCCAAAGTATGCTGACAGCAAGTTTCGGCTACTGCGGC 60

Qy 61 ACAACGACAGAGTACTCGCGGCGACGGGTGCGAGTGCAGTTCGGGCGGCGGCGGCG 120
Db 61 ACAACGACAGAGTACTCGCGGCGACGGGTGCGAGTGCAGTTCGGGCGGCGGCGGCG 120

Qy 121 GGCAGCAGTTCGGGCGGCTGCGCAAGTGGCTAGCGTTCGACCGGCTCTCTTCTTCAAC 180
Db 121 GGCAGCAGTTCGGGCGGCTGCGCAAGTGGCTAGCGTTCGACCGGCTCTCTTCTTCAAC 180

Qy 181 GGCATCAAGAACACAGGCGGAGCGGCTGCGAGGCGCAAGAACTTCTACCCGAGCGCG 240
Db 181 GGCATCAAGAACACAGGCGGAGCGGCTGCGAGGCGCAAGAACTTCTACCCGAGCGCG 240

Qy 241 TTCTGAGCGCGTCAAGGCGTACCCAGGCTTGCAGGCTTGCAGGCTTCTGTAAGTCAACTAC 300
Db 241 TTCTGAGCGCGTCAAGGCGTACCCAGGCTTGCAGGCTTGCAGGCTTCTGTAAGTCAACTAC 300

Qy 301 AAGCGCGAGATCGCGGCTTCTTTCGCGCAGCCAGCGTGCAGTTCGCGGCTCTCTTCTTCAAC 360
Db 301 AAGCGCGAGATCGCGGCTTCTTTCGCGCAGCCAGCGTGCAGTTCGCGGCTCTCTTCTTCAAC 360

Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCGGCTGCGAGGCGAGTGCAGGCG 420
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTCTGCGACCGGCTGCGAGGCGAGTGCAGGCG 420

Qy 421 GCGCGCGGCGAGAGTACTAGCGGCGGCGCGGCTGCGAGTCTCGTGGAACTACAACTAC 480
Db 421 GCGCGCGGCGAGAGTACTAGCGGCGGCGCGGCTGCGAGTCTCGTGGAACTACAACTAC 480

Qy 481 GGGCGCGCGGAGGAGCATCGGCTTTCGAGCGGCTCGGCGGACCCCGCGAGGCTGCGCGG 540
Db 481 GGGCGCGCGGAGGAGCATCGGCTTTCGAGCGGCTCGGCGGACCCCGCGAGGCTGCGCGG 540

Qy 541 GACGCGGTGCGGCTTCAAGGCGGCGCTCTGCTTCTGATGAAACAGTGCACCGGTG 600
Db 541 GACGCGGTGCGGCTTCAAGGCGGCGCTCTGCTTCTGATGAAACAGTGCACCGGTG 600

Qy 601 ATGCGCGAGGCTTTCGGGCGGCGGCTTTCGAGGCGGCTTTCGAGTGCAGCGG 660
Db 601 ATGCGCGAGGCTTTCGGGCGGCGGCTTTCGAGGCGGCTTTCGAGTGCAGCGG 660

Qy 661 AACAAACCGCGGCGGCGGCGGCTTTCGAGGCGGCTTTCGAGTGCAGCGGCTC 720
Db 661 AACAAACCGCGGCGGCGGCGGCTTTCGAGGCGGCTTTCGAGTGCAGCGGCTC 720

Qy 721 GGCCTGACCCAGGCGGCGGCGGCTTTCGAGTGCAGCGGCTC 753
```

```
Db 721 GGGCTGACCCAGGGCCCACTCACTTGCTGA 753
|||||
US-10-389-432B-51
; Sequence 51, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 489492000300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: 4N1/23_G4 nucleic acid
US-10-389-432B-51

Query Match 96.8%; Score 729.2; DB 18; Length 750;
Best Local Similarity 98.3%; Pred. No. 1.5e-182;
Matches 737; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TCGATGACAGAACTCGCGCTGCAGCCAAAGTATGTCAGCAAGTTTCGGTACTCGGCG 60
Db 1 TCGATGACAGAACTCGCGCTGCAGCCAAAGTATGTCAGCAAGTTTCGGTACTCGGCG 60
Qy 61 ACAACCGACAGTACTCGCGCGACGGGTGCGAGTCGCGGCCGCTCGCGCGCGCGCG 120
Db 61 ACGACCGACAGTACTCGCGCGACGGGTGCGAGTCGCGGCCGCTCGCGCGCGCGCG 120
Qy 121 GGCAGAGTGGCGCGGTGTCGAACTGCTGAGCGTCTGACCGGCTCTCTTCTTCAAC 180
Db 121 GGCAGAGTGGCGCGGTGTCGAACTGCTGAGCGTCTGACCGGCTCTCTTCTTCAAC 180
Qy 181 GGCATCAAGAACCAAGCGCGGTGCGAGGCGCAAGAACTTCTACACCCGAGCGCG 240
Db 181 GGCATCAAGAACCAAGCGCGGTGCGAGGCGCAAGAACTTCTACACCCGAGCGCG 240
Qy 241 TTCTGAGCGCGGTCAAGCGGTACCAGGGCTTCCGCCATGCGCGGTTCACAGGTGCGCGG 300
Db 241 TTCTGAGCGCGGTCAAGCGGTACCAGGGCTTCCGCCATGCGCGGTTCACAGGTGCGCGG 300

Db 721 GGGCTGACCCAGGGCCCACTCACTTGCTGA 753
|||||
US-10-692-367-55
; Sequence 55, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-55

Query Match 96.4%; Score 725.8; DB 19; Length 753;
Best Local Similarity 97.7%; Pred. No. 1.2e-181;
Matches 736; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TCGATGACAGAACTCGCGCTGCAGCCAAAGTATGTCAGCAAGTTTCGGTACTCGGCG 60
Db 1 TCGATGACAGAACTCGCGCTGCAGCCAAAGTATGTCAGCAAGTTTCGGTACTCGGCG 60
Qy 61 ACAACCGACAGTACTCGCGCGACGGGTGCGAGTCGCGGCCGCTCGCGCGCGCGCG 120
Db 61 ACAACCGACAGTACTCGCGCGACGGGTGCGAGTCGCGGCCGCTCGCGCGCGCGCG 120
Qy 121 GGCAGAGTGGCGCGGTGTCGAACTGCTGAGCGTCTGACCGGCTCTCTTCTTCAAC 180
Db 121 GGCAGAGTGGCGCGGTGTCGAACTGCTGAGCGTCTGACCGGCTCTCTTCTTCAAC 180
Qy 181 GGCATCAAGAACCAAGCGCGGTGCGAGGCGCAAGAACTTCTACACCCGAGCGCG 240
Db 181 GGCATCAAGAACCAAGCGCGGTGCGAGGCGCAAGAACTTCTACACCCGAGCGCG 240
Qy 241 TTCTGAGCGCGGTCAAGCGGTACCAGGGCTTCCGCCATGCGCGGTTCACAGGTGCGCGG 300
Db 241 TTCTGAGCGCGGTCAAGCGGTACCAGGGCTTCCGCCATGCGCGGTTCACAGGTGCGCGG 300
```



```
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE2:
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-77

Query Match      96.0%; Score 722.6; DB 19; Length 753;
Best Local Similarity 97.5%; Pred. No. 8.2e-181;
Matches 734; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 TCGATGCAGAACTCGCGCTGCGAGCAAACTATGTCGACGAACTTCGCTACTGCGGC 60
Db 1 TCGATGCAGAACTCGCGCTGCGAGCAAACTATGTCGACGAACTTCGCTACTGCGGC 60

Qy 61 ACAACGACGAGTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 120
Db 61 ACACGACGAGTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 120

Qy 121 GGCAGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 180
Db 121 GGCAGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 180

Qy 181 GGCATCAAGAACACGAGCGCGGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 240
Db 181 GGCATCAAGAACACGAGCGCGGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 240

Qy 241 TTCCTGAGCGCGTCAAGCGCTAACCAGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 300
Db 241 TTCCTGAGCGCGTCAAGCGCTAACCAGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 300

Qy 301 AAGCGCGAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 360
Db 301 AAGCGCGAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 360

Qy 361 ATCAGCGAGATCAAGAACACGAGCGCGGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 420
Db 361 ATCAGCGAGATCAAGAACACGAGCGCGGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 420

Qy 421 GCGCGGCGGAGAAAGTACTACGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 480
Db 421 GCGCGGCGGAGAAAGTACTACGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 480

Qy 481 GCGCGCGGCGGAGGAGTACTACGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 540
Db 481 GCGCGCGGCGGAGGAGTACTACGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 540

Qy 541 GACGCGCGTGGTGGCGTTCAAGCGGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 600
Db 541 GACGCGCGTGGTGGCGTTCAAGCGGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 600

Qy 601 ATGCGCGAGGCTTCGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 660
Db 601 ATGCGCGAGGCTTCGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 660

Qy 661 AACAAACCCCGCCAGATGAAGCGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 720
Db 661 AACAAACCCCGCCAGATGAAGCGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 720

Qy 721 GCGCTGACCCAGGCGGCGGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 753
Db 721 GCGCTGACCCAGGCGGCGGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 753
```

## RESULT 7

```
US-10-692-367-81
; Sequence 81, Application US/10692367
; Publication No. US200500595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
```

```
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; FEATURE2:
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-81
```

```
Query Match      95.5%; Score 719.4; DB 19; Length 753;
Best Local Similarity 97.2%; Pred. No. 5.7e-180;
Matches 732; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 TCGATGCAGAACTCGCGCTGCGAGCAAACTATGTCGACGAACTTCGCTACTGCGGC 60
Db 1 TCGATGCAGAACTCGCGCTGCGAGCAAACTATGTCGACGAACTTCGCTACTGCGGC 60

Qy 61 ACAACGACGAGTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 120
Db 61 ACACGACGAGTACTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 120

Qy 121 GGCAGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 180
Db 121 GGCAGCAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 180

Qy 181 GGCATCAAGAACACGAGCGCGGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 240
Db 181 GGCATCAAGAACACGAGCGCGGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 240

Qy 241 TTCCTGAGCGCGTCAAGCGCTAACCAGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 300
Db 241 TTCCTGAGCGCGTCAAGCGCTAACCAGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 300

Qy 301 AAGCGCGAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 360
Db 301 AAGCGCGAGTGGCGGCTGCGGCGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 360

Qy 361 ATCAGCGAGATCAAGAACACGAGCGCGGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 420
Db 361 ATCAGCGAGATCAAGAACACGAGCGCGGAGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 420

Qy 421 GCGCGGCGGAGAAAGTACTACGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 480
Db 421 GCGCGGCGGAGAAAGTACTACGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 480

Qy 481 GCGCGCGGCGGAGGAGTACTACGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 540
Db 481 GCGCGCGGCGGAGGAGTACTACGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 540

Qy 541 GACGCGCGTGGTGGCGTTCAAGCGGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 600
Db 541 GACGCGCGTGGTGGCGTTCAAGCGGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 600

Qy 601 ATGCGCGAGGCTTCGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 660
Db 601 ATGCGCGAGGCTTCGCGGCGGCGGTGCGAAGTGGCTAGCGTCCGTCAGCGGCTCTTCAAC 660

Qy 661 AACAAACCCCGCCAGATGAAGCGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 720
Db 661 AACAAACCCCGCCAGATGAAGCGCGGCTTCCGCGGCGAGCGGTGCGAAGTGGCTAGCGGCTCTTCAAC 720
```

Qy 661 AACAAACCCGCCAGATGAACGCGCATCGGCTACTACAGCAGTAGTCTGCGGCCAGCTC 720  
Db 661 AACAAACCCGCCAGATGAACGCGCATCGGCTACTACAGCAGTAGTCTGCGGCCAGCTC 720  
Qy 721 GCGGTGACCCAGGCGCCAACTCCTCCTGCTGA 753  
Db 721 GCGGTGACCCAGGCGCCAACTCCTCCTGCTGA 753

## RESULT 8

US-10-692-367-35  
; Sequence 35, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 753  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; NAME/KEY: CDS  
; LOCATION: (1)...(753)  
US-10-692-367-35

Query Match 95.3%; Score 717.8; DB 19; Length 753;  
Best Local Similarity 97.1%; Pred. No. 1.5e-179;  
Matches 731; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
Qy 1 TCGATGAGAACTCGCGTGCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
Db 1 TCGATGAGAACTCGCGTGCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60  
Qy 61 AACACGACGAGTACTCGCGGACGGGTGCAGTCCGGCCCGTCCCGCTCGGGCGGCGC 120  
Db 61 ACGACCGACGAGTACTCGCGGACGGGTGCAGTCCGGCCCGTCCCGCTCGGGCGGCGC 120  
Qy 121 GGCAGCAGTGCAGGCGGTGGTGCAGCGTGGCTAGCGTTCGACGGGCTCCTTCTTCAAC 180  
Db 121 GGCAGCAGTGCAGGCGGTGGTGCAGCGTGGCTAGCGTTCGACGGGCTCCTTCTTCAAC 180  
Qy 181 GGCAATCAAGAACACGAGCGCGGAGCGGGTGCAGGGGCAAGAACTTCTACCCCGGAGCGC 240  
Db 181 GGCAATCAAGAACACGAGCGCGGAGCGGGTGCAGGGGCAAGAACTTCTACCCCGGAGCGC 240  
Qy 241 TTCTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATATGCGGGTTCAGAGTGCAGGGC 300  
Db 241 TTCTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATATGCGGGTTCAGAGTGCAGGGC 300  
Qy 301 AAGCGCAGATCGCGGCTTCTTCGCGCACGCCACGACGAGACCGGGCATTTCTGTATC 360  
Db 301 AAGCGCAGATCGCGGCTTCTTCGCGCACGCCACGACGAGACCGGGCATTTCTGTATC 360

Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTACTTGGGACCCGACAGGCGAGTGGCCGTGC 420  
Db 361 ATCAACGAGATCAACAAGAGCAACGCTACTTGGGACCCGACAGGCGAGTGGCCGTGC 420  
Qy 421 GCGCGGGGCGAGAAGTACTACGGGCGCGCGCTCGAGATCTCGTGGAACTACAACCTAC 480  
Db 421 GCGCGGGGCGAGAAGTACTACGGGCGCGCGCTCGAGATCTCGTGGAACTACAACCTAC 480  
Qy 481 GGGCGCGGGGAGGAGACATCGGCTTCGACGGGCTGGGGACCCCGGACGGTGGCGCG 540  
Db 481 GGGCGCGGGGAGGAGACATCGGCTTCGACGGGCTGGGGACCCCGGACGGTGGCGCG 540  
Qy 541 GAGCGCGTGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTCACCGTGTG 600  
Db 541 GAGCGCGTGTGGCGTTCAAGGCGGCGCTCTGGTTCTGGATGAACAACGTCACCGTGTG 600  
Qy 601 ATGCGCAGGGCTTCGGGCGCACATCAGGGCCCATCAACGGCGGCTCGAGTGGGAGGG 660  
Db 601 ATGCGCAGGGCTTCGGGCGCACATCAGGGCCCATCAACGGCGGCTCGAGTGGGAGGG 660  
Qy 661 AACAAACCCCGCCAGATGAACGCGCATCGGCTACTTACAAGCAGTACTGCCGACGCTC 720  
Db 661 AACAAACCCCGCCAGATGAACGCGCATCGGCTACTTACAAGCAGTACTGCCGACGCTC 720  
Qy 721 GCGGTGACCCAGGCGCCCAACCTCCTGCTGA 753  
Db 721 GCGGTGACCCAGGCGCCCAACCTCCTGCTGA 753

## RESULT 9

US-10-425-114-19751  
; Sequence 19751, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 19751  
; LENGTH: 1037  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-014-E10\_FLI  
US-10-425-114-19751

Query Match 95.2%; Score 717.2; DB 17; Length 1037;  
Best Local Similarity 97.6%; Pred. No. 2.2e-179;  
Matches 728; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
Qy 6 GCAGAACTCGGGTGCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGCAAC 65  
Db 124 GCAGAACTCGGGTGCAGCCAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGCAAC 183  
Qy 66 CGACGAGTACTGCGGCGACGGGTGCAGTGGGGCCCGTGCCTCGGGCGGCGGCGGAG 125  
Db 184 CGACGAGTACTGCGGCGACGGGTGCAGTGGGGCCCGTGCCTCGGGCGGCGGCGGAG 243  
Qy 126 CAGTGGCGGCGGTGGTGCAGAAAGTGGCTAGCGTTCGTCACCGGCTCTTCTTCAACGGCAT 185  
Db 244 CAGTGGCGGCGGTGGTGCAGAAAGTGGCTAGCGTTCGTCACCGGCTCTTCTTCAACGGCAT 303  
Qy 186 CAGAAACGAGCGCGGAGCGGTCGAGGGCAGAACTTCTACACCGGAGCGGTTTCCT 245  
Db 304 CAGAGCCAGCGCGGAGCGGTCGAGGGCAGAACTTCTACACCGGAGCGGTTTCCT 363

246 GAGCGCGCTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCA CAGGTGCAAGGCAAGCG 305  
|  
|  
|  
Db 364 GAGCGCGCTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCA CAGGTGCAAGGCAAGCG 423  
|  
|  
|  
Qy 306 CGAGATCGCGCGCTTCCTCGGCGACGCCACGACGAGACCGGGCATTTCTGTTACATCAG 365  
|  
|  
|  
Db 424 CGAGATCGCGCGCTTCCTCGGCGACGCCACGACGAGACCGGGCATTTCTGTTACATCAG 483  
|  
|  
|  
Qy 366 CGAGATCAGCAGAGCAACGCTTACTGCGAACCCGACCAAGAGGCGAGTGGCGCGCGC 425  
|  
|  
|  
Db 484 CGAGATCAACAGAGCAACGCTTACTGCGAACCCGACCAAGAGGCGAGTGGCGCGCGC 543  
|  
|  
|  
Qy 426 GGGCAGAGTACTACGGGCGGGCGCGCTCGAGATCTCGTGAACCTACAACTACGGGCG 485  
|  
|  
|  
Db 544 GGGCAGAGTACTACGGGCGGGCGCGCTCGAGATCTCGTGAACCTACAACTACGGGCG 603  
|  
|  
|  
Qy 486 CGCGGGAGGACATCGCTTCGACGGGCTCGGGGACCCCGGCGAGGTGGCGCGGAGCG 545  
|  
|  
|  
Db 604 CGCGGGAGGACATCGCTTCGACGGGCTCGGGGACCCCGGCGAGGTGGCGCGGAGCG 663  
|  
|  
|  
Qy 546 CGTGTGCGCTTCAAGGCGGCGCTCTGTTCTGGATGAACACGTCGACCGTGTGATGCC 605  
|  
|  
|  
Db 664 GGTGTGCGCTTCAAGGCGGCGCTCTGTTCTGGATGAACACGTCGACCGTGTGATGCC 723  
|  
|  
|  
Qy 606 GCAGGCTTCGGCGGCACATCAGGCGGCATCAACGGCGCGCTCGAGTGGCGGGAACAA 665  
|  
|  
|  
Db 724 GCAGGCTTCGGCGGCACATCAGGCGGCATCAACGGCGCGCTCGAGTGGCGGGAACAA 783  
|  
|  
|  
Qy 666 CCGCGCCAGATGAACGGCGGCATCGCTTCTACAGCAGTACTCGCCAGCTCGGCGT 725  
|  
|  
|  
Db 784 CCGCGCCAGATGAACGGCGGCATCGCTTCTACAGCAGTACTCGCCAGCTCGGCGT 843  
|  
|  
|  
Qy 726 CGACCCAGGCGCCCAACCTCACTTGT 751  
|  
|  
|  
Db 844 CGACCCAGGCGCCCAACCTCACTTGT 869  
|  
|  
|

## RESULT 10

US-10-692-367-43  
; Sequence 43, Application US/10692367  
; Publication No. US2005005955A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 54916200320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 753  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(753)  
US-10-692-367-43

Query Match 95.1%; Score 716.2; DB 19; Length 753;  
Best Local Similarity 96.9%; Pred. No. 4e-179;  
Matches 730; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
Qy 1 TCGATGCAAGTCTCGCGCTCGCAGCAAACTATGCTGACAGCAAGTTTCGGCTACTGCGGC 60  
|  
|  
|  
Db 1 TCGATGCAAGTCTCGCGCTCGCAGCAAACTATGCTGACAGCAAGTTTGGCTACTTGGCG 60  
|  
|  
|  
Qy 61 ACAACCAAGTACTGCGCGAGTGGGTGCGAGTGGCGCGCTCGCGTTCGGGCGGCGG 120  
|  
|  
|  
Db 61 ACAGACGACGAGTACTGCGCGAGCGGTGCGAGTGGCGCGCTCGCGTTCGGGCGGCGG 120  
|  
|  
|  
Qy 121 GGCAGCAGTGGCGCGGTGGTGGCAAGTGGCTAGCGTCAACGGCTCTCTTCTTCAAC 180  
|  
|  
|  
Db 121 GGCAGCAGTGGCGCGGTGGTGGCAAGTGGCTAGCGTCAACGGCTCTCTTCTTCAAC 180  
|  
|  
|  
Qy 181 GGCATCAAGAACCAAGGCGCGGTGGAGGGCAAGAACTTCTACACCCGAGGCGCG 240  
|  
|  
|  
Db 181 GGCATCAAGAACCAAGGCGCGGTGGAGGGCAAGAACTTCTACACCCGAGGCGCG 240  
|  
|  
|  
Qy 241 TTCTGAGCGCGCTCAAGGCGTACCCAGGTTCGCCCATGCGCGGTCAACAGTGCAGGCG 300  
|  
|  
|  
Db 241 TTCTGAGCGCGCTCAAGGCGTACCCAGGTTCGCCCATGCGCGGTCAACAGTGCAGGCG 300  
|  
|  
|  
Qy 301 AAGCGCAGATCGCGCGCTTCTTTCGCGCAACGCCACGAGACCGGGCATTTCTGTATC 360  
|  
|  
|  
Db 301 AAGCGCAGATCGCGCGCTTCTTTCGCGCATGTTCGCGACGAGACCGGGCATTTCTGTATC 360  
|  
|  
|  
Qy 361 ATCAGCAGATCAGCAAGAGCAACGCTTCTGCGACCCGACCAAGAGGCGAGTGGCGTGC 420  
|  
|  
|  
Db 361 ATCAGCAGATCAGCAAGAGCAACGCTTCTGCGACCCGACCAAGAGGCGAGTGGCGTGC 420  
|  
|  
|  
Qy 421 GCGCGCGGCGAGTACTACGGGCGCGCTCGCGCTCGAGATCTCTGGAACCTACAACTAC 480  
|  
|  
|  
Db 421 GCGCGCGGCGAGTACTACGGGCGCGCTCGCGCTCGAGATCTCTGGAACCTACAACTAC 480  
|  
|  
|  
Qy 481 GGGCGCGGGGAGGAGATCGGCTTCGAGGGGCTCGGGGACCCCGGCGAGGTGGCGCGG 540  
|  
|  
|  
Db 481 GGGCGCGGGGAGGAGATCGGCTTCGAGGGGCTCGGGGACCCCGGCGAGGTGGCGCGG 540  
|  
|  
|  
Qy 541 GAGCGCGTGGTGGGCTTCAAGGCGGCGCTCTGCTTCTGGATGAACAACTGTCACCGTGTG 600  
|  
|  
|  
Db 541 GAGCGCGTGGTGGGCTTCAAGGCGGCGCTCTGCTTCTGGATGAACAACTGTCACCGTGTG 600  
|  
|  
|  
Qy 601 ATGCGCAGGCGTTCGGCGCCCATCAGGGCCATCAACGGCGCTCGAGTGCAGCGG 660  
|  
|  
|  
Db 601 ATGCGCAGGCGTTCGGCGCCCATCAGGGCCATCAACGGCGCTCGAGTGCAGCGG 660  
|  
|  
|  
Qy 661 AACAAACCCCGCCAGATGAACGGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTC 720  
|  
|  
|  
Db 661 AACAAACCCCGCCAGATGAACGGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTC 720  
|  
|  
|  
Qy 721 GGGTGCAGCCAGGCGCCCAACCTCACTTGTCTGA 753  
|  
|  
|  
Db 721 GGGTGCAGCCAGGCGCCCAACCTCACTTGTCTGA 753  
|  
|  
|

## RESULT 11

US-10-304-928-1  
; Sequence 1, Application US/10304928  
; Publication No. US20030101484A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100D  
; CURRENT APPLICATION NUMBER: US/10/304,928  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/522,714  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 60/125,915  
; PRIOR FILING DATE: 1999-03-24



; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (51)...(893)  
US-10-304-928-1

Query Match 95.0%; Score 715.6; DB 15; Length 1094;  
Best Local Similarity 97.5%; Pred. No. 5.8e-179;  
Matches 727; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 6 GCAGAACTGGCGCTCCAGCCCAACGATGCTGCAGCAAGTTCCGGCTACTGCGGCACAAC 65  
Db 149 GCAGAACTGGCGCTCCAGCCCAACGATGCTGCAGCAAGTTTGGCTACTGCGGCACGAC 208  
Qy 66 CGACGAGTACTGCGCGCAGCGGTGCCAGTGGGCGCCGTCGCGCTCGGCGCGCGCGCGAG 125  
Db 209 CGACGAGTACTGCGCGCAGCGGTGCCAGTGGGCGCCGTCGCGCTCGGCGCGCGCGAG 268  
Qy 126 CAGTGGCGCGGTGGTGCAGACGTGGCTAGCGTCCGCTCACCGGCTCTTCTTCAACGGCAT 185  
Db 269 CAGTGGCGCGGTGGTGCAGACGTGGCTAGCGTCCGCTCACCGGCTCTTCTTCAACGGCAT 328  
Qy 186 CAAGAAACAGGCCCGGAGCGGTGCGAGGGCAAGACTTCTACCCGGAGCGGTTCCT 245  
Db 329 CAAGAGCCAGGCCCGGAGCGGTGCGAGGGCAAGACTTCTACCCGGAGCGGTTCCT 388  
Qy 246 GAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGCGGGTGCAGGTGAGGCGCAAGCG 305  
Db 389 GAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGCGGGTGCAGGTGAGGCGCAAGCG 448  
Qy 306 CGAGATCGCGCTTCTTCGCGCAGCGCCAGCAGCAGACCGGCAATTTCTGTATCATCAG 365  
Db 449 CGAGATCGCGCTTCTTCGCGCAGCGCCAGCAGCAGACCGGCAATTTCTGTATCATCAG 508  
Qy 366 CGAGATCAGCAGCAGCAGCTACTGCGACCCGACCAAGAGGAGTGGCGCGCGCG 425  
Db 509 CGAGATCAACAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGGCGCGCGCG 568  
Qy 426 GGGCGAGAGTACTACGGCGCGCGCGCTGCAGATCTCTGGGAATCAACTACGGGCG 485  
Db 569 GGGCGAGAGTACTACGGCGCGCGCGCTGCAGATCTCTGGGAATCAACTACGGGCG 628  
Qy 486 CGCGGGAGGGAATCGGCTTCGACCGGCTTCGGGACCCCGGACGGGTGGCGCGGACGC 545  
Db 629 CGCGGGAGGGAATCGGCTTCGACCGGCTTCGGGACCCCGGACGGGTGGCGCGGACGC 688  
Qy 546 CGTGTGGCGTTCAAGCGCGCTCTGGTTCTGATGAACAACTGCAACCGTGTGATGCC 605  
Db 689 CGTGTGGCGTTCAAGCGCGCTCTGGTTCTGATGAACAACTGCAACCGTGTGATGCC 748  
Qy 606 GCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTCCAGTGCAGCGGAAACA 665  
Db 749 GCAGGGTTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTTCAGTGGCGGGGAAACA 808  
Qy 666 CCGCGCCAGATGAACCGCGCGATCGGCTACTAAGCAGTACTTCCGCGCCAGCTCGGCGT 725  
Db 809 CCGCGCCAGATGAACCGCGCGCTCGGCTACTAAGCAGTACTTCCGCGCCAGCTCGGCGT 868  
Qy 726 GCAGCCAGGGCCCACTCTTCT 751  
Db 869 GCAGCCAGGGCCCACTCTTCT 894

RESULT 12  
US-10-389-432B-35  
; Sequence 35, Application US/10389432B  
; Publication No. US20040250309A1  
; GENERAL INFORMATION:

; APPLICANT: Muller, Mathias  
; APPLICANT: Simmons, Carl  
; APPLICANT: True, Thom  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE  
; FILE REFERENCE: 489492000300  
; CURRENT APPLICATION NUMBER: US/10/389,432B  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 750  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
; OTHER INFORMATION: rl AH8 nucleic acid  
US-10-389-432B-35

Query Match 94.9%; Score 714.8; DB 18; Length 750;  
Best Local Similarity 97.1%; Pred. No. 9.3e-179;  
Matches 728; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
Qy 1 TCGATGCAGAACTCGCGCTGCCAGCCAAAGCTATGCTGCAGCAAGTTCCGGCTACTGCGGC 60  
Db 1 TCGATGCAGAACTCGCGCTGCCAGCCAAAGCTATGCTGCAGCAAGTTCCGGCTACTGCGGC 60  
Qy 61 ACAACCGACGAGTACTGCGCGCAGCGGTGCAGTCCGGGCCCGCTCGGCGCGCGGC 120  
Db 61 ACAGACGACGAGTACTGCGCGCAGCGGTGCAGTCCGGGCCCGCTCGGCGCGCGGC 120  
Qy 121 GGACGAGTGGCGCGCGGTGTCGACGCTGGCTAGCGTCTGCTACCGGCTCTTCTTCAAC 180  
Db 121 GGACGAGTGGCGCGCGGTGTCGACGCTGGCTAGCGTCTGCTACCGGCTCTTCTTCAAC 180  
Qy 181 GGATCAAGAAACAGCGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCCGAGGCGCG 240  
Db 181 GGATCAAGAGCAAGCGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCCGAGGCGCG 240  
Qy 241 TTCTGAGCGCTCAAGGCGTACCAGGTTTCCGCGATGCGGGTCAAGGTCAGAGTGCAGGGC 300  
Db 241 TTCTGAGCGCTCAAGGCGTACCAGGTTTCCGCGATGCGGGTCAAGGTCAGAGTGCAGGGC 300  
Qy 301 AAGCGGAGATCGCGCTTCTTTCGCGCAGCCAGCAGAGACCGGGCAATTTCTGTATC 360  
Db 301 AAGCGGAGATCGCGCTTCTTTCGCGCAGCCAGCAGAGACCGGGCAATTTCTGTATC 360  
Qy 361 ATCAGCGAGATCAGCAAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGCAGCGTGC 420  
Db 361 ATCAGCGAGATCAGCAAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGCAGCGTGC 420  
Qy 421 GCGCGGGGAGAACTACTACGGCGCGCGCTGTCAGATCTCGTGGAACTCAACATCAG 480  
Db 421 GCGCGGGGAGAACTACTACGGCGCGCGCTGTCAGATCTCGTGGAACTCAACATCAG 480  
Qy 481 GGGCGCGGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGGAGGGTGGCGCGG 540  
Db 481 GGGCGCGGGGAGGAGCATCGGCTTCGACGGGCTCGGGGACCCCGGAGGGTGGCGCGG 540  
Qy 541 GAGCGCGTGGTGGCTTCAAGCGCGCGCTCTGGTTCTGGATGAACAACTGCACCGTGTG 600  
Db 541 GAGCGCGTGGTGGCTTCAAGCGCGCGCTCTGGTTCTGGATGAACAACTGCACCGTGTG 600  
Qy 601 ATGCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAACCGCGCGCTTCGAGTGCAGCGG 660  
Db 601 ATGCGCGAGGCTTCGGCGCCACCATCAGGGCCATCAACCGCGCGCTTCGAGTGCAGCGG 660  
Qy 661 AACAAACCCCGCAGATGAACCGCGCGCTCTTCTACAGCAGTACTCCCGCAGCTC 720  
Db 661 AACAAACCCCGCAGATGAACCGCGCGCTCTTCTTCTACAGCAGTACTCCCGCAGCTC 720



```
QY 721 GCGTCGACCCAGGGCCCAACCTCACTTGC 750
Db 721 GCGTCGACCCAGGGCCCAACCTCACTTGC 750

RESULT 13
US-10-692-367-21
; Sequence 21, Application US/10692367
; Publication No. US200500595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-10-692-367-21

Query Match 94.9%; Score 714.6; DB 19; Length 753;
Best Local Similarity 96.8%; Pred. No. 1.1e-178;
Matches 729; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TCGATGCAGAACTCGCGCTGCAGCAAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGC 60
Db 1 TCGATGCAGAACTCGCGGTGCGCGTCTGCTGCAGCCGGTTCGGGTACTGCGGC 60

QY 61 ACACCCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTGCAGTCCGGCGCGGC 120
Db 61 ACACCCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTGCAGTCCGGCGCGGC 120

QY 121 GGCAGCAGTGGCGGGTGGTGCAGAACTGCTAGCGTCTGCACGGCTCTTCTTCAAC 180
Db 121 GGCAGCAGTGGCGGGTGGTGCAGAACTGCTAGCGTCTGCACGGCTCTTCTTCAAC 180

QY 181 GGCATCAAGAACACGAGCCGGAGCGGGTGCAGGGCAAGAACTTCTACACCCGAGCGCG 240
Db 181 GGCATCAAGAACACGAGCCGGAGCGGGTGCAGGGCAAGAACTTCTACACCCGAGCGCG 240

QY 241 TTCCTGAGCGCGTCAAGCGGTACCCAGGCTTGCAGACCCGACCAAGAGGCAAGTGGCGGTGC 420
Db 241 TTCCTGAGCGCGTCAAGCGGTACCCAGGCTTGCAGACCCGACCAAGAGGCAAGTGGCGGTGC 420

US-10-692-367-43
; Sequence 43, Application US/10389432B
; Publication No. US20040250309A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias
; APPLICANT: Simmons, Carl
; APPLICANT: True, Thom
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: NOVEL COMPOSITIONS WITH CHITINASE
; FILE REFERENCE: 489492000300
; CURRENT APPLICATION NUMBER: US/10/389,432B
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
; OTHER INFORMATION: 4NI/95_H3 nucleic acid
US-10-389-432B-43

Query Match 94.7%; Score 713.2; DB 18; Length 750;
Best Local Similarity 96.9%; Pred. No. 2.5e-178;
Matches 727; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 TCGATGCAGAACTCGCGCTGCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGC 60
Db 1 TCGATGCAGAACTCGCGCTGCAGCCAAACGTATGCTGCAGCAAGTTCGGCTACTGCGGC 60

QY 61 ACACCCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTGCAGTCCGGCGCGGC 120
Db 61 ACACCCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTGCAGTCCGGCGCGGC 120

QY 121 GGCAGCAGTGGCGGGTGGTGCAGAACTGCTAGCGTCTGCACGGCTCTTCTTCAAC 180
Db 121 GGCAGCAGTGGCGGGTGGTGCAGAACTGCTAGCGTCTGCACGGCTCTTCTTCAAC 180

QY 181 GGCATCAAGAACACGAGCCGGAGCGGGTGCAGGGCAAGAACTTCTACACCCGAGCGCG 240
Db 181 GGCATCAAGAACACGAGCCGGAGCGGGTGCAGGGCAAGAACTTCTACACCCGAGCGCG 240

QY 241 TTCCTGAGCGCGTCAAGCGGTACCCAGGCTTGCAGACCCGACCAAGAGGCAAGTGGCGGTGC 300
Db 241 TTCCTGAGCGCGTCAAGCGGTACCCAGGCTTGCAGACCCGACCAAGAGGCAAGTGGCGGTGC 300

QY 301 AAGCCGAGATCGCGCGCTTCTTGCAGCGCCAGCGACGAGACCGGSCATTTCTGTTAC 360
Db 301 AAGCCGAGATCGCGCGCTTCTTGCAGCGCCAGCGACGAGACCGGSCATTTCTGTTAC 360

QY 361 ATCAGCGAGATCAGCAAGACGACGCTTCTGCGACCCGACCAAGAGGCAAGTGGCGGTGC 420
Db 361 ATCAGCGAGATCAGCAAGACGACGCTTCTGCGACCCGACCAAGAGGCAAGTGGCGGTGC 420
```

```
Db 241 TTCTGAGCGCGTCAAGGCGTACCCAGGCTTCGCCCATGCGGCTCCGAGTGCAGGCG 300
Qy 301 AAGCGGAGATCGCGCGCTTCTTCGCGACGCCACGACGAGACCGGGCATTTCTGTAC 360
Db 301 AAGCGGAGATTCGCGCGCTTCTTCGCGCATGTCAACGACGAGACCGGGCATTTCTGTAC 360
Qy 361 ATACGCGAGATCAGCAGAGCAACGCTTACTGCGACCCGACCAAGAGGCGAGTGCCTGC 420
Db 361 ATACGCGAGATCAACAAGAGCAACGCTTACTGCGACCCGACCAAGAGGCGAGTGCCTGC 420
Qy 421 GCCGCGGCGGAGAGTACTACGCGCGCGCGCGCGCTGCGAGATCTCGTGAACCTACA 480
Db 421 GCCGCGGCGGAGAGTACTACGCGCGCGCGCGCTGCGAGATCTCGTGAACCTACA 480
Qy 481 GGGCGCGCGGAGGAGCAATCGGCTTCGACGCGGCTCGGGGACCCCGGAGGGTGGCGGG 540
Db 481 GGGCGCGCGGAGGAGCAATCGGCTTCGACGCGGCTCGGGGACCCCGGAGGGTGGCGGG 540
Qy 541 GACGCGGTGGGCTTCAAGCGCGCGCTCTGCTTCTGGATGAACAACGTCACCGGTG 600
Db 541 GACGCGGTGGGCTTCAAGCGCGCGCTCTGCTTCTGGATGAACAACGTCACCGGTG 600
Qy 601 ATGCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAACGCGCGCTCGAGTGGACGGG 660
Db 601 ATGCGCGAGGCTTCGCGCGCACCATCAGGCGCATCAACGCGCGCTCGAGTGGACGGG 660
Qy 661 AACAAACCGCGCGAGATGAACGCGCGCATCGGCTACTCAAGAGAGTACTGCGCGCAGT 720
Db 661 AACAAACCGCGCGAGATGAACGCGCGCATCGGCTACTCAAGAGAGTACTGCGCGCAGT 720
Qy 721 GCGCTGCGACCCAGGCGCCCACTCACTTGC 750
Db 721 GCGCTGCGACCCAGGCGCCCACTCACTTGC 750
```

## RESULT 15

US-10-692-367-67

; Sequence 67, Application US/10692367

; Publication No. US20050050595A1

; GENERAL INFORMATION:

; APPLICANT: Muller, Mathias L.

; APPLICANT: True, Thom

; APPLICANT: Simmons, Carl R.

; APPLICANT: Yalpani, Nasser

; TITLE OF INVENTION: Novel compositions with chitinase

; FILE OF INVENTION: activity

; FILE REFERENCE: 54916200320

; CURRENT APPLICATION NUMBER: US/10/692,367

; CURRENT FILING DATE: 2003-10-22

; PRIOR APPLICATION NUMBER: 10/389,432

; PRIOR FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: 10/290,086

; PRIOR FILING DATE: 2002-11-06

; PRIOR APPLICATION NUMBER: 60/337,029

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: 60/420,666

; PRIOR FILING DATE: 2002-10-22

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 67

; LENGTH: 765

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Variant sequence produced by shuffling techniques

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)....(765)

US-10-692-367-67

Query Match

Best Local Similarity 94.5%; Score 711.8; DB 19; Length 765;

96.9%; Pred. No. 5.8e-178;

```
Matches 741; Conservative 0; Mismatches 12; Indels 12; Gaps 1;
Qy 1 TCGATGAGAACTCGCGCTCCAGCCAAACGATGCTGCAGCAAGTTTCGCTACTCGGC 60
Db 1 TCGATGAGAACTCGCGCTCCAGCCAAACGATGCTGCAGCAAGTTTCGCTACTCGGC 60
Qy 61 ACAACCGACGAGTACTGCGCGGACGCGGTGCGAGTTCGGGCCCGCTCGCGCGCGGC 120
Db 61 ACAACCGACGAGTACTGCGCGGACGCGGTGCGAGTTCGGGCCCGCTCGCGCGCGGC 120
Qy 121 GGCAGCAGTGGCGGC-----GGTGGTGGAAACGCTGGCTAGCTGCTCACCAGC 168
Db 121 GGCAGCAGTGGCGGC-----GGTGGTGGAAACGCTGGCTAGCTGCTCACCAGC 180
Qy 169 TCCTTCTTCAACCGCATCAAGAACCCAGGCGCGGAGCGGTGCGAGGGCAAGAACTTCTAC 228
Db 181 TCCTTCTTCAACCGCATCAAGAACCCAGGCGCGGAGCGGTGCGAGGGCAAGAACTTCTAC 240
Qy 229 ACCCGAGCGCGTTCTTCAAGCGCGCTCAAGCGCGTACCCAGGCTTCGCCCATGGCGGTCA 288
Db 241 ACCCGAGCGCGTTCTTCAAGCGCGCTCAAGCGCGTACCCAGGCTTCGCCCATGGCGGTCA 300
Qy 289 CAGGTGAGGCGAAGCGCGAGATCGCGCTTCTTCGCGCACGCCACGACGACGAGCCGG 348
Db 301 CAGGTGAGGCGAAGCGCGAGATTCGCGCTTCTTCGCGCACGCCACGACGAGACCGGG 360
Qy 349 CATTTCTTTACATCAGCAGAGATCAGCAAGAGAAACGCTTACTGCGACCCGACCAAGAG 408
Db 361 CATTTCTTGTACATCAGCAGAGATCAACAGAGAACGCTTACTGCGACCCGACCAAGAG 420
Qy 409 CAGTGGCGGTGCGCGCGCGGCGAGAGTACTACGGGCGCGCGCTGCGATCTCGTGG 468
Db 421 CAGTGGCGGTGCGCGCGCGGCGAGAGTACTACGGGCGCGCGCTGCGATCTCGTGG 480
Qy 469 AACTACAACTACGCGGCGCGCGGAGGAGATCGGCTTCGACGCGGCTCGGCGACCCCGGC 528
Db 481 AACTACAACTACGCGGCGCGCGGAGGAGATCGGCTTCGACGCGGCTCGGCGACCCCGGC 540
Qy 529 AGGTGGCGGAGACGCGGCTGCGGCTTCAAGCGCGCGCTCTGCTTCTGGATGAACAAC 588
Db 541 AGGTGGCGGAGACGCGGCTGCGGCTTCAAGCGCGCGCTCTGCTTCTGGATGAACAAC 600
Qy 589 GTGCACCGTGTGATGCGCGCAGGCGCTTCGCGCCCAACCATCAGGGCCATCAACGGCGGCTC 648
Db 601 GTGCACCGTGTGATGCGCGCAGGCGCTTCGCGCCCAACCATCAGGGCCATCAACGGCGGCTC 660
Qy 649 GAGTGGACGCGGAAACAAACCCCGCCAGATGAACGCGCGCATCGGCTACTACAGCAGTAC 708
Db 661 GAGTGGACGCGGAAACAAACCCCGCCAGATGAACGCGCGCATCGGCTACTACAGCAGTAC 720
Qy 709 TGGCGCCAGCTCGGCGTCGACCCAGGGCCCAACCTCACTTGTGTA 753
Db 721 TGGCGCCAGCTCGGCGTCGACCCAGGGCCCAACCTCACTTGTGTA 765
```

Search completed: May 23, 2005, 17:32:11

Job time : 388.609 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 12:20:11 ; Search time 2155.94 Seconds  
(without alignments)  
13294.634 Million cell updates/sec

Title: US-10-692-367-69  
Perfect score: 753  
Sequence: 1 tcgatgcagactcggtgctg.....ggcccaacctcactgtgtga 753

Scoring table:  
IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g881:\*  
9: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	663.4	88.1	855	4	BG837663 Zm10_01e1
2	643	85.4	1179	3	AY103546 Zea mays
3	619.6	82.3	767	7	C0524416 3530_1_16
4	599.6	79.6	737	6	CD435649 EL01N0364
5	598.6	79.5	958	4	BG837479 Zm10_10h0
6	550.8	73.1	710	6	CD443492 Zm10_10h0
7	546.8	72.6	837	7	CN133023 OX1_9_D11
8	536.8	71.3	628	4	BM736454 952051A06
9	533.2	70.8	625	5	BM895383 952073H05
10	526.6	69.9	820	6	CD995497 QB825f07
11	522.6	69.4	578	6	CD994156 QB813f07
12	521.2	69.2	575	6	CD994132 QB813e04
13	520.6	69.1	578	6	CD994454 QB815f08
14	519.6	69.0	741	6	CD994869 QB818d07
15	519.6	69.0	753	6	CD994885 QB818e05
16	508.6	67.5	754	6	CD995176 QB820h11
17	502.4	66.7	647	6	CA197556 SCBPAD106
18	498.8	66.2	550	6	CF001565 QB84f06.x
19	498.8	66.2	559	6	CD999920 QB810a02
20	498.8	66.2	562	6	CF000010 QB811a02
21	498.8	66.2	562	6	CF000228 QB813e12
22	498.8	66.2	562	6	CF000357 QB815b09
23	498.8	66.2	562	6	CF000565 QB817b11
24	498.8	66.2	562	6	CF000643 QB818a05

25	498.8	66.2	573	6	CF000161	CF000161 QB812g06.
26	498.8	66.2	573	6	CF000412	CF000412 QB815g11.
27	498.8	66.2	574	6	CD999947	CD999947 QB810c07.
28	498.8	66.2	574	6	CF000325	CF000325 QB814g11.
29	498.8	66.2	587	6	CF002068	CF002068 QB8f07.x
30	498.8	66.2	587	6	CF002109	CF002109 QB8h11.x
31	498.8	66.2	606	6	CF001250	CF001250 QB82a02.x
32	498.8	66.2	606	6	CF001262	CF001262 QB82b02.x
33	498.8	66.2	606	6	CF001900	CF001900 QB87c09.x
34	498.8	66.2	742	6	CF001316	CF001316 QB82e05.p
35	497.8	66.1	573	6	CF000017	CF000017 QB811a12.
36	497.8	66.0	603	6	CF001775	CF001775 QB86c07.x
37	497.2	66.0	627	6	CF001901	CF001901 QB87c10.x
38	497.2	66.0	641	6	CF011507	CF011507 QB8jhl1.x
39	497.2	66.0	695	6	CF014634	CF014634 QBL17d09.
40	497.2	66.0	746	6	CF001249	CF001249 QB82a02.p
41	497.2	66.0	751	6	CF014225	CF014225 QBL14a03.
42	494.6	65.7	626	6	CF001317	CF001317 QB82e05.x
43	494	65.6	585	6	CF002103	CF002103 QB88h06.x
44	494	65.6	647	6	CF011391	CF011391 QB8b07.x
45	494	65.6	744	6	CF000853	CF000853 QB81a05.p

## ALIGNMENTS

RESULT 1  
BG837663/c 855 bp mRNA linear EST 25-MAY-2001  
LOCUS Zm10\_01e10.A Zm10.AAFC\_ECORC\_Fusarium\_graminearum\_corn\_silk Zea  
DEFINITION mays CDNA Clone Zm10\_01e10, mRNA sequence.  
ACCESSION BG837663  
VERSION BG837663.1 GI:14203986  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 855)  
AUTHORS Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De  
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A.,  
Spott,D., and Tinker,N.A.  
TITLE Expressed Sequence Tags from Maize Silk Six Hours After Silk  
Channel Inoculation with Fusarium graminearum  
JOURNAL Unpublished (2001)  
COMMENT Contact: Harris, Linda J.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,  
CANADA  
Tel: (613) 759-1314  
Fax: (613) 759-6566  
Email: harrielj@agr.gc.ca  
Location/Qualifiers  
1. 855  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="CO388"  
/db\_xref="taxon:4577"  
/clone="Zm10\_01e10"  
/tissue\_type="Silk"  
/dev\_stage="4-5 days post-silk emergence"  
/clone\_lib="Zm10\_AAFC\_ECORC\_Fusarium\_graminearum\_corn\_silk"

Site 2: XhoI; Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;  
in the morning (-10 am) with 1 ml of a macroconidial  
suspension (500,000 spores/ml) of Fusarium graminearum and  
silk channels were collected and immediately frozen in  
liquid nitrogen 6 hours later. RNA was extracted from  
silk tissue between 1 cm below and above the inoculation  
point in the silk channel, RNA from five silk channels was



Qy 525 CGGACGGTGGCGGAGCGCGTGGCGTTCAAGCGCGCTCTGGTTCTGGATGAA 584  
|  
Db 688 CAACAGGGTGGCGGAGCGCGGTGATCGGTTTCAAGACGGCGCTCTGGTTCTGGATGAA 747  
|  
Qy 585 CAACGTGCACCGTGTGATCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGC 644  
|  
Db 748 CAAGTGCACCGTGTGATCGCGAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGC 807  
|  
Qy 645 GCTCAGTGTGCAACGGGCAACCCCGCCAGATGAACGGCGCGATCGGCTACTACAAGCA 704  
|  
Db 808 CTTCTCAGTGTGCAACGGGCAACCCCGCCAGATGAACGGCGCGCTCGGCTACTACAAGCA 867  
|  
Qy 705 GTACTGCGCGAGCTCGCGTGCAGCCAGGCGCCCAACTCACTTGCT 751  
|  
Db 868 GTACTGCGAGCTCGCGTGCAGCCAGGCGCCCAACTCACTTGCT 914  
|

## RESULT 3

CO524416

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

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JOURNAL

COMMENT

CO524416 767 bp mRNA linear EST 15-JUL-2004  
3530\_1\_161\_1 E12.Y.1 3530 - Full length cDNA library created by  
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.  
CO524416  
CO524416.1 GI:50329290  
EST.  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 767)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 3530\_1\_161\_1 row: E column: 12.

Location/Qualifiers

1. 767

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="multiple"

/dev\_stage="varies by tissue"

/lab\_host="DH10B"

/clone\_lib="3530 - Full length cDNA library created by

Invitrogen from multiple tissues"

/note="Organ: silks, husks, ears, pollen, shoot tips,

leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT

6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery

Project contracted with Invitrogen to produce a

normalized, full length library in a pSport clone. This

is a Gateway compatible vector, permitting clone movement

to new vector backbones for expression in diverse host

cells using recombination rather than restriction enzymes.

Details of the vector and sequencing primers are available

at ZmDB in the EST library description tables. poly(A) +

mRNA was prepared by Invitrogen, and equimolar amounts of

RNA from each of the 12 tissue samples were mixed together

for selection of mRNA with a 5' cap. After synthesis of

cDNA, a normalization step was conducted against the

mixture of RNA sources. This step effected a 20X to 80X

reduction in common transcript types. Tissues prepared: 1.

just emerging silks; 2. inner husks from ears of sample

#1; 3. 20 day aleurone; 4. immature tassels, stages from

1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm

vegetative shoot tips from 15 day old seedlings; all  
leaves with an expanded or partially expanded sheath  
were removed; 8. mature leaf tissue; 9. 0.5 cm long root  
tips from 15 day old seedlings; 10. 10 day whole seed; 11.  
12 day endosperm and embryo; 12. 17 day endosperm and  
embryo. All of the sequenced clones in project 3530 will  
be archived at the University of Arizona along with the  
unigene clones from the Maize Gene Discovery EST  
sequencing projects. Clones can be ordered through the  
ZmDB web site or directly from the University of Arizona  
(http://www.genome.arizona.edu/orders/). High density  
filters containing over 18,000 clones can also be ordered  
from the University of Arizona."

## ORIGIN

Query Match 82.3%; Score 619.6; DB 7; Length 767;

Best Local Similarity 97.8%; Pred. No. 7.6e-122;

Matches 628; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 6 GCAGAACTGGCGTGCAGCAAAACGTATGCTGAGCAAGTTGGCTACTGCGGCACAAAC 65  
|  
Db 126 GCAGAACTGGCGTGCAGCAAAACGTATGCTGAGCAAGTTGGCTACTGCGGCACAAAC 185  
|  
Qy 66 CGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTCCGCTCGGCGCGCGCGGCGAG 125  
|  
Db 186 CGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCCGTCCGCTCGGCGCGCGCGGCGAG 245  
|  
Qy 126 CAGTGGCGGCGGTGTGCGAAAGTGGCTAGCGTGTGTCACCGGCTCTTCTTCAACGGCAT 185  
|  
Db 246 CAGTGGCGGCGGTGTGCGAAAGTGGCTAGCGTGTGTCACCGGCTCTTCTTCAACGGCAT 305  
|  
Qy 186 CAGAAACAGCGCGGAGCGGGTGCAGAGGGCAAGAACTTCTACACCGGAGCGGCTTCT 245  
|  
Db 306 CAGAGAGCAGCGCGGAGCGGGTGCAGAGGGCAAGAACTTCTACACCGGAGCGGCTTCT 365  
|  
Qy 246 GAGCGCGCTCAAGCGGTACCCAGGCTTTCGCCCATGGCGGGTTCACAGTGCAGGGCAAGCG 305  
|  
Db 366 GAGCGCGCTCAAGCGGTACCCAGGCTTTCGCCCATGGCGGGTTCACAGTGCAGGGCAAGCG 425  
|  
Qy 306 CGAGATCGCGCGCTTCTTCGCGCAACCGCTACGAGCGAGACCGGGCATTTCTGTTACATCAG 365  
|  
Db 426 CGAGATCGCGCGCTTCTTCGCGCAACCGCTACGAGCGAGACCGGGCATTTCTGTTACATCAG 485  
|  
Qy 366 CGAGATCAGCAAGAGCAACCGCTTCTGCGCAACCGCTTCTGCGAGCGAGCGGCTGCGCGCGC 425  
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Db 486 CGAGATCAGCAAGAGCAACCGCTTCTGCGCAACCGCTTCTGCGAGCGAGCGGCTGCGCGCGC 545  
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Qy 426 GGGGCGAGAGTACTACGGGCGCGCGCTGCGAGTCTCGTGGAACTACAACTACGGGCGC 485  
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Db 546 GGGGCGAGAGTACTACGGGCGCGCGCTGCGAGTCTCGTGGAACTACAACTACGGGCGC 605  
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Qy 486 CGCGGGGAGGAGCAATCGGCTTCCAGCGGCTCGGGGACCCCGGCGAGGGTGGCGCGGAGCGC 545  
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Db 606 CGCGGGGAGGAGCAATCGGCTTCCAGCGGCTCGGGGACCCCGGCGAGGGTGGCGCGGAGCGC 665  
|  
Qy 546 CTTGCTGGCGTTCAAGCGCGCGCTTCTGCTTCTGATGAACAACTGACACCGTGTGATGCC 605  
|  
Db 666 CTTGCTGGCGTTCAAGCGCGCGCTTCTGCTTCTGATGAACAACTGACACCGTGTGATGCC 725  
|  
Qy 606 GCAGGGCTTCGGGCGCCACCATCAGGGCGCATCAACGGCGCGCT 647  
|  
Db 726 GCAGGGCTTCGGGCGCCACCATCAGGGCGCATCAACGGCGCGCT 767  
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## RESULT 4

CD435649

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CD435649 737 bp mRNA linear EST 03-JUN-2003

EL01N0364B04.b Endosperm\_3 Zea mays cDNA, mRNA sequence.

CD435649

CD435649.1 GI:31351292

EST.

Zea mays

Zea mays

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 737)

REFERENCE  
AUTHORS  
Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F., Larkins, B., Becraft, P., and Messing, J.

TITLE  
Characterization of the maize endosperm transcriptome and its comparison to the rice genome

JOURNAL  
Genome Res. 14 (10), 1932-1937 (2004)

COMMENT  
Contact: Lai, Jinsheng  
Dr. Joachim Messing's lab  
Waksman Institute, Rutgers University  
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA  
Tel: 732-445-3801  
Fax: 732-445-5735  
Email: jlai@waksman.rutgers.edu  
Seq primer: T3.

FEATURES  
source  
1. 737  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W22"  
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ORIGIN  
Query Match 79.6%; Score 599.6; DB 6; Length 737;  
Best Local Similarity 96.0%; Pred. No. 1.4e-117;  
Matches 641; Conservative 0; Mismatches 14; Indels 13; Gaps 2;

QY 6 GCAGAACTCGCGCTGCCAGCCAAACGATATGTCGACGAAGTTCGGCTACTCGGCACAAC 65  
DB 82 GCAGAACTCGCGCTGCCAGCCAAACGATCTGTCGACGAAGTTCGGCTACTCGGCACGAC 141  
QY 66 CGACGAGTACTGCGCGGACCGGTCGCCAGTCGCGGCCGTCGCGCTCGCGCGCGCGCGAG 125  
DB 142 CGACGAGTACTGCGCGGACCGGTCGCCAGTCGCGGCCGTCGCGCTCGCGCGGC----- 193  
QY 126 CAGTGGCGGGCTGCTGCGCAAGTGGCTAGGCTGTCACCGGCTCTCTTCTCAACGGCAT 185  
DB 194 -----GGCGGGCGGTGTCGAACGTCGGTAGCGTGTCTACCGGCTCTCTTCTCAACGGCAT 249  
QY 186 CAAGAACCAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGCGGTTCCT 245  
DB 250 CAAGAACCAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGCGGTTCCT 309  
QY 246 GAGCGCGCTCAAGCGCTACCCAGGCTTTCGCCCATGGCGGGTTCACAGTGCAGGCGCAAGCG 305  
DB 310 GAGCGCGCTCAAGCGCTACCCAGGCTTTCGCCCATGGCGGGTTCGAGTGCAGGCGCAAGCG 369  
QY 306 CGAGATCGCGCTCTTTCGGGCAAGCGGACGACGAGACCGGGATTTCTGTATCATCAG 365  
DB 370 CGAGATCGCGCTCTTTCGGGCAAGCGGACGACGAGACCGGGATTTCTGTATCATCAG 429  
QY 366 CGAGATCAGCAGACGACGCTACTCGGACCGGCTGCGAGCGAGCGGTGCGCGCGC 425  
DB 430 CGAGATCAACAGAGCAACGCTACTCGGACCGGCTGCGAGCGAGGTGCGCGCGC 489  
QY 426 GGGGCGAGAAGTACTACCGGGCGCGCGCGCTGCGAGTCTCGTGGAACTTCAACTACGCGGC 485  
DB 490 GGGGCGAGAAGTACTACCGGGCGCGCGCGCTGCGAGTCTCGTGGAACTTCAACTACGCGGC 549  
QY 486 CGCGGGAGGGAATCGGCTTCGACGGGCTCGGGGACCGCGGACGGGTGGCGGGGACGC 545  
DB 550 CGCGGGAGGGAATCGGCTTCGACGGGCTCGGGGACCGCGGACGGGTGGCGGGGACGC 609  
QY 546 CGTGGTGGCGTTCAAGCGCGGCTCTGTTCTGATGAAACAACGTGACAC-CGTGTGATGC 604  
DB 610 CGTGGTGGCGTTCAAGCGCGGCTCTGTTCTGATGAAACAACGTGACACCGGGGTGTTGC 669

QY 605 CGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGGCTCGAGTGCAGCGGGAACA 664  
DB 670 CGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGGCTCGAGTGCAGCGGGAACA 729  
QY 665 ACCCGGCC 672  
DB 730 ACCCGGCC 737

RESULT 5  
EG837479  
LOCUS  
DEFINITION  
Zm10\_10h09\_A Zm10\_AAFCECORC\_Fusarium\_graminearum\_corn\_silk Zea  
mays cDNA Clone Zm10\_10h09, mRNA sequence.

ACCESSION  
EG837479  
VERSION  
EG837479.1 GI:14203802  
KEYWORDS  
EST.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS  
1 (bases 1 to 958)  
Harris, L.J., Balcerzak, M., Allard, S., Saparno, A., Couroux, P., De Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S., Singh, J.A., Sprott, D., and Tinker, N.A.

TITLE  
Expressed Sequence Tags from Maize Silk Six Hours After Silk Channel Inoculation with Fusarium graminearum

JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Harris, Linda J.  
Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA  
Tel: (613) 759-1314  
Fax: (613) 759-6566  
Email: harrisjl@agr.gc.ca.

FEATURES  
source  
1. 958  
/organism="Zea mays"  
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/tissue\_type="Silk"  
/dev\_stage="4-5 days post-silk emergence"  
/clone\_lib="Zm10\_AAFCECORC\_Fusarium\_graminearum\_corn\_silk"  
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Field-grown corn was silk channel-inoculated in the morning (~10 am) with 1 ml of a macroconidial suspension (500,000 spores/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel. RNA from five silk channels was pooled."

ORIGIN  
Query Match 79.5%; Score 598.6; DB 4; Length 958;  
Best Local Similarity 89.9%; Pred. No. 2.3e-117;  
Matches 683; Conservative 6; Mismatches 56; Indels 15; Gaps 4;

QY 6 GCAGAACTCGCGCTGCCAGCCAAACGATATGTCGACG- AAGTTCGGCTACTCGGCACAA 64  
DB 31 GCAGAACTCGCGCTGCCAGCCAAACGATATGTCGACGAAAGTTCGGCTACTCGGCACGA 90  
QY 65 CCAGCAGTACTCGCGCGACGCGGTGCCAGTCCGCGCCCGTCCGCTCGGGCGCGCGGCA 124  
DB 91 CCAGCAGTACTCGCGCGACGCGGTGCCAGTCCGCGCCCGTCCGCTCGGGCGCGGCG 150  
QY 125 GCAGTGGCG-----GGGTGGTGCAGACGTGGCTAGCTGTCACCGGCTCCT 172  
:



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Db 151 SCGGCGCGGAGCGGAGGCGAGTGGCGGTGCGAACGTGGCTAAAGTGGTCAAGCGCGCGT 210
Qy 173 TCTTCAACGGGATCAAGAACAGGCGCGGAGCGGTCGAGGGGCAAGAACTTCTACACCC 232
Db 211 TCTTCAACGGGATCAAGAACAGGCGCGGAGCGGTCGAGGGGCAAGAACTTCTACACCC 270
Qy 233 GGAGCGGTTCTCGAGCGCGTCAAGCGTCAAGCGTACCGAGGCTTCGCCATGGGGTCAAGG 292
Db 271 GGAGCGGTTCTCGAGCGCGTCAAGCGTCAAGCGTACCGAGGCTTCGCCATGGGGGAGG 329
Qy 293 TGCAGGGCAAGCGCGAGATCGCGCTTCTTTCGCGCACGCCACGACGACGAGACCGGGCAT 352
Db 330 TGCAGGGCAAGCGCGAGATCGCGCTTCTTTCGCGCACGCCACGACGAGACCGGACAT 389
Qy 353 TCTGTTCATCAGCGAGATCAGAGAGCAAGCGCTACTCGGACCCGACCAAGAGGAGT 412
Db 390 TCTGTTCATCAGCGAGATCAAGAGAGCAAGCGCTACTCGGACCGCAAGCAAGGCGAGT 449
Qy 413 GGCGTCGCGCGCGGCGGAGGAGTACTACGGGCGCGGCGCTCGAGATCTCGTGGAACT 472
Db 450 GGCGTCGCGCGCGGCGGAGGAGTACTACGGGCGCGGCGCTCGAGATCTCGTGGAACT 509
Qy 473 ACAACTACGGGCGCGCGGAGGAGTACTACGGGCGCGGCGCTCGAGATCTCGTGGAACT 532
Db 510 ACAACTACGGGCGCGCGGAGGAGTACTACGGGCGCGGCGCTCGAGATCTCGTGGAACT 569
Qy 533 TGGCGGCGGAGCGCGTGGTTCAGAGCGGCGCTCTCGTTCGATGAACAAACGTGC 592
Db 570 TGGCGGAGGAGCGCGTGCATCGCGTTCAGAGCGGCGCTCTCGTTCGATGAACAAACGTGC 629
Qy 593 ACCGTGTGATCGCGCGGCTTCGGCGCCACCATCAGGCGCCATCAAGCGCGCTCGAGT 652
Db 630 ACCGTGTGATCGCGCGGCTTCGGCGCCACCATCAGGCGCCATCAAGCGCGCTCGAGT 689
Qy 653 GCGACGGGAACAAACCGCGCCAGATGAACGCGCGCTACTACAGCAGTACTGCG 712
Db 690 GCGACGGGAACAAACCGCGCCAGATGAACGCGCGCTACTACAGCAGTACTGCG 749
Qy 713 GCGAGTGGCGGTGCAACCA-GGGCCCAACTCACTTGCT 751
Db 750 AGCMCTCCGCGTGSACCCAGGGGCCCAACCTCACTTGCT 789
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RESULT 6
CD43492
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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CD43492
EL01N0427B11.b EndospERM_4 Zea mays cDNA, mRNA sequence.
CD43492
CD43492.1 GI:31359135
EST.
```

```
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
```

```
REFERENCE
AUTHORS
```

```
Laikins, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
Laikins, B., Becraft, P. and Messing, J.
```

```
TITLE
Characterization of the maize endospERM transcriptome and its
comparison to the rice genome
```

```
JOURNAL
COMMENT
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
```

```
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
```

```
FEATURES
source
1..710
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
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```
ORIGIN
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Query Match
Best Local Similarity
Matches 571; Conservative
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73.1%; Score 550.8; DB 6; Length 710;
Pred. No. 3.5e-107;
0; Mismatches 12; Indels 3; Gaps 1;
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Qy 6 GCAGAACTCGCGGTGCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCAACAC 65
Db 125 GCAGAACTCGCGGTGCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCAACAC 184
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Qy 66 CGACGAGTACTGTCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCAACAC 122
Db 185 CGACGAGTACTGTCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCAACAC 244
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Qy 123 CAGCAGTGGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCGGCTACTCGGCTACT 182
Db 245 CGCAGTGGTGGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCGGCTACTCGGCT 304
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Qy 183 CATCAAGAACCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCGGCTACT 242
Db 305 CATCAAGAACCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCGGCTACT 364
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Qy 243 CTTGAGCGCGTCAAGGCGTACCGAGGCTTCGCGGTCGAGCAAGTTCGGCTACTCG 302
Db 365 CTTGAGCGCGTCAAGGCGTACCGAGGCTTCGCGGTCGAGCAAGTTCGGCTACTCG 424
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Qy 303 GCGCAGATCGCGCTTCTTCGCGCAAGTTCGCGGTCGAGCAAGTTCGGCTACTCGG 362
Db 425 GCGCAGATCGCGCTTCTTCGCGCAAGTTCGCGGTCGAGCAAGTTCGGCTACTCGG 484
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Qy 363 CAGCGAGATCAGCAAGGCAAGTTCGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCG 422
Db 485 CAGCGAGATCAGCAAGGCAAGTTCGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCG 544
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Qy 423 CCGCGGCGGAGGAGTACTACCGGCTTCGAGCGGTCGCGGTCGAGCAAGTTCGGCT 482
Db 545 CCGCGGCGGAGGAGTACTACCGGCTTCGAGCGGTCGCGGTCGAGCAAGTTCGGCT 604
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```
Qy 483 GCGCGGCGGAGGAGTACTACCGGCTTCGAGCGGTCGCGGTCGAGCAAGTTCGGCT 542
Db 605 GCGCGGCGGAGGAGTACTACCGGCTTCGAGCGGTCGCGGTCGAGCAAGTTCGGCT 664
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Qy 543 CCGCGTGGTGGCGTTCAGGCGGCTTCGCTTCTGGATGAACAC 588
Db 665 CCGCGTGGTGGCGTTCAGGCGGCTTCGCTTCTGGATGAACAC 710
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RESULT 7
LOCUS
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DEFINITION
Ox1_9 D11.g1_A002 Oxidatively-stressed leaves and roots Sorghum
bicolor cDNA clone Ox1_9 D11_A002 5', mRNA sequence.
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```
ACCESSION
VERSION
KEYWORDS
SOURCE
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```
ORGANISM
Sorghum bicolor (sorghum)
Sorghum bicolor
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```
REFERENCE
AUTHORS
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```
TITLE
JOURNAL
COMMENT
```

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/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="EndospERM of 7-23DAP"
/clone_lib="EndospERM_4"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
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Query Match
Best Local Similarity
Matches 571; Conservative
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73.1%; Score 550.8; DB 6; Length 710;
Pred. No. 3.5e-107;
0; Mismatches 12; Indels 3; Gaps 1;
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```
Qy 6 GCAGAACTCGCGGTGCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCAACAC 65
Db 125 GCAGAACTCGCGGTGCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCAACAC 184
```

```
Qy 66 CGACGAGTACTGTCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCAACAC 122
Db 185 CGACGAGTACTGTCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCAACAC 244
```

```
Qy 123 CAGCAGTGGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCGGCTACTCGGCTACT 182
Db 245 CGCAGTGGTGGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCGGCTACTCGGCT 304
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Qy 183 CATCAAGAACCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCGGCTACT 242
Db 305 CATCAAGAACCGCGGAGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCGGCTACT 364
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Qy 243 CTTGAGCGCGTCAAGGCGTACCGAGGCTTCGCGGTCGAGCAAGTTCGGCTACTCG 302
Db 365 CTTGAGCGCGTCAAGGCGTACCGAGGCTTCGCGGTCGAGCAAGTTCGGCTACTCG 424
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```
Qy 303 GCGCAGATCGCGCTTCTTCGCGCAAGTTCGCGGTCGAGCAAGTTCGGCTACTCGG 362
Db 425 GCGCAGATCGCGCTTCTTCGCGCAAGTTCGCGGTCGAGCAAGTTCGGCTACTCGG 484
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```
Qy 363 CAGCGAGATCAGCAAGGCAAGTTCGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCG 422
Db 485 CAGCGAGATCAGCAAGGCAAGTTCGCGGTCGAGCAAGTTCGGCTACTCGGCTACTCG 544
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```
Qy 423 CCGCGGCGGAGGAGTACTACCGGCTTCGAGCGGTCGCGGTCGAGCAAGTTCGGCT 482
Db 545 CCGCGGCGGAGGAGTACTACCGGCTTCGAGCGGTCGCGGTCGAGCAAGTTCGGCT 604
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```
Qy 483 GCGCGGCGGAGGAGTACTACCGGCTTCGAGCGGTCGCGGTCGAGCAAGTTCGGCT 542
Db 605 GCGCGGCGGAGGAGTACTACCGGCTTCGAGCGGTCGCGGTCGAGCAAGTTCGGCT 664
```

```
Qy 543 CCGCGTGGTGGCGTTCAGGCGGCTTCGCTTCTGGATGAACAC 588
Db 665 CCGCGTGGTGGCGTTCAGGCGGCTTCGCTTCTGGATGAACAC 710
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CN133023 837 bp mRNA linear EST 01-APR-2004
Ox1_9 D11.g1_A002 Oxidatively-stressed leaves and roots Sorghum
bicolor cDNA clone Ox1_9 D11_A002 5', mRNA sequence.
```

```
ACCESSION
VERSION
KEYWORDS
SOURCE
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```
ORGANISM
Sorghum bicolor (sorghum)
Sorghum bicolor
```

```
REFERENCE
AUTHORS
```

```
TITLE
JOURNAL
COMMENT
```



Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
the Human Genome Center, University of Tokyo Institute of Medical  
Science; plant material and RNA prepared at Texas A & M University;  
sequencing done in the Laboratory for Genomics and Bioinformatics,  
University of Georgia. Sequence ends have been trimmed to exclude  
vector and regions below Phred quality 16. Three-prime sequences  
are presented as their reverse complement and have been trimmed to  
exclude polyA.

## FEATURES

## ORIGIN

Query Match	72.6%;	Score 546.8;	DB 7;	Length 837;
Best Local Similarity	87.2%;	Pred. No. 2.5e-106;		
Matches 628;	Conservative 0;	Mismatches 77;	Indels 15;	Gaps 2;
Qy	6	GCAGAACTCGGGCTGCCAGCGCAAAACGATATGCTGCAGCAGAAATTCGGCTACTCGCGGCACAAAC	65	
Db	133	GCAGAACTACGGCTGCCAGGACAGTTACTGCTGCAGCDAGTTCGGTTACTCGGCGACGAC	192	
Qy	66	CGACGAGTACTCGCGCGACACGGGTGCGAGTCCGGCCCGTGCCTCGGCGCGCGCGCGGCGAG	125	
Db	193	CGACGAGTACTCTCGCGCGACACGGGTGCCAGTCCGGGCCCGTGCCTCGCGCGCGCGCGAGCA-	251	
Qy	126	CAGTGGCGGGGTGCTGCGAACGTTGGCTTAGCGTTCGTCAACCGGCTCTCTTCTTCAACGGCAT	185	
Db	252	-----GTGGAGTGGGAACGTGGCTGTGCACGACGGATCTCTTCAACGAGAT	303	
Qy	186	CAAGAAACGAGCCGGGACGCGGTGCGAGGGCAAGAACTTCTACACCCGGAGCGCGTTCT	245	
Db	304	CAAGAAACGAGCCGGGAAACGGGTGCGAGGGCAAGAACTTCTACACCCGGAGCGCGTTCT	363	
Qy	246	GAGCGCGTCAAGCGGTACACAGAGTTCGCCCATGGCGGCTCACAGGTGCGAGGGCAAGCG	305	
Db	364	GAGCGCGCGACCGGTACAAAGGCTTCG-----GTGGCAGTCCGTTGCGAGGCAAGCG	417	
Qy	306	CGAGATCGCGCCTTCTTCGCGCACCGCCACGACGAGACCGGGGCATTTCTGTATCATCAG	365	
Db	418	CGAGATCGCGCCTTCTTCGCGCCACATCACGCAACGAGACCGGACATTTCTGTCTACATCAG	477	
Qy	366	CGAGATCAGCAAGACGACGCTACTGCGACCGCACAGGAGGCGAGTGGCGGTGCGCGCG	425	
Db	478	CGAGATCAACAAAGAACCAACGCTTACTTGGGATCTCGAGCAACAGGCGAGTGGCGGTGCGCGC	537	
Qy	426	GGGCGAAGATCTACCGGGCGGGCCCGCTCGAGATCTCTGTGGAATCAACTACGCGGCC	485	
Db	538	GGGTCAAGTACTACGGGCGGGCCCGCTGCAATCTGTGGGAATCAACTACGAGGCC	597	

Qy	486	CGCGGGAGGACATCGGCTTCACACGGCTCGGGACCCCGGCAGCGGTGCGCGGACGC	545
Db	598	TGCGGGAGGAGCATCGGCTTCGACGGCTTCGGAAACCCCGGACAGGTTGGCGCAAGACGC	657
Qy	546	CGTGGTGGCGTTCAGAGCGCGCGCTCTGGTCTTCGATGAAACAACGTGCACCGTGTGATGCC	605
Db	658	CGTGGTGGCGTTCAGAGCGCGCGCTCTGGTCTTCGATGAAACAACGTGCACCGGTTGATGTC	717
Qy	606	GCAGGGGTTTCGGCGCCACCATCATAGGCGCCATCAACGGCGCGCTCGAGTGCACGGGAACAA	665
Db	718	GCAGGGGTTTCGGCGCCACCATCATAGGCGCCATCAACGGCGCGCTCGAGTGCACGGCAAGAA	777
Qy	666	CCCCGCCAGATGAACGGCGCGCATCGGCTACTACAGCAGTACTGCCCGCAGCTCGGCGT	725
Db	778	TACTGCCAGATGAACGGCGCGCGTGGGCTACTACAGCAGTACTGCCCGCAGCTCGGCGT	837

  

RESULT	8
LOCUS	BW736454
DEFINITION	952051A06.x1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea mays CDNA, mRNA sequence.
ACCESSION	BW736454
VERSION	BW736454.1
KEYWORDS	EST.
SOURCE	GI:19057787
ORGANISM	Zea mays
REFERENCE	Zea mays
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
TITLE	1 (bases 1 to 628)
JOURNAL	Walbot, V.
COMMENT	Maize ESTs from various cDNA libraries sequenced at Stanford University Unpublished (1999) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 952051 row: A column: 06. Location/Qualifiers 1..628 /organism="Zea mays" /mol_type="mRNA" /cultivar="BMS (Black Mexican Sweet)" /db_xref="taxon:4577" /tissue_type="suspension culture" /dev_stage="mixed logarithmic and stationary growth phases" /lab_host="DH10B" /clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)" /notes="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

  

FEATURES	source

## ORIGIN

Query Match 71.3%; Score 536.8; DB 4; Length 628;  
Best Local Similarity 93.0%; Pred. No. 3.4e-104;  
Matches 573; Conservative 0; Mismatches 42; Indels 1; Gaps 1;  
Ov 136 GGTGTCGGAACGTGGCTAGCGTGTCAACGGGCTCTTTCTTTAAACGGCATCAAGAACGAG 195

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Db 3 GGGCGGGGAACTGGCTTACGT GGCAGCAGCGGTTCTTCAACGGGATCAAGAACAG 61
Qy 196 GCCGGGACGGGTCGAGGGCAAGAATCTTACACCCGGAGCGGTTCTCTGAGCGCGTC 255
Db 62 GCCGGGACGGGTCGAGGGCAAGAATCTTACACCCGGAGCGGTTCTCTGAGCGCGTC 121
Qy 256 AAGCGGTACCCAGGCTTCCCATGGCGGTTCAGGTGAGGGCAAGCGGAGATCGCC 315
Db 122 AACAACTACCCGGGCTTCGCCCATGGCGGAGCGAGTGGAGGCAAGCGGAGATCGCC 181
Qy 316 GCCTTCTTCGGCGACGCCACGACGAGACCGGGCATTTCTGTATCATCAGCGAGATCAGC 375
Db 182 GCCTTCTTCGGCGACGTCAGCGACGAGACCGGATTTCTGTATCATCAGCGAGATCAAC 241
Qy 376 AAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGGCGGTGCGCGCGGCGAGAG 435
Db 242 AAGAGCAACGCTTACTGCGACCGCAAGCAAGGCAAGTGGCGGTGCGCGCGGCGAGAG 301
Qy 436 TACTACGGGCGCGCGCTGCGATCTCGTGGAACTACAACTACGGGCGCGCGGAGG 495
Db 302 TACTACGGGCGCGCGCTGCGATCTCGTGGAACTACAACTACGGGCGCGCGGAGG 361
Qy 496 GACATCGGCTTCGACGGGCTCGCGGACCCCGCAGGGTGGCGCGGAGCGCGTGTGCG 555
Db 362 GACATCGGCTTCAGGGGCTCGCGACCCCGCAAGAGGTTGGCGGAGCGCGTGTGCG 421
Qy 556 TTCAAGGCGGCGCTCTGTTCTGATGAACAACTGCAACCGTGTGATGCCAGGGCTTC 615
Db 422 TTCAAGGCGGCGCTCTGTTCTGATGAACAACTGCAACCGTGTGATGCCAGGGCTTC 481
Qy 616 GGCGGCAACCATCAGGCGCATCAAGCGCGCTCGAGTGGCGGAGCAACACCCCGCGAG 675
Db 482 GGCGGCAACCATCAGGCGCATCAAGCGCGCTCGAGTGGCGGAGCAACACCCCGCGAG 541
Qy 676 ATGAACGCGCGCTCTGCTACTACAGCAGTACTGCGCGCAGCTCGGCGTGCAGCCAGGG 735
Db 542 ATGAACGCGCGCTCTGCTACTACAGCAGTACTGCGCGCAGCTCGGCGTGCAGCCAGGG 601
Qy 736 CCCAACTCACTTGT 751
Db 602 CCCAACTCACTTGT 617
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RESULT 9  
BM895383  
LOCUS 952073H05.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea  
DEFINITION BM895383 625 bp mRNA linear EST 11-MAR-2002  
may8 cDNA, mRNA sequence.

ACCESSION BM895383  
VERSION BM895383.1 GI:19350851  
KEYWORDS EST.  
SOURCE Zea mays

## ORGANISM

Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 625)  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished (1999)  
CONTACT: Walbot V  
DEPARTMENT OF Biological Sciences  
STANFORD UNIVERSITY  
855 California Ave, Palo Alto, CA 94304, USA

TELEPHONE: 650 723 2227  
FAX: 650 725 8221

EMAIL: walbot@stanford.edu

PLATE: 952073 row: H column: 05.

LOCATION/Qualifiers  
1. - 625

ORGANISM="Zea mays"

## FEATURES

source

CD995497

LOCUS

CD995497

820 bp

mRNA

linear

EST 16-JUL-2003

/mol\_type="mRNA"  
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/tissue\_type="suspension culture"  
/dev\_stage="mixed logarithmic and stationary growth phases"  
/lab\_host="DH10B"  
/clone\_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"  
/notes="vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

## ORIGIN

Query Match 70.8%; Score 533.2; DB 5; Length 625;  
Best Local Similarity 92.1%; Pred. No. 2e-103;  
Matches 573; Conservative 0; Mismatches 48; Indels 1; Gaps 1;

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Qy 119 GCGGCACAGTGGCGGCGGTGGTGGAACTGGGTAGCGTGTCAACGGCTCTCTTCTTCA 178
Db 5 GCTGTGCGGAGGAGTGGCGGTGCGAACTGGGTAAAG-GGTGAGGACGCTTCTTCA 63
Qy 179 ACGCATCAAGAACCCAGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCG 238
Db 64 ACGCATCAAGAACCCAGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGGAGCG 123
Qy 239 CGTTCTGAGCGCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCAAGGTGCA 298
Db 124 GCTTCTGAGCGCGTCAAGGCGTACCCAGGCTTCGCCCATGGCGGGTCAAGGTGCA 183
Qy 299 GCAAGCGGAGATCGCGCGCTTCTTTCGGGACGCGACGCGAGACCGGGATTTCTGTT 358
Db 184 GCAAGCGGAGATCGCGCGCTTCTTTCGGGACGCGACGCGAGACCGGGATTTCTGTT 243
Qy 359 ACATCAGCGAGATCAGCAAGAGCAACGCTTACTGCGACCGGACCAAGAGGAGTGGCGGT 418
Db 244 ACATCAGCGAGATCAGCAAGAGCAACGCTTACTGCGACCGGACCAAGAGGAGTGGCGGT 303
Qy 419 GCGCGCGGCGGAGAGTACTTACGCGGCGCGCGCTGCGAGATCTCGTGGAACTACAACT 478
Db 304 GCGCGCGGCGGAGAGTACTTACGCGGCGCGCGCTGCGAGATCTCGTGGAACTACAACT 363
Qy 479 ACGGCGCGGCGGAGGAGATCGGCTTTCAGCGGGCTCGGGGACCGCGGAGGTGGCGG 538
Db 364 ACGGCGCGGCGGAGGAGATCGGCTTTCAGCGGGCTCGGGGACCGCGGAGGTGGCGG 423
Qy 539 GGGACGCGGTGGCGGTTCAGAGCGCGCGCTCTGTTCTGTGATGAAACAGTGCACCGTG 598
Db 424 AGGACGCGGTGATGCGCTTCAAGACGCGCGCTCTGTTCTGTGATGAAACAGTGCACCGTG 483
Qy 599 TGATGCGGAGGCGTTCGGCGGCGGACCACTCAGGGGCGATCAACGGCGCGCTCGAGTGCAG 658
Db 484 TGATGCGGAGGCGTTCGGCGGCGGACCACTCAGGGGCGATCAACGGCGCGCTCGAGTGCAG 543
Qy 659 GGAACAAACCCCGCCAGATGAAACGCGGCGATTCGGCTACTACAGCAGTACTTGGCGCGG 718
Db 544 GGAACAAACCCCGCCAGATGAAACGCGGCGATTCGGCTACTACAGCAGTACTTGGCGCGG 603
Qy 719 TCGCGGTGCGACCCAGGGGCGCAA 740
Db 604 TCGCGGTGCGACCCAGGGGCGCAA 625
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RESULT 10

CD995497

LOCUS

CD995497

820 bp

mRNA

linear

EST 16-JUL-2003

DEFINITION QBB25f07.xg QBB Zea mays cDNA clone QBB25f07, mRNA sequence.  
ACCESSION CD995497  
VERSION CD995497.1 GI:32855816  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE 1 (bases 1 to 820)  
AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).  
FEATURES  
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/mol\_type="mRNA"  
/cultivar="F2"  
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/clone="QBB25f07"  
/tissue\_type="embryo"  
/clone\_lib="QBB"  
ORIGIN  
Query Match 69.9%; Score 526.6; DB 6; Length 820;  
Best Local Similarity 96.6%; Pred. No. 5e-102;  
Matches 538; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 195 GCGCGGAGCGGCTGCGAGGGCAAGAACTTCTACACCGGAGCGGCTTCTGAGCGCGT 254  
Db 45 GCGCGTGNCGGGTGCAGGGGCAAGAACTTCTACACCGGAGCGGCTTCTGAGCGCGT 104  
Qy 255 CAAGCGGTACCCAGGCTTGCCTCATGCGGGTCAAGGTGAGGCGAAGCGAGATCGC 314  
Db 105 CAAGCGGTACCCAGGCTTGCCTCATGCGGGTCAAGGTGAGGCGAAGCGAGATCGC 164  
Qy 315 CGCTTCTTCGCGACGCGCAGCAGACCGGCGATTTCTGTATCATCAGCAGATCAG 374  
Db 165 CGCTTCTTCGCGACGCGCAGCAGACCGGCGATTTCTGTATCATCAGCAGATCAA 224  
Qy 375 CAAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGGCGCGCGCGGGCAGAA 434  
Db 225 CAAGAGCAACGCTTACTGCGACCCGACCAAGAGGAGTGGCGCGCGGGGCGAGAA 284  
Qy 435 GTACTAGCGGCGCGCGCGCTGCGAGATCTCTGTGAACTAACAATACGGGCGCGGGAG 494  
Db 285 GTACTAGCGGCGCGCGCGCTGCGAGATCTCTGTGAACTAACAATACGGGCGCGGGAG 344  
Qy 495 GGACATCGGCTTCGACGGGCTCGGGGACCCCGGAGGAGTGGCGGGGACCGCGTGGC 554  
Db 345 GGCCATCGGCTTCGACGGGCTCGGGGACCCCGGAGGAGTGGCGGGGACCGCGTGGC 404  
Qy 555 GTTCAAGCGCGGCTCTGTTCTGGATGAACAAAGTGCACCGTGTGATGCGCGAGGGCTT 614  
Db 405 GTTCAAGCGCGGCTCTGTTCTGGATGAACAAAGTGCACCGTGTGATGCGCGAGGGTTC 464  
Qy 615 CGGCGCCACATCAAGGGGCATCAACGGCGCGCTCGAGTGCAGCGGGAACAAACCGGCCCA 674  
Db 465 CGGCGCCACCAACGAGGGGCATCAACGGCGCGCTCGAGTGCAGCGGGAACAAACCGGCCCA 524  
Qy 675 GATGAACCGCGCATCGGCTACTCAAGCAGTACTCGCGCAGCTCGGCGTCAACCCAGG 734  
Db 525 GATGAACCGCGCGTTCGGCTACTACAGCAGTACTCGCGCAGCTCGGCGTCAACCCAGG 584  
Qy 735 GCCCAACCTCACTTGTCT 751

Db 585 GCCCAACCTCACTTGTCT 601  
RESULT 11  
CD994156  
LOCUS QBB13f07.xg QBB Zea mays cDNA clone QBB13f07, mRNA linear EST 16-JUL-2003  
DEFINITION QBB13f07.xg QBB Zea mays cDNA clone QBB13f07, mRNA sequence.  
ACCESSION CD994156  
VERSION CD994156.1 GI:32854475  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE 1 (bases 1 to 578)  
AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).  
FEATURES  
Location/Qualifiers  
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/tissue\_type="embryo"  
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ORIGIN  
Query Match 69.4%; Score 522.6; DB 6; Length 578;  
Best Local Similarity 96.6%; Pred. No. 3.6e-101;  
Matches 534; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 199 GGGAGCGGGTGCAGGGCAAGAACTTCTACACCGGAGCGGCTTCTGAGCGCGTCAAG 258  
Db 1 GGGAGCGGGTGCAGGGCAAGAACTTCTACACCGGAGCGGCTTCTGAGCGCGTCAAG 60  
Qy 259 GCGTACCCAGGCTTCGCCCATGCGGGTCAAGGTGAGGCGAAGCGGAGATCGCGCC 318  
Db 61 GCGTACCCAGGCTTCGCCCATGCGGGTCAAGGTGAGGCGAAGCGGAGATCGCGCC 120  
Qy 319 TTCTTCGCGACGCGCACGACGAGACCGGCGATTTCTGTATCATCAGCAGATCAGCAAG 378  
Db 121 TTCTTCGCGACGCGCACGACGAGACCGGCGATTTCTGTATCATCAGCAGATCAGCAAG 180  
Qy 379 AGCAACCCCTACTGCGACCCGACCAAGAGGAGTGGCGCGCGCGGGGCGAGAGTAC 438  
Db 181 AGCAACCCCTACTGCGACCCGACCAAGAGGAGTGGCGCGCGGGGCGAGAGTAC 240  
Qy 439 TAGGGGCGGGCGCGCTGCGAGATCTCTGTGAACTAACAATACGGGCGCGGGGAGGAG 498  
Db 241 TAGGGGCGGGCGCGCTGCGAGATCTCTGTGAACTAACAATACGGGCGCGGGGAGGAG 300  
Qy 499 ATCGGCTTCGACGGGCTCGGGGACCCCGGAGGAGTGGCGGGGAGCGCGTGGTGGCGTTC 558  
Db 301 ATCGGCTTCGACGGGCTCGGGGACCCCGGAGGAGTGGCGGGGAGCGCGTGGTGGCGTTC 360  
Qy 559 AAGCGCGCGCTCTGTTCTGGATGAACAAAGTGCACCGTGTGATGCGCGAGGGCTTCGGC 618  
Db 361 AAGCGCGCGCTCTGTTCTGGATGAACAAAGTGCACCGTGTGATGCGCGAGGGCTTCGGC 420  
Qy 619 GCCCAACCTCAAGGGGCATCAAGCGGCGCGCTCGAGTGCAGCGGGAACAAACCCCGCCAGATG 678

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Db 421 GCCACCAGGGCCATCAACGGCGCCCTCGAGTGGCGGGGACCAACCCCGCCAGATG 480
Qy 679 AACGGCGCCATCGGTACTATAAGCAGTACTGCGCCAGCTGCGGTGCGATCCAGGGGCC 738
Db 481 AACGGCGCGTGGGTACTATACAGGCAGTACTGCGCCAGCTCGGCGTGCAGCCCGGGGCC 540
Qy 739 AACCTCACTTGT 751
Db 541 AACCTCACTTGT 553

RESULT 12
CD994132
LOCUS QBB13e04.xg QBB Zea mays cDNA clone QBB13e04, mRNA linear EST 16-JUL-2003
DEFINITION CD994132
ACCESSION CD994132
VERSION CD994132.1 GI:32854451
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 575)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..575
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/db_xref="taxon:4577"
/clone="QBB13e04"
/tissue_type="embryo"
/clone_lib="QBB"

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Best Local Similarity 96.7%; Pred. No. 7.1e-101;
Matches 532; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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Db 1 AGCGGTGCGAGGCAAGAACTTCTACACCGGAGCGGTTCTGAGCGCGTCAAGGCG 60
Qy 262 TACCAGGCTTCGCCCATGGCGGTCAAGTGCAGGGCAGCGGATCGCGCTTC 321
Db 61 TACCAGGCTTCGCCCATGGCGGTGCGAGTGCAGGGCAAGCGGAGATCGCGCTTC 120
Qy 322 TTCCGCAACGCGACGACGACCGGGCATTTCTTACATCAGCGAGATCAGCAAGGC 381
Db 121 TTCCGCAACGCGACGACGACCGGGCATTTCTTACATCAGCGAGATCAGCAAGGC 180
Qy 382 AACGCTACTCGACCCGACCAAGAGCAGTGGCGGTGCGCGCGGGGCGAGTACTAC 441
Db 181 AACGCTACTCGACCCGACGACGACCGGGCATTTCTTACATCAGCGAGATCAGCAAGGC 240
Qy 442 GGGCGCGCGCTCGAGATCTCTGGAATCTAACTACCGGCGCGGGGAGGAGCATC 501
Db 241 GGGCGCGCGCTCGAGATCTCTGGAATCTAACTACCGGCGCGGGGAGGAGCATC 300
Qy 502 GGTTCGACGGGCTCGGGGACCCCGGAGGCTGGCGGGAGCGCGGTGGCGTTCAAG 561
Db 301 GGTTCGACGGGCTCGGGGACCCCGGAGGCTGGCGGGAGCGCGGTGGCGTTCAAG 360
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Qy 562 GCGGCGCTCTGGTTCTGATGAACAAAGTCACCGTGTGATGCCGAGGGCTTCGGCGCC 621
Db 361 GCGGCGCTCTGGTTCTGATGAACAAAGTCACCGGTTGTCGCGCAGGGGTTCGGCGCC 420
Qy 622 ACCATCAGGGCCATCAACGGCGCGTCTGAGTGCAGCGGAACAACCCCGCCAGATGAAC 681
Db 421 ACCACCGGGCCATCAACGGCGCGTCTGAGTGCAGCGGAACAACCCCGCCAGATGAAC 480
Qy 682 GCGGCATCGGCTACTACAAGCAGTACTGCGCGCAGCTCGGCGTCGACCCAGGGGCCAAC 741
Db 481 GCGGCGTGGCTACTACAGGCACTACTGCGCGCAGCTCGGCGTCGACCCCGGGGCCAAC 540
Qy 742 CTCACCTTGT 751
Db 541 CTCACCTTGT 550

RESULT 13
CD994454
LOCUS QBB15f08.xg QBB Zea mays cDNA clone QBB15f08, mRNA linear EST 16-JUL-2003
DEFINITION CD994454
ACCESSION CD994454
VERSION CD994454.1 GI:32854773
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 578)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QBB15f08"
/tissue_type="embryo"
/clone_lib="QBB"

ORIGIN
Query Match 69.1%; Score 520.6; DB 6; Length 578;
Best Local Similarity 96.4%; Pred. No. 9.5e-101;
Matches 532; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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Db 6 GGAGCGGTGCGAGGGCAAGAACTTCTACACCGGAGCGGTTCTCTGAGCGCGTCAAGG 65
Qy 260 CGTACCCAGGCTTCGCCCATGGCGGTGTCAGGTGTCAGGGCAAGCGGAGATCGCGCT 319
Db 66 CGTACCCAGGCTTCGCCCATGGCGGTGTCAGGTGTCAGGGCAAGCGGAGATCGCGCT 125
Qy 320 TCTTCGCGCAGCGCAGCAGCAGCGGGCATTTCTGTACATCAGCGAGATCAGCAAGA 379
Db 126 TCTTCGCGCAGCGCAGCAGCAGCGGGCATTTCTGTCTACATCAGCGAGATCAGCAAGA 185
Qy 380 GCAACGCTTACTGCGACCCCGACCAAGAGGAGTGGCGGTGGCGCGGGGAGAGTACT 439
Db 186 GCAACGCTTACTGCGACCCCGACCAAGAGGAGTGGCGGTGGCGCGGGGAGAGTACT 245
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Db	61	TACCCAGGCTTTCGCCCATGCGGTCTACAGGTGAGGGCAAGCGCGAGATGCGCGCTTC	120
Qy	322	TTGCGGCACGCCACGACGAGACCGGGCATTTCTGTACATCAGCGGAGATCAGCAAGGC	381
Db	121	TTGCGGCACGCCACGACGAGACCGGGCATTTCTGTACTTTCAGCGAGATCAACAGAGC	180
Qy	382	AACGCTACTGCGACCCGACCAAGAGGCAAGTGGCGCGTGGCGCGGCGGAGAGTACTAC	441
Db	181	AAGCCTTACTGCGACCCGAGCAAGAGGCAAGTGGCGCGTGGCGCGGCGGAGAGTACTAC	240
Qy	442	GGGCGCGCGCGCTGCGAGATCTGTGGAACATAAACTACGGGCGCGCGGAGGGGACATC	501
Db	241	GGGCGCGCGCGCTGCGAGATCTGTGGAACATAAACTACGGGCGCGCGGAGGGGCAATC	300
Qy	502	GGCTTCGACGGGCTCGGGGACCCCGGAGGTTGGCGGAGCGCGTGTGGCGTTCAAG	561
Db	301	GGCTTCGACGGGCTCGGGGACCCCGGAGGTTGGCGGAGCGCGTGTGGCGTTCAAG	360
Qy	562	GCGCGCTCTGGTTCTCGATGAACAAAGTGCACCGTGTGATGCGCAGGGCTTCGGCGCC	621
Db	361	GCGCGCTCTGGTTCTCGATGAACAGCGTGCACGGGTTGGTCCGCGAGGGTTCCGGCGCC	420
Qy	622	ACCATCAGGCGCATCAACGGCGCGCTCGAGTGCACGGGAAACAACCCGCCAGATGAAC	681
Db	421	ACCATCAGGCGCATCAACGGCGCGCTCGAGTGCACGGGAAACAACCCGCCAGATGAAC	480
Qy	682	GCGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTCGGCGTTCGACCCAGGGCCCCAAC	741
Db	481	GCGCGCATCGGCTACTACAGCAGTACTGCGCGCAGCTCGGCGTTCGACCCAGGGCCCCAAC	540
Qy	742	CTCACTTGCT	751
Db	541	CTCACTTGCT	550

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Job time : 2157.94 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2005, 12:19:56 ; Search time 113.905 Seconds  
(without alignments)  
848.864 Million cell updates/sec

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Perfect score: 1408  
Sequence: 1 SMQNCQPNVCCSKFYCG.....GYKQYRQLGVDPGNLTC 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1408	100.0	250	8	ADS92686 Chitinase
2	1377	97.8	250	8	ADS92668 Chitinase
3	1372	97.4	250	8	ADS92698 Chitinase
4	1366	97.0	254	8	ADS92684 Chitinase
5	1363	96.8	250	8	ADS92694 Chitinase
6	1360	96.6	250	8	ADS92672 Chitinase
7	1358	96.4	250	8	ADS92660 Chitinase
8	1357.5	96.4	257	8	ADS92688 Chitinase
9	1351	96.0	248	8	ADS92618 Maize chi
10	1351	96.0	250	8	ADS92666 Chitinase
11	1351	96.0	281	3	AABI8894 A maize C
12	1350	95.9	250	8	ADS92670 Chitinase
13	1349	95.8	256	8	ADS92690 Chitinase
14	1348	95.7	250	8	ADS92638 Chitinase
15	1348	95.7	256	8	ADS92664 Chitinase
16	1344	95.5	256	8	ADS92676 Chitinase
17	1342	95.3	256	8	ADS92678 Chitinase
18	1341	95.2	250	8	ADS92652 Chitinase
19	1336.5	94.9	249	8	ADS92696 Chitinase
20	1335.5	94.9	257	8	ADS92682 Chitinase
21	1335	94.8	256	8	ADS92700 Chitinase
22	1328.5	94.4	257	8	ADS92646 Chitinase
23	1328.5	94.4	257	8	ADS92650 Chitinase
24	1325.5	94.1	259	8	ADS92656 Chitinase
25	1324.5	94.1	259	8	ADS92692 Chitinase

26	1323	94.0	250	8	ADS92674	AdS92674 Chitinase
27	1322.5	93.9	257	8	ADS92662	AdS92662 Chitinase
28	1321.5	93.9	257	8	ADS92680	AdS92680 Chitinase
29	1319	93.7	250	8	ADS92648	AdS92648 Chitinase
30	1318.5	93.6	257	8	ADS92628	AdS92628 Chitinase
31	1314.5	93.4	269	8	ADS92634	AdS92634 Maize chi
32	1312	93.2	250	8	ADS92644	AdS92644 Chitinase
33	1309.5	93.0	257	8	ADS92654	AdS92654 Chitinase
34	1303	92.5	270	8	ADS92636	AdS92636 Maize chi
35	1300.5	92.4	257	8	ADS92640	AdS92640 Chitinase
36	1285	91.3	256	8	ADS92658	AdS92658 Chitinase
37	1283.5	91.2	257	8	ADS92624	AdS92624 Chitinase
38	1271.5	90.3	255	8	ADS92617	AdS92617 Maize chi
39	1265.5	89.9	280	8	ADS92635	AdS92635 Maize chi
40	1258.5	89.4	280	8	ADS92633	AdS92633 Maize chi
41	1255	89.1	254	8	ADS92642	AdS92642 Chitinase
42	1253	89.0	258	8	ADS92632	AdS92632 Chitinase
43	1245	88.4	258	8	ADS92620	AdS92620 Chitinase
44	1244.5	88.4	251	8	ADS92630	AdS92630 Chitinase
45	1242.5	88.2	251	8	ADS92622	AdS92622 Chitinase

## ALIGNMENTS

## RESULT 1

ADS92686  
ID ADS92686 standard; protein; 250 AA.

XX ADS92686;

XX 02-DEC-2004 (first entry)

XX Chitinase variant polypeptide #32.

XX Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX Synthetic.

XX WO2004037194-A2.

PD 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

PR 06-NOV-2002; 2002US-00290086.

PR 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

PA (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

DR N-PSDB; ADS92685.

XX New chitinase polynucleotides and polypeptides, useful in producing

plants with enhanced resistance against a fungus or a nematode.

PS Claim 3; SEQ ID NO 70; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides encoding them. A method of enhancing plant resistance to a fungus or nematode comprises introducing into a plant a recombinant expression cassette comprising a promoter operably linked to a chitinase polynucleotide of the invention. The plant is maize or soybean. The fungus is from the genus Fusarium. The nematode is from the genus Heterodera. The polynucleotides and polypeptides are useful in enhancing plant resistance to a fungus or nematode. This sequence represents a chitinase variant polypeptide of the invention.

XX Sequence 250 AA;

Query Match	100.0%	Score 1408;	DB 8;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 1.6e-115;		
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Qy	1	SMQCGGQPNVCCSKFGYCGTTDBYCGDGCQGPCRSGGGSSGGGGANVASVVTGSPFN	60	
Db	1	SMQCGGQPNVCCSKFGYCGTTDBYCGDGCQGPCRSGGGSSGGGGANVASVVTGSPFN	60	
Qy	61	G1KNOAGSGCBGKKNFYTRSAFLSAVKAYPGFAHGSGSQVGKRETAAPFAHATHETGHFCY	120	
Db	61	G1KNOAGSGCBGKKNFYTRSAFLSAVKAYPGFAHGSGSQVGKRETAAPFAHATHETGHFCY	120	
Qy	121	ISETSKSNAYCDPTKRWPCAAQKQYXGRGPLQIJSWNNYNGPACRDGFGDLGDPGRVAR	180	
Db	121	ISETSKSNAYCDPTKRWPCAAQKQYXGRGPLQIJSWNNYNGPACRDGFGDLGDPGRVAR	180	
Qy	181	DAVAFKAALWFWMNNVHRVMPQFGGATIRAINGALECDGNNPAQMNARIQYKQYCRQL	240	
Db	181	DAVAFKAALWFWMNNVHRVMPQFGGATIRAINGALECDGNNPAQMNARIQYKQYCRQL	240	
Qy	241	GVDPGPNLTC	250	
Db	241	GVDPGPNLTC	250	

RESULT 2	
ADS92668	
ID	ADS92668 standard; protein; 250 AA.
XX	
AC	ADS92668;
XX	
DT	02-DEC-2004 (first entry)
XX	
XX	Chitinase variant polypeptide #23.
DE	
XX	Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
KW	
XX	Synthetic.
OS	
XX	WO2004037194-A2.
PN	
XX	06-MAY-2004.
PD	
XX	
XX	22-OCT-2003; 2003WO-US033588.
PF	
XX	
XX	22-OCT-2002; 2002US-0420666P.
PR	
XX	06-NOV-2002; 2002US-00290086.
PR	
XX	14-MAR-2003; 2003US-00389432.
XX	
XX	(VERD-) VERDIA INC.
PA	(PION-) PIONEER HI-BRED INT INC.
PA	
XX	
PI	Muller ML, True T, Simmons CR, Yalpani N;
XX	
XX	WPI; 2004-365417/34.
DR	N-PSDB; ADS92667.
DR	
XX	
PT	New chitinase polynucleotides and polypeptides, useful in producing
PT	plants with enhanced resistance against a fungus or a nematode.
XX	
PS	Claim 3; SEQ ID NO 52; 197pp; English.
PS	
XX	
XX	The invention relates to chitinase polypeptides and the polynucleotides
CC	encoding them. A method of enhancing plant resistance to a fungus or
CC	nematode comprises introducing into a plant a recombinant expression
CC	cassette comprising a promoter operably linked to a chitinase
CC	polynucleotide of the invention. The plant is maize or soybean. The
CC	fungus is from the genus Fusarium. The nematode is from the genus
CC	Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC	plant resistance to a fungus or nematode. This sequence represents a
CC	chitinase variant polypeptide of the invention.
XX	

Seq	Sequence	250 AA;
Query Match	97.8%; Score 1377; DB 8; Length 250;	
Best Local Similarity	97.2%; Pred. No. 8.6e-113;	
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Db	1	SMQNCGQPNVCSKFGYCGTTDEYCGDGCQGPCRSGGGSGGGGGANVASVVTGSFFN 60
Qy	61	GIXNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSSQVQCKREIAAFFAHATHETHGHFCY 120
Db	61	GIXSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSSQVQCKREIAAFFAHATHETHGHFCY 120
Qy	121	ISEISKSNAYCDPTKRWPCAAQKQYVGRGPIQISWNYNYPGAGRDITGFDGLGDPGRVAR 180
Db	121	ISEINKSNAYCDPTKRWPCAAQKQYVGRGPIQISWNYNYPGAGRAIGFDGLGDPGRVAR 180
Qy	181	DAVAFKAALWFWMNNVHRVYMPQGFATIRAINGALECCGNNPAQMNARIGYYKOYCRQL 240
Db	181	DAVAFKAALWFWMNNVHRVYMPQGFATIRAINGALECCGNNPAQMNARVGYTRYOYCRQL 240
Qy	241	GVDPGPNLTC 250
Db	241	GVDPGPNLTC 250
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ID	ADSS92698	standard; protein; 250 AA.
XX		
AC	ADSS92698;	
XX		
DT	02-DEC-2004	(first entry)
XX		
DE		Chitinase variant polypeptide #38.
XX		
KW		Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.
XX		
OS		Synthetic.
XX		
FN	MO2004037194-A2.	
XX		
PD	06-MAY-2004.	
XX		
PF	22-OCT-2003; 2003WO-US033588.	
XX		
PR	22-OCT-2002; 2002US-0420666P.	
PR	06-NOV-2002; 2002US-00290086.	
PR	14-MAR-2003; 2003US-00389432.	
XX		
PA	(VERD-) VERDIA INC.	
PA	(PION-) PIONEER HI-BRED INT INC.	
XX		
FI	Muller ML, True T, Simmons CR, Yalpani N;	
XX		
DR	WPI; 2004-365417/34.	
DR	N-PSDB; ADS92697.	
XX		
PT	New chitinase polynucleotides and polypeptides, useful in producing	
PT	plants with enhanced resistance against a fungus or a nematode.	
XX		
PS	Claim 3; SEQ ID NO 82; 197pp; English.	
XX		
CC	The invention relates to chitinase polypeptides and the polynucleotides	
CC	encoding them. A method of enhancing plant resistance to a fungus or	
CC	nematode comprises introducing into a plant a recombinant expression	
CC	casette comprising a promoter operably linked to a chitinase	
CC	polynucleotide of the invention. The plant is maize or soybean. The	
CC	fungus is from the genus Fusarium. The nematode is from the genus	
CC	Heterodera. The polynucleotides and polypeptides are useful in enhancing	
CC	plant resistance to a fungus or nematode. This sequence represents a	
CC	chitinase variant polypeptide of the invention.	

XX Sequence 250 AA;  
SQ  
Query Match 97.4%; Score 1372; DB 8; Length 250;  
Best Local Similarity 97.2%; Pred. No. 2.4e-112;  
Matches 243; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 SMQNGCGPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGSGGGGANNVAVVTGSPFN 60  
Db 1 SMQNGCGPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGSGGGGANNVAVVTGSPFN 60  
Qy 61 GIKNQAGSGCGKPNFYTRSAFLSAVKAYPGFAHGGSOVQGRKREIAAPFAHATHETGFCY 120  
Db 61 GIKNQAGSGCGKPNFYTRSAFLSAVKAYPGFAHGGSOVQGRKREIAAPFAHATHETGFCY 120  
Qy 121 ISEISKSNAAYCDPTKRWPCAAAGQKYTGGRPLQISWNNYNGPAGRDIGFDGLGDPGRVAR 180  
Db 121 ISEINKSNAYCDPTKRWPCAAAGQKYTGGRPLQISWNNYNGPAGRDIGFDGLGDPGRVAR 180  
Qy 181 DAVAFKAAALFWFNNVHRVMPQFGATIRAINGALECDGNPAQMNARIQYKQYCRQL 240  
Db 181 DAVAFKAAALFWFNNVHRVMPQFGATIRAINGALECDGNPAQMNARIQYKQYCRQL 240  
Qy 241 GVDPGNLTC 250  
Db 241 GVDEGNLTC 250

RESULT 4  
ADS92684  
ID ADS92684 standard; protein; 254 AA.  
XX AC ADS92684;  
XX DT 02-DEC-2004 (first entry)  
XX DE Chitinase variant polypeptide #31.  
XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX OS Synthetic.  
XX PN WO2004037194-A2.  
XX PD 06-MAY-2004.  
XX PF 22-OCT-2003; 2003WO-US033588.  
XX PR 22-OCT-2002; 2002US-0420666P.  
XX PR 06-NOV-2002; 2002US-00290086.  
XX PR 14-MAR-2003; 2003US-00389432.  
XX PA (VERD-) VERDIA INC.  
XX PA (PION-) PIONEER HI-BRED INT INC.  
XX PI Muller ML, True T, Simmons CR, Yalpani N;  
XX DR WPI; 2004-365417/34.  
XX DR N-PSDB; ADS92683.  
XX PT New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX PS Claim 3; SEQ ID NO 68; 197pp; English.  
XX CC The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing  
XX plant resistance to a fungus or nematode. This sequence represents a

CC chitinase variant polypeptide of the invention.  
XX SQ Sequence 254 AA;

Query Match 97.0%; Score 1366; DB 8; Length 254;  
Best Local Similarity 95.7%; Pred. No. 8.1e-112;  
Matches 243; Conservative 3; Mismatches 4; Indels 4; Gaps 1;  
Qy 1 SMQNGCGPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGSGGGGANNVAVVTG 56  
Db 1 SMQNGCGPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGSGGGGANNVAVVTG 60  
Qy 57 SPFNGIKNOAGSGCGKPNFYTRSAFLSAVKAYPGFAHGGSOVQGRKREIAAPFAHATHETG 116  
Db 61 SPFNGIKNOAGSGCGKPNFYTRSAFLSAVKAYPGFAHGGSOVQGRKREIAAPFAHATHETG 120  
Qy 117 HFCYISISKSNAAYCDPTKRWPCAAAGQKYTGGRPLQISWNNYNGPAGRDIGFDGLGDPG 176  
Db 121 HFCYISINKSNAYCDPTKRWPCAAAGQKYTGGRPLQISWNNYNGPAGRDIGFDGLGDPN 180  
Qy 177 RVARDAVVAFKAAALFWFNNVHRVMPQFGATIRAINGALECDGNPAQMNARIQYKQY 236  
Db 181 RVAQDAVVAFKAAALFWFNNVHRVMPQFGATIRAINGALECDGNPAQMNARIQYKQY 240  
Qy 237 CRQLGVDPGNLTC 250  
Db 241 CRQLGVDPGNLTC 254

RESULT 5  
ADS92694  
ID ADS92694 standard; protein; 250 AA.  
XX AC ADS92694;  
XX DT 02-DEC-2004 (first entry)  
XX DE Chitinase variant polypeptide #36.  
XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
XX OS Synthetic.  
XX PN WO2004037194-A2.  
XX PD 06-MAY-2004.  
XX PF 22-OCT-2003; 2003WO-US033588.  
XX PR 22-OCT-2002; 2002US-0420666P.  
XX PR 06-NOV-2002; 2002US-00290086.  
XX PR 14-MAR-2003; 2003US-00389432.  
XX PA (VERD-) VERDIA INC.  
XX PA (PION-) PIONEER HI-BRED INT INC.  
XX PI Muller ML, True T, Simmons CR, Yalpani N;  
XX DR WPI; 2004-365417/34.  
XX DR N-PSDB; ADS92693.  
XX PT New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX PS Claim 3; SEQ ID NO 78; 197pp; English.  
XX CC The invention relates to chitinase polypeptides and the polynucleotides  
XX encoding them. A method of enhancing plant resistance to a fungus or  
XX nematode comprises introducing into a plant a recombinant expression  
XX cassette comprising a promoter operably linked to a chitinase  
XX polynucleotide of the invention. The plant is maize or soybean. The  
XX fungus is from the genus Fusarium. The nematode is from the genus  
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing

CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 250 AA;

Query Match 96.8%; Score 1363; DB 8; Length 250;  
 Best Local Similarity 96.0%; Pred. No. 1.5e-111;  
 Matches 240; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSFFN 60  
 |||||  
 DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSFFN 60  
 |||||

QY 61 GIKNQAGSGCGKGFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFPAHATHETGHFCY 120  
 |||||  
 DB 61 GIKNQAGSGCGKGFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFPAHATHETGHFCY 120  
 |||||

QY 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180  
 |||||  
 DB 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180  
 |||||

QY 181 DAVVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
 |||||  
 DB 181 DAVVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
 |||||

QY 241 GVDPGPNLTC 250  
 |||||  
 DB 241 GVDPGPNLTC 250  
 |||||

## RESULT 6

ADSS2672  
 ID ADS92672 standard; protein; 250 AA.

XX AC ADS92672;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polypeptide #25.

XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX OS Synthetic.

XX PN W02004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX DR N-PSDB; ADS92671.

XX PT New chitinase polynucleotides and polypeptides, useful in producing  
 plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 3; SEQ ID NO 56; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
 encoding them. A method of enhancing plant resistance to a fungus or  
 nematode comprises introducing into a plant a recombinant expression  
 cassette comprising a promoter operably linked to a chitinase  
 polynucleotide of the invention. The plant is maize or soybean. The  
 fungus is from the genus *Fusarium*. The nematode is from the genus

CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX SQ Sequence 250 AA;

Query Match 96.6%; Score 1360; DB 8; Length 250;  
 Best Local Similarity 96.0%; Pred. No. 2.7e-111;  
 Matches 240; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSFFN 60  
 |||||

DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSFFN 60  
 |||||

QY 61 GIKNQAGSGCGKGFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFPAHATHETGHFCY 120  
 |||||

DB 61 GIKNQAGSGCGKGFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFPAHATHETGHFCY 120  
 |||||

QY 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180  
 |||||

DB 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGFLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180  
 |||||

QY 181 DAVVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
 |||||

DB 181 DAVVAFKAALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNARIYYKQYCRQL 240  
 |||||

QY 241 GVDPGPNLTC 250  
 |||||

DB 241 GVDPGPNLTC 250  
 |||||

## RESULT 7

ADSS2660

ID ADS92660 standard; protein; 250 AA.

XX AC ADS92660;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polypeptide #19.

XX KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.

XX OS Synthetic.

XX PN W02004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

XX DR N-PSDB; ADS92659.

XX PT New chitinase polynucleotides and polypeptides, useful in producing  
 plants with enhanced resistance against a fungus or a nematode.

XX PS Claim 3; SEQ ID NO 44; 197pp; English.

XX CC The invention relates to chitinase polypeptides and the polynucleotides  
 encoding them. A method of enhancing plant resistance to a fungus or  
 nematode comprises introducing into a plant a recombinant expression  
 cassette comprising a promoter operably linked to a chitinase  
 polynucleotide of the invention. The plant is maize or soybean. The

CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 250 AA;

Query Match 96.4%; Score 1358; DB 8; Length 250;  
 Best Local Similarity 95.6%; Pred. No. 4e-111;  
 Matches 239; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGANVASVVTGSFEN 60  
 DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGANVANVTDFFN 60  
 QY 61 GIKNOAGSGCGKGFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAPFAHATHETGHFCY 120  
 DB 61 GIKNOAGSGCGKGFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAPFAHVTHTGHFCY 120  
 QY 121 ISEISKSNAYCDPTKROWPCAGQKYGRGLOISWNYNYPAGRDIGFDGLGDPGRVAR 180  
 DB 121 ISEINKSNAYCDPTKROWPCAGQKYGRGLOISWNYNYPAGRAIGFDGLGDPGRVAR 180  
 QY 181 DAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALCEGNNPAQMNARIGYIKQYCRQL 240  
 DB 181 DAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALCEGNNPAQMNARIGYIKQYCRQL 240  
 QY 241 GVDFGPNLTC 250  
 DB 241 GVDFGPNLTC 250

RESULT 8  
 ADS92688  
 ID ADS92688 standard; protein; 257 AA.  
 XX  
 AC ADS92688;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #33.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 XX  
 PR 06-NOV-2002; 2002US-00290086.  
 XX  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 XX WPI; 2004-365417/34.  
 DR N-PSDB; ADS92687.  
 XX  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 XX Claim 3; SEQ ID NO 72; 197pp; English.  
 XX  
 XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase

CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 257 AA;

Query Match 96.4%; Score 1357.5; DB 8; Length 257;  
 Best Local Similarity 94.2%; Pred. No. 4.6e-111;  
 Matches 242; Conservative 4; Mismatches 4; Indels 7; Gaps 1;  
 QY 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGG-----CGANVASV 53  
 DB 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGGANVANV 60  
 QY 54 VTGSPFNGIKNOAGSGCGKGFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAPFAHATH 113  
 DB 61 VTDAFPNGIKNOAGSGCGKGFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAPFAHATH 120  
 QY 114 ETGHFCYISISKSNAAYCDPTKROWPCAGQKYGRGLOISWNYNYPAGRDIGFDGLG 173  
 DB 121 ETGHFCYISINKSNAYCDPTKROWPCAGQKYGRGLOISWNYNYPAGRAIGFDGLG 180  
 QY 174 DPGRVARDAVAFKAALWFMMNNVHRVMPQGFATIRAINGALCEGNNPAQMNARIGY 233  
 DB 181 DPGRVARDAVAFKAALWFMMNNVHRVMPQGFATIRAINGALCEGNNPAQMNARIGY 240  
 QY 234 KOYCRQLGVDPGNLTC 250  
 DB 241 KOYCRQLGVDPGNLTC 257

RESULT 9  
 ADS92618  
 ID ADS92618 standard; protein; 248 AA.  
 XX  
 AC ADS92618;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Maize chitinase B polypeptide #1.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*;  
 XX maize; chitinase B; plant.  
 XX  
 OS Zea mays.  
 XX  
 PN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 XX  
 PR 06-NOV-2002; 2002US-00290086.  
 XX  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 XX WPI; 2004-365417/34.  
 DR  
 XX New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 XX Disclosure; SEQ ID NO 2; 197pp; English.  
 XX  
 XX The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase

CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC maize chitinase B polypeptide of the invention.

XX  
 SQ Sequence 248 AA;

Query Match 96.0%; Score 1351; DB 8; Length 248;  
 Best Local Similarity 96.0%; Pred. No. 1.6e-110;  
 Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 QNCQCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANVASVVTGSPFNGI 62  
 DB 1 QNCQCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANVASVVTGSPFNGI 60  
 QY 63 KNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFAFAHATHETGHFCYIS 122  
 DB 61 KSOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFAFAHATHETGHFCYIS 120  
 QY 123 EISKSNAICDPTKQWPCAAQKYYGRGPIQISWNYNYGPAGRDIGFDGLDGPGRVARD 182  
 DB 121 EINKSNAYCDPTKQWPCAAQKYYGRGPIQISWNYNYGPAGRAIGFDGLDGPGRVARD 180  
 QY 183 VVAFKAALWFWMNNVHRVMPQGFATIRAINGALECDGNNPAQNNRIGYKQYCRQLGV 242  
 DB 181 VVAFKAALWFWMNSVHGVVQGFATIRAINGALECCGNNPAQNNRIGYKQYCRQLGV 240  
 QY 243 DPGPNLTC 250  
 DB 241 DPGPNLTC 248

RESULT 10

ID ADS92666 standard; protein; 250 AA.

AC ADS92666;

DT 02-DEC-2004 (first entry)

DE Chitinase variant polypeptide #22.

KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.

OS Synthetic.

XX WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

PR 06-NOV-2002; 2002US-00290086.

PR 14-MAR-2003; 2003US-00389432.

FA (VERD-) VERDIA INC.

FA (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

DR N-PSDB; ADS92665.

XX New chitinase polynucleotides and polypeptides, useful in producing

PT plants with enhanced resistance against a fungus or a nematode.

XX Claim 3; SEQ ID NO 50; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides

CC encoding them. A method of enhancing plant resistance to a fungus or

CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.

XX  
 SQ Sequence 250 AA;

Query Match 96.0%; Score 1351; DB 8; Length 250;  
 Best Local Similarity 94.8%; Pred. No. 1.7e-110;  
 Matches 237; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANVASVVTGSPFN 60  
 DB 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGAGANVASVVTGSPFN 60  
 QY 61 GIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGKREIAAFAFAHATHETGHFCY 120  
 DB 61 GIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGTEVEGKREIAAFAFAHATHETGHFCY 120  
 QY 121 ISEISKNAYCDPTKQWPCAAQKYYGRGPIQISWNYNYGPAGRDIGFDGLDGPGRVAR 180  
 DB 121 ISEISKNAYCDPTKQWPCAAQKYYGRGPIQISWNYNYGPAGRAIGFDGLDGPGRVAR 180  
 QY 181 DAVVAFKAALWFWMNNVHRVMPQGFATIRAINGALECDGNNPAQNNRIGYKQYCRQL 240  
 DB 181 DAVVAFKAALWFWMNSVHGVVQGFATIRAINGALECCGNNPAQNNRIGYKQYCRQL 240  
 QY 241 GVDPGPNLTC 250  
 DB 241 GVDPGPNLTC 250

RESULT 11

ID AAB18894 standard; protein; 281 AA.

AC AAB18894;

DT 08-FEB-2001 (first entry)

DE A maize chitinase polypeptide designated ZmCh2.

KW Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase family 18;  
 KW pathogen control; disease resistance; molecular marker.

OS Zea mays.

XX WO200056908-A2.

XX 28-SEP-2000.

XX 09-MAR-2000; 2000WO-US006121.

XX 24-MAR-1999; 99US-0125915P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Simmons CR, Yalpani N;

XX WPI; 2000-628269/60.

DR N-PSDB; AAA96222.

XX New maize chitinase genes encoding seven chitinases of glucosyl hydrolase  
 PT family 19 are useful for enhancing disease resistance in crop plants by  
 PT modulating its expression in plants.

XX Claim 11; Page 65-66; 96pp; English.

XX The present sequence represents a maize chitinase polypeptide. The

CC specification describes glucosyl hydrolase family 19 chitinases

CC (AAB18894, AAB18896, AAB18899, and AAB18902-05), and glucosyl hydrolase  
 CC family 18 chitinases (AAB18895, AAB18897-98 and AAB18900-01). The level of  
 CC chitinase in plants can be modulated to enhance disease resistance in  
 CC crop plants and for control of pathogens. The chitinase polynucleotides  
 CC are also useful as molecular markers for genotype in a plant, and for  
 CC sequence shuffling  
 XX  
 SQ Sequence 281 AA;

Query Match 96.0%; Score 1351; DB 3; Length 281;  
 Best Local Similarity 96.0%; Pred. No. 1.9e-110;  
 Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 3 QNCGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSPFNGI 62  
 Db 34 QNCGCOPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSPFNGI 93  
 Qy 63 KNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSOVQGKREIAAFPAHATHETGHFCYIS 122  
 Db 94 KSQAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSOVQGKREIAAFPAHATHETGHFCYIS 153  
 Qy 123 EISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 182  
 Db 154 EINKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRAIGFDGLGDPGRVARD 213  
 Qy 183 VVAFKAALWFNNVHVRVMPQFGATTIRAINGALCECDGNPAQNNARIGYKYQYCRQLGV 242  
 Db 214 VVAFKAALWFNNVHVRVMPQFGATTIRAINGALCECDGNPAQNNARIGYKYQYCRQLGV 273  
 Qy 243 DPGPNLTC 250  
 Db 274 DPGPNLTC 281

RESULT 12  
 ADS92670  
 ID ADS92670 standard; protein; 250 AA.  
 XX  
 AC ADS92670;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #24.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92669.  
 XX  
 PT New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 54; 197pp; English.  
 XX  
 CC The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or

CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus Fusarium. The nematode is from the genus  
 CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polypeptide of the invention.  
 XX  
 SQ Sequence 250 AA;

Query Match 95.9%; Score 1350; DB 8; Length 250;  
 Best Local Similarity 94.4%; Pred. No. 2e-110;  
 Matches 236; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSPFN 60  
 Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGSGGGGGANVASVVTGSPFN 60  
 Qy 61 GIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSOVQGKREIAAFPAHATHETGHFCY 120  
 Db 61 GIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSOVQGKREIAAFPAHATHETGHFCY 120  
 Qy 121 ISEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVAR 180  
 Db 121 ISEINKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFNGLADPNRVAQ 180  
 Qy 181 DAVVAFKAALWFNNVHVRVMPQFGATTIRAINGALCECDGNPAQNNARIGYKYQYCRQL 240  
 Db 181 DAVIAFKSALWFNNVHVRVMPQFGATTIRAINGALCECDGNPAQNNARVGYRYQYCRQL 240  
 Qy 241 GVDGPNLTC 250  
 Db 241 GVDGPNLTC 250

RESULT 13  
 ADS92690  
 ID ADS92690 standard; protein; 256 AA.  
 XX  
 AC ADS92690;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Chitinase variant polypeptide #34.  
 XX  
 KW Chitinase; plant resistance; fungus; nematode; Fusarium; Heterodera.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004037194-A2.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 22-OCT-2003; 2003WO-US033588.  
 XX  
 PR 22-OCT-2002; 2002US-0420666P.  
 PR 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX  
 PA (VERD-) VERDIA INC.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Muller ML, True T, Simmons CR, Yalpani N;  
 XX  
 DR WPI; 2004-365417/34.  
 DR N-PSDB; ADS92689.  
 XX  
 PT New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX  
 PS Claim 3; SEQ ID NO 74; 197pp; English.  
 XX  
 CC The invention relates to chitinase polypeptides and the polynucleotides



CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
SQ Sequence 256 AA;

Query Match 95.8%; Score 1349; DB 8; Length 256;  
Best Local Similarity 93.8%; Pred. No. 2.6e-110;  
Matches 240; Conservative 4; Mismatches 6; Indels 6; Gaps 1;  
QY 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGG-----GGANVASV 54  
DB 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGANVASV 60  
QY 55 TGSFNGIKNOAGSGCGKPNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHE 114  
DB 61 TDSFNGIKNOAGSGCGKPNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHE 120  
QY 115 TGHFICYISEISKSNAAYCDPTKRWPCAAGQKYGRGLQISWNNYGPAGRDIGFDGLGD 174  
DB 121 TGHFICYINEINKSNAYCDPTKRWPCAAGQRYGRGLQISWNNYGPAGRAIGFDGLGD 180  
QY 175 PGRVARDVAFAKALWFNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIGYYK 234  
DB 181 PGRVARDVAFAKALWFNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIGYYK 240  
QY 235 QYCRQLGVDPGNLTC 250  
DB 241 QYCRQLGVDPGNLTC 256

RESULT 14  
ADS92638  
ID ADS92638 standard; protein; 250 AA.  
XX  
AC ADS92638;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polypeptide #8.  
XX  
KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
XX  
OS Synthetic.  
XX  
PN W02004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
XX  
PR 06-NOV-2002; 2002US-00290086.  
XX  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
XX  
DR N-PSDB; ADS92637.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 3; SEQ ID NO 22; 197pp; English.  
XX

CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX  
SQ Sequence 250 AA;

Query Match 95.7%; Score 1348; DB 8; Length 250;  
Best Local Similarity 95.2%; Pred. No. 3e-110;  
Matches 238; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
QY 1 SMQNGCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGANVASVVTGSFFN 60  
DB 1 SMQNGCGASGLCCSRFGYCGTTDEYCGDGCQSGPCRSGGGSSGGANVASVVTGSFFN 60  
QY 61 GIKNOAGSGCGKPNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHEGHFCY 120  
DB 61 GIKNOAGSGCGKPNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHEGHFCY 120  
QY 121 ISBISKSNAAYCDPTKRWPCAAGQKYGRGLQISWNNYGPAGRDIGFDGLGDGPRVAR 180  
DB 121 ISBISKSNAAYCDPTKRWPCAAGQKYGRGLQISWNNYGPAGRAIGFDGLGDGPRVAR 180  
QY 181 DAVVAFAKALWFNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIGYYKQYCRQL 240  
DB 181 DAVVAFAKALWFNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIGYYKQYCRQL 240  
QY 241 GVDPGPNLTC 250  
DB 241 RVDPGPNLTC 250

RESULT 15  
ADS92664  
ID ADS92664 standard; protein; 256 AA.  
XX  
AC ADS92664;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polypeptide #21.  
XX  
KW Chitinase; plant resistance; fungus; nematode; *Fusarium*; *Heterodera*.  
XX  
OS Synthetic.  
XX  
PN W02004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
XX  
PR 06-NOV-2002; 2002US-00290086.  
XX  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
XX WPI; 2004-365417/34.  
XX  
DR N-PSDB; ADS92663.  
XX  
XX New chitinase polynucleotides and polypeptides, useful in producing  
XX plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 3; SEQ ID NO 48; 197pp; English.  
XX

XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polypeptide of the invention.  
XX

SQ Sequence 256 AA;

Query Match 95.7%; Score 1348; DB 8; Length 256;  
Best Local Similarity 93.8%; Pred. No. 3.1e-110;  
Matches 240; Conservative 4; Mismatches 6; Indels 6; Gaps 1;  
Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSPCRSGGGSGG-----GGANVASV 54  
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSPCRSGGGSGGGGGGGGGANVASV 60  
Qy 55 TGSFFNGIKNQAGSGCGKFNFTRS AFLSAVKAYPGFAHGSSQVGKREIAAFPAHATHE 114  
Db 61 TGSFFNGIKNQAGSGCGKFNFTRS AFLSAVKAYPGFAHGSSQVGKREIAAFPAHVTHE 120  
Qy 115 TGHEFCYISEISKSNAYCDPTKRWPCAAGQKYGRGPIQISWNYNGPAGRDIGFDGLGD 174  
Db 121 TGHPRYISEVKNKNAYCDPTKRWPCAAGQKYGRGPIQISWNYNGPAGRAIGFDGLGD 180  
Qy 175 PGRVARDAVAFKAALWFMMNHRVMPQGFATIRAINGALECDGNNPAQMNARIGYK 234  
Db 181 PGRVARDAVAFKAALWFMMNHRVMPQGFATIRAINGALECDGNNPAQMNARVGYR 240  
Qy 235 QYCRQLGVDPGPNLTC 250  
Db 241 QYCRQLGVDPGPNLTC 256

Search completed: May 24, 2005, 12:50:20  
Job time : 114.905 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2005, 12:41:36 ; Search time 30.572 Seconds  
(without alignments)  
610.437 Million cell updates/sec

Title: US-10-692-367-70  
Perfect score: 1408  
Sequence: 1 SMQNCQPNVCCSKFGYCG.....GYKQYCRQLGVDPPNLTLC 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgm2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgm2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgm2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgm2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1351	96.0	281	4	US-09-522-714-2
2	861	61.2	271	4	US-09-522-714-22
3	685.5	48.7	183	4	US-09-522-714-30
4	627.5	44.6	328	3	US-07-791-931-5
5	621.5	44.1	310	1	US-07-704-288C-6
6	621.5	44.1	310	1	US-08-379-259-6
7	621.5	44.1	330	1	US-07-704-288C-8
8	621.5	44.1	330	1	US-08-379-259-8
9	621	44.1	310	3	US-07-791-931-6
10	620	44.0	324	1	US-08-047-413-11
11	620	44.0	324	3	US-08-229-050-11
12	620	44.0	324	3	US-08-801-563-11
13	620	44.0	329	2	US-08-475-427-13
14	620	44.0	329	2	US-07-842-165-13
15	602.5	42.8	314	1	US-07-704-288C-7
16	602.5	42.8	314	1	US-08-379-259-7
17	592	42.0	336	1	US-07-704-288C-3
18	592	42.0	336	1	US-08-093-372-2
19	592	42.0	336	1	US-08-379-259-3
20	588	41.8	319	4	US-09-534-229C-3
21	581	41.3	302	2	US-08-475-427-6
22	581	41.3	302	2	US-07-842-165-6
23	563	40.0	328	3	US-07-791-931-7
24	557.5	39.6	318	1	US-07-704-288C-9
25	557.5	39.6	318	1	US-08-379-259-9
26	552.5	39.2	323	4	US-09-534-229C-2
27	535.5	38.0	328	4	US-09-125-891-2

28 535.5 38.0 328 4 US-09-125-891-4 Sequence 4, Appli  
29 504.5 35.8 254 2 US-08-475-427-1 Sequence 1, Appli  
30 504.5 35.8 254 2 US-07-842-165-1 Sequence 1, Appli  
31 504.5 35.8 254 3 US-08-448-398-3 Sequence 3, Appli  
32 498 35.4 316 3 US-07-791-931-8 Sequence 8, Appli  
33 490 34.8 284 4 US-09-522-714-24 Sequence 24, Appli  
34 477 33.9 266 1 US-08-812-025-10 Sequence 10, Appli  
35 477 33.9 266 3 US-07-791-931-10 Sequence 10, Appli  
36 477 33.9 266 3 US-09-138-873A-10 Sequence 10, Appli  
37 462 32.8 405 4 US-09-902-540-11954 Sequence 11954, A  
38 456.5 32.4 271 4 US-09-266-965-141 Sequence 141, App  
39 392 27.8 372 3 US-07-791-931-4 Sequence 4, Appli  
40 384.5 27.3 252 4 US-09-522-714-20 Sequence 20, Appli  
41 378.5 26.9 256 4 US-09-534-229C-1 Sequence 1, Appli  
42 377 26.8 259 4 US-09-522-714-18 Sequence 18, Appli  
43 371.5 26.4 253 3 US-07-791-931-9 Sequence 9, Appli  
44 367.5 26.1 250 1 US-08-162-475A-4 Sequence 4, Appli  
45 366.5 26.0 253 1 US-08-162-475A-5 Sequence 5, Appli

#### ALIGNMENTS

RESULT 1  
US-09-522-714-2  
; Sequence 2, Application US/09522714  
; Patent No. 6563020  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Valpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants  
; FILE REFERENCE: 1100  
; CURRENT APPLICATION NUMBER: US/09/522.714  
; EARLIER FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/125,915  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-09-522-714-2

Query Match 96.0%; Score 1351; DB 4; Length 281;  
Best Local Similarity 96.0%; Pred. No. 4.6e-113;  
Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSPFNGI 62  
Db 34 QNCGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSPFNGI 93  
Qy 63 KNQAGSCGCKNFYTRSAPLSAVKAYPGFAGGSOVQGREIAAFPAHAHETHGHPCVIS 122  
Db 94 KQAGSCGCKNFYTRSAPLSAVKAYPGFAGGSOVQGREIAAFPAHAHETHGHPCVIS 153  
Qy 123 EISKSNAYCDPTKQWPCAAQKYYGRGLQISWNTYNYGPAGRDIGFDGLGDPGRVARD 182  
Db 154 EINKSNAYCDPTKQWPCAAQKYYGRGLQISWNTYNYGPAGRDIGFDGLGDPGRVARD 213  
Qy 183 VVAFKAALWFMWNNVHRVMPQGFATRAINGALECDGNPNPAQWNAHIGYKQYCRQLGV 242  
Db 214 VVAFKAALWFMWNNVHRVMPQGFATRAINGALECDGNPNPAQWNAHIGYKQYCRQLGV 273  
Qy 243 DPGPNLTC 250  
Db 274 DPGPNLTC 281

RESULT 2  
US-09-522-714-22  
; Sequence 22, Application US/09522714









Db 64 IISSEMFQMLKRNDCQKGFYSYNAFINAARSPFGTSGDTTARKKEIAAFAQT 123  
Qy 112 THET-----GHFCYISEISKSNAICDPTKRWPCAAQKQYGRGPLOISWNY 158  
Db 124 SHETGGWATAPDPYAWGYCWLREQSPGDYCTPS-GQWPCAPGRKYFGRGP1QISHNY 182  
Qy 159 NYGPAGRIDGFDGLDGRVARDVAFKALWFMNN-----VHRVMPQ----- 203  
Db 183 NYGPCRAIGVDLLNPDVATDPVIFSKSALWFMWMTQSPKPSCHDVIGRWQPSADR 242  
Qy 204 -----GFGATIRAINGALECDGNPAQMARIGYKQYCRQLGVDGPNLTC 250  
Db 243 AANRLPGFVITNIINGLEGCGRTDSRVQDRIGFYRRYCSILGVSFGDNLDC 295

RESULT 10  
US-08-047-413-11  
; Sequence 11, Application US/08047413  
; Patent No. 5670706  
; GENERAL INFORMATION:  
; APPLICANT: Cornelissen, Bernardus J.C.  
; APPLICANT: Melchers, Leo S.  
; APPLICANT: Meulenhoff, Elisabeth J.S.  
; APPLICANT: van Roekel, Jeroen S.C.  
; APPLICANT: Sela-Buurlage, Marianne B.  
; APPLICANT: Vloemans, Alexandra A.  
; APPLICANT: Woloshuk, Charles P.  
; APPLICANT: Bol, John F.  
; APPLICANT: Linthorst, Hubertus J.M.  
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR  
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/047,413  
; FILING DATE: 19-APR-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/647,831  
; FILING DATE: 29-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20022.00  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-047-413-11

Query Match 44.0%; Score 620; DB 1; Length 324;  
Best Local Similarity 42.0%; Pred. No. 1.3e-47;  
Matches 123; Conservative 43; Mismatches 79; Indels 48; Gaps 9;  
Qy 1 SMQNG-----CQPNVCCSKFGYCGTTEBYCGDG-CQSGPCRSGGGSGGGANVAS 52

Db 22 SARQCGSQAGARCASGLCCSKFGWCGNTINDYCGNQCQS-QC-----PGPTPPGGGDLGS 77  
Qy 53 VVTGSGFNG-1KNQAGSGCGKQNFYTRSAFLSAVKAYPGFAHGGSOVQGRKEIAAFAHA 111  
Db 78 IISSEMFQMLKRNDCQKGFYSYNAFINAARSPFGTSGDTTARKKEIAAFAQT 137  
Qy 112 THET-----GHFCYISEISKSNAICDPTKRWPCAAQKQYGRGPLOISWNY 158  
Db 138 SHETGGWATAPDPYAWGYCWLREQSPGDYCTPS-GQWPCAPGRKYFGRGP1QISHNY 196  
Qy 159 NYGPAGRIDGFDGLDGRVARDVAFKALWFMNN-----VHRVMPQ----- 203  
Db 197 NYGPCRAIGVDLLNPDVATDPVIFSKSALWFMWMTQSPKPSCHDVIGRWQPSADR 256  
Qy 204 -----GFGATIRAINGALECDGNPAQMARIGYKQYCRQLGVDGPNLTC 250  
Db 257 AANRLPGFVITNIINGLEGCGRTDSRVQDRIGFYRRYCSILGVSFGDNLDC 309

RESULT 11  
US-08-229-050-11  
; Sequence 11, Application US/08229050  
; Patent No. 6066491  
; GENERAL INFORMATION:  
; APPLICANT: Cornelissen, Bernardus J.C.  
; APPLICANT: Melchers, Leo S.  
; APPLICANT: Meulenhoff, Elisabeth J.S.  
; APPLICANT: van Roekel, Jeroen S.C.  
; APPLICANT: Sela-Buurlage, Marianne B.  
; APPLICANT: Vloemans, Alexandra A.  
; APPLICANT: Woloshuk, Charles P.  
; APPLICANT: Bol, John F.  
; APPLICANT: Linthorst, Hubertus J.M.  
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR  
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT  
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/229,050  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/647,831  
; FILING DATE: 29-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20022.00  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-229-050-11





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; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-704-288C-7

Query Match      42.8%; Score 602.5; DB 1; Length 314;
Best Local Similarity 43.6%; Pred. No. 4.7e-46;
Matches 122; Conservative 38; Mismatches 77; Indels 43; Gaps 9;

Qy 7 CQNVCCSKFGYCGTTDEYCGDG-CQSGPCRSGGGSGGGGANVASVVTGSPFNGIKNQ 65
Db 27 CAPGLCCSKFGWCNTNDYCGPGNCQS-QCPGGPGPSGDLGG-----VISNSMFDQMLNH 80
Qy 66 AG-SGCEGK-NFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHET----- 115
Db 81 RNDNACQCKNPFYSYNAFISAGSFGFGTTGDTARKREIAAFLAQTSHETTCGWPSAP 140
Qy 116 -----GHFCYISEISKSNAYCDPTKROWPCAAGQKYYGRGPLQISWNNYGPAGRDIGFD 170
Db 141 DGPYAWGYCFLEQGSFGDYCTPSS-QWPCAPGRKYFGRGPIQISHNNYNGPCGRAIGVD 199
Qy 171 GLGDPGRVARDVAVFAKALWFNN-----NVHRVMP-----QGFGATIR 210
Db 200 LLNPNDLVATDSVISFKSAIFWMTPOSXPSPSCHDVITGRWPSCADQAAANRVPGFVITN 259
Qy 211 AINGALECDGNNPAQMNARIGYKQYCRQLGVDPGNLTC 250
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Job time : 31.572 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)  
936.991 Million cell updates/sec

Title: US-10-692-367-70  
Perfect score: 1408  
Sequence: 1 SMQNGQPNVCCSKFCYCG.....GYKQYCRQLGVDPGNLTC 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1408	100.0	250	17	US-10-692-367-70 Sequence 70, Appl
2	1377	97.8	250	17	US-10-692-367-52 Sequence 52, Appl
3	1372	97.4	250	17	US-10-692-367-82 Sequence 82, Appl
4	1366	97.0	254	17	US-10-692-367-68 Sequence 68, Appl
5	1363	96.8	250	17	US-10-692-367-78 Sequence 78, Appl
6	1360	96.6	250	17	US-10-692-367-56 Sequence 56, Appl
7	1358	96.4	250	17	US-10-692-367-44 Sequence 44, Appl
8	1357.5	96.4	257	17	US-10-692-367-72 Sequence 72, Appl
9	1351	96.0	248	17	US-10-692-367-2 Sequence 2, Appl
10	1351	96.0	250	17	US-10-692-367-50 Sequence 50, Appl
11	1351	96.0	281	14	US-10-304-928-2 Sequence 2, Appl
12	1350	95.9	280	17	US-10-692-367-54 Sequence 54, Appl
13	1349	95.8	256	17	US-10-692-367-74 Sequence 74, Appl

14	1348	95.7	250	17	US-10-692-367-22 Sequence 22, Appl
15	1348	95.7	256	17	US-10-692-367-48 Sequence 48, Appl
16	1344	95.5	256	17	US-10-692-367-60 Sequence 60, Appl
17	1342	95.3	256	17	US-10-692-367-62 Sequence 62, Appl
18	1341	95.2	250	17	US-10-692-367-36 Sequence 36, Appl
19	1336.5	94.9	249	17	US-10-692-367-80 Sequence 80, Appl
20	1335.5	94.9	257	17	US-10-692-367-66 Sequence 66, Appl
21	1335	94.8	256	17	US-10-692-367-84 Sequence 84, Appl
22	1328.5	94.4	257	17	US-10-692-367-30 Sequence 30, Appl
23	1328.5	94.4	257	17	US-10-692-367-34 Sequence 34, Appl
24	1325.5	94.1	259	17	US-10-692-367-40 Sequence 40, Appl
25	1324.5	94.1	259	17	US-10-692-367-76 Sequence 76, Appl
26	1323	94.0	250	17	US-10-692-367-58 Sequence 58, Appl
27	1322.5	93.9	257	17	US-10-692-367-46 Sequence 46, Appl
28	1321.5	93.9	257	17	US-10-692-367-64 Sequence 64, Appl
29	1319	93.7	250	17	US-10-692-367-32 Sequence 32, Appl
30	1318.5	93.6	257	17	US-10-692-367-12 Sequence 12, Appl
31	1314.5	93.4	269	17	US-10-692-367-18 Sequence 18, Appl
32	1312	93.2	250	17	US-10-692-367-28 Sequence 28, Appl
33	1309.5	93.0	257	17	US-10-692-367-38 Sequence 38, Appl
34	1303	92.4	270	17	US-10-692-367-20 Sequence 20, Appl
35	1300.5	92.4	257	17	US-10-692-367-24 Sequence 24, Appl
36	1285	91.3	256	17	US-10-692-367-42 Sequence 42, Appl
37	1283.5	91.2	257	17	US-10-692-367-8 Sequence 8, Appl
38	1271.5	90.3	255	17	US-10-692-367-1 Sequence 1, Appl
39	1271.5	90.3	303	15	US-10-425-114-57156 Sequence 57156, A
40	1269	90.1	301	15	US-10-425-114-63860 Sequence 63860, A
41	1269	90.1	302	15	US-10-425-114-71741 Sequence 71741, A
42	1265.5	89.9	280	17	US-10-692-367-19 Sequence 19, Appl
43	1264	89.8	293	15	US-10-425-114-64209 Sequence 64209, A
44	1264	89.8	288	15	US-10-425-114-52906 Sequence 52906, A
45	1258.5	89.4	280	17	US-10-692-367-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-10-692-367-70  
; Sequence 70, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Salmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; TITLE OF INVENTION: activity  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 70  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-70

Query Match 100.0%; Score 1408; DB 17; Length 250;  
Best Local Similarity 100.0%; Pred. No. 5.2e-110;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASVVTGSFFN 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASVVTGSFFN 60

Qy 61 GIKNQAGSGCGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120
Db 61 GIKNQAGSGCGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120

Qy 121 ISEISKSNAVCDPTRQWPCCAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEISKSNAVCDPTRQWPCCAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVAR 180

Qy 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPQMNARIGYYKQYCRQL 240
Db 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPQMNARIGYYKQYCRQL 240

Qy 241 GVDPGPNLTC 250
Db 241 GVDPGPNLTC 250

RESULT 2
US-10-692-367-52
; Sequence 52, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2002-11-06
; PRIOR FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-52

Query Match 97.8%; Score 1377; DB 17; Length 250;
Best Local Similarity 97.2%; Pred. No. 2.1e-107;
Matches 243; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASVVTGSFFN 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASVVTGSFFN 60

Qy 61 GIKNQAGSGCGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120
Db 61 GIKNQAGSGCGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120

Qy 121 ISEISKSNAVCDPTRQWPCCAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEISKSNAVCDPTRQWPCCAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVAR 180

Qy 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPQMNARIGYYKQYCRQL 240
Db 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPQMNARIGYYKQYCRQL 240
```

```
Qy 241 GVDPGPNLTC 250
Db 241 GVDPGPNLTC 250

RESULT 3
US-10-692-367-82
; Sequence 82, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR FILING DATE: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2002-11-06
; PRIOR FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-82

Query Match 97.4%; Score 1372; DB 17; Length 250;
Best Local Similarity 97.2%; Pred. No. 5.4e-107;
Matches 243; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASVVTGSFFN 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQSGGSGGGANVASVVTDAFFN 60

Qy 61 GIKNQAGSGCGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120
Db 61 GIKNQAGSGCGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120

Qy 121 ISEISKSNAVCDPTRQWPCCAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEISKSNAVCDPTRQWPCCAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVAR 180

Qy 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPQMNARIGYYKQYCRQL 240
Db 181 DAVVAFAKALWFNNVHVRVMPQFGATIRAINGALECDGNPQMNARIGYYKQYCRQL 240

Qy 241 GVDPGPNLTC 250
Db 241 GVDPGPNLTC 250

RESULT 4
US-10-692-367-68
; Sequence 68, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR FILING DATE: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2002-11-06
; PRIOR FILING DATE: 2001-11-07
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-68
```

```
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 254
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-68

Query Match          97.0%; Score 1366; DB 17; Length 254;
Best Local Similarity 95.7%; Pred. No. 1.7e-106;
Matches 243; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGSSGG-----GGANVASVVTG 56
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGSSGGGGGGGGGGGGGGANVASVVTG 60

Qy 57 SFFNGIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETG 116
Db 61 SFFNGIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETG 120

Qy 117 HFCYISEISKSNAYCDPTKRWPCAAQGYGRGLQISWNYNYGPAGRDIGFDGLGDPG 176
Db 121 HFCYISEISKSNAYCDPTKRWPCAAQGYGRGLQISWNYNYGPAGRAIGFDGLGDPN 180

Qy 177 RVADAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALBCEGNNPAQMNARIQYKQY 236
Db 181 RVADAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALBCEGNNPAQMNARVGYTKQY 240

Qy 237 CRQLGVDGPNLTC 250
Db 241 CRQLGVDGPNLTC 254

RESULT 5
US-10-692-367-78
; Sequence 78, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 250
; TYPE: PR1

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-56

Query Match          96.6%; Score 1360; DB 17; Length 250;
Best Local Similarity 96.0%; Pred. No. 5.5e-106;
Matches 240; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGSSGGGGGGGGGGANVASVVTGSPFN 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGSSGGGGGGGGGGANVASVVTGSPFN 60

Qy 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETGHPCY 120
Db 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETGHPCY 120

Qy 121 ISEISKSNAYCDPTKRWPCAAQGYGRGLQISWNYNYGPAGRDIGFDGLGDPNVRAR 180
Db 121 ISEISKSNAYCDPTKRWPCAAQGYGRGLQISWNYNYGPAGRAIGFDGLGDPNVRAR 180

Qy 181 DAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALBCEGNNPAQMNARIQYKQYCRQL 240
Db 181 DAVVAFKAALWFMMNNVHRVMPQGFATIRAINGALBCEGNNPAQMNARIQYKQYCRQL 240

Qy 241 GVDGPNLTC 250
Db 241 GVDGPNLTC 250

RESULT 6
US-10-692-367-56
; Sequence 56, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 250
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-56

Query Match          96.6%; Score 1360; DB 17; Length 250;
Best Local Similarity 96.0%; Pred. No. 5.5e-106;
Matches 240; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGSSGGGGGGGGGGANVASVVTGSPFN 60
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDQSGPCRSQGGSSGGGGGGGGGGANVASVVTGSPFN 60

Qy 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETGHPCY 120
Db 61 GIKNQAGSGCGKKNFYTRSAFLSAVKAYPGFAHGSQVQGRREIAAPFAHATHETGHPCY 120
```



Qy 121 ISEISKNAYCDPTKRWPCAAQKYYGRGPIQISWNNYGPAGRDIGFDGLDGPGRVAR 180  
Db 121 ISEISKNAYCDPTKRWPCAAQKYYGRGPIQISWNNYGPAGRDIGFDGLDGPGRVAR 180  
Qy 181 DAVAFKAALFWMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYKYQYCRQL 240  
Db 181 DAVAFKAALFWMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYKYQYCRQL 240  
Qy 241 GVDGPNLTC 250  
Db 241 GVDGPNLTC 250

## RESULT 7

US-10-692-367-44  
; Sequence 44, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-44

Query Match 96.4%; Score 1358; DB 17; Length 250;  
Best Local Similarity 95.6%; Pred. No. 8e-106;  
Matches 239; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGGANVASVVTGSPFN 60  
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGGANVANVTDAFFN 60  
Qy 61 GIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHAHATHETGHFCY 120  
Db 61 GIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSEVERKREIAAFPAHVTHTGHFCY 120  
Qy 121 ISEISKNAYCDPTKRWPCAAQKYYGRGPIQISWNNYGPAGRDIGFDGLDGPGRVAR 180  
Db 121 ISEISKNAYCDPTKRWPCAAQKYYGRGPIQISWNNYGPAGRDIGFDGLDGPGRVAR 180  
Qy 181 DAVAFKAALFWMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYYKYQYCRQL 240  
Db 181 DAVAFKAALFWMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARVGIYKYQYCRQL 240  
Qy 241 GVDGPNLTC 250  
Db 241 GVDGPNLTC 250

## RESULT 8

US-10-692-367-72

; Sequence 72, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/337,029  
; PRIOR FILING DATE: 2001-11-07  
; PRIOR APPLICATION NUMBER: 60/420,666  
; PRIOR FILING DATE: 2002-10-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 72  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Variant sequence produced by shuffling techniques  
US-10-692-367-72

Query Match 96.4%; Score 1357.5; DB 17; Length 257;  
Best Local Similarity 94.2%; Pred. No. 9.1e-106;  
Matches 242; Conservative 4; Mismatches 4; Indels 7; Gaps 1;

Qy 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGG-----GGANVASV 53  
Db 1 SMQNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSSGGGGGGGGGGANVANV 60  
Qy 54 VTGSFFNGIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHAHATH 113  
Db 61 VTDAFFNGIKNOAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHAHATH 120  
Qy 114 ETGHFCYISISKNAYCDPTKRWPCAAQKYYGRGPIQISWNNYGPAGRDIGFDGLG 173  
Db 121 ETGHFCYISISKNAYCDPTKRWPCAAQKYYGRGPIQISWNNYGPAGRDIGFDGLG 180  
Qy 174 DPGHVARDAVAFKAALFWMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYY 233  
Db 181 DPGHVARDAVAFKAALFWMNNVHRVMPQGFATIRAINGALECDGNNPAQMNARIYY 240  
Qy 234 KOYCRQLGVDGPNLTC 250  
Db 241 KOYCRQLGVDGPNLTC 257

## RESULT 9

US-10-692-367-2  
; Sequence 2, Application US/10692367  
; Publication No. US20050050595A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Mathias L.  
; APPLICANT: True, Thom  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Novel compositions with chitinase  
; FILE REFERENCE: 549162000320  
; CURRENT APPLICATION NUMBER: US/10/692,367  
; CURRENT FILING DATE: 2003-10-22  
; PRIOR APPLICATION NUMBER: 10/389,432  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 10/290,086  
; PRIOR FILING DATE: 2002-11-06

```
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Zea mays
US-10-692-367-2

Query Match
  Score 96.0%; DB 17; Length 248;
  Best Local Similarity 96.0%; Pred. No. 3.1e-105;
  Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSFFNGI 62
Db 1 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSFFNGI 60

QY 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 122
Db 61 KSOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 120

QY 123 EISKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVARDA 182
Db 121 EINKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVARDA 180

QY 183 VVAFKAALWFMNNSVHGVVPGFGATTIRAINGALCEGNNPAQMNARIGYTKQYCRQLGV 242
Db 181 VVAFKAALWFMNNSVHGVVPGFGATTIRAINGALCEGNNPAQMNARIGYTKQYCRQLGV 240

QY 243 DPGPNLTC 250
Db 241 DPGPNLTC 248

RESULT 10
US-10-692-367-50
; Sequence 50, Application US/10692367
; Publication No. US200500595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-50

Query Match
  Score 96.0%; DB 17; Length 250;
  Best Local Similarity 94.8%; Pred. No. 3.1e-105;
  Matches 237; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Zea mays
US-10-692-367-2

Query Match
  Score 96.0%; DB 17; Length 248;
  Best Local Similarity 96.0%; Pred. No. 3.1e-105;
  Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSFFNGI 62
Db 1 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSFFNGI 60

QY 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 122
Db 61 KSOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 120

QY 123 EISKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVARDA 182
Db 121 EINKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVARDA 180

QY 183 VVAFKAALWFMNNSVHGVVPGFGATTIRAINGALCEGNNPAQMNARIGYTKQYCRQLGV 242
Db 181 VVAFKAALWFMNNSVHGVVPGFGATTIRAINGALCEGNNPAQMNARIGYTKQYCRQLGV 240

QY 243 DPGPNLTC 250
Db 241 DPGPNLTC 248

RESULT 11
US-10-304-928-2
; Sequence 2, Application US/10304928
; Publication No. US20030101484A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100D
; CURRENT APPLICATION NUMBER: US/10/304,928
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/522,714
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/125,915
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Zea mays
US-10-304-928-2

Query Match
  Score 96.0%; DB 14; Length 281;
  Best Local Similarity 96.0%; Pred. No. 3.5e-105;
  Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSFFNGI 62
Db 34 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGANVASVVTGSFFNGI 93

QY 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 122
Db 94 KSOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAPFAHATHETGHFCYIS 153

QY 123 EISKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVARDA 182
Db 154 EINKSNAYCDPTKRWPCAAAGQKYYGRGPLQISWNNYGPAGRDIGFDGLGDPGRVARDA 213

QY 183 VVAFKAALWFMNNSVHGVVPGFGATTIRAINGALCEGNNPAQMNARIGYTKQYCRQLGV 242
Db 214 VVAFKAALWFMNNSVHGVVPGFGATTIRAINGALCEGNNPAQMNARIGYTKQYCRQLGV 273

QY 243 DPGPNLTC 250
Db 274 DPGPNLTC 281

RESULT 12
US-10-367-54
; Sequence 54, Application US/10692367
; ; ;
```

```
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-54

Query Match          95.9%; Score 1350; DB 17; Length 250;
Best Local Similarity 94.4%; Pred. No. 3.8e-105;
Matches 236; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQSGGSGGGANVASVVTGSPFN 60
Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQSGGSGGGANVASVVTGSPFN 60

Qy 61 GIKQAGSGCGKGFYTRSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHEGHFCY 120
Db 61 GIKQAGSGCGKGFYTRSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHEGHFCY 120

Qy 121 ISEISKSNAAYCDPTKRWPCAAAGQKYGRGKPLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180
Db 121 ISEISKSNAAYCDPTKRWPCAAAGQKYGRGKPLQISWNYNYGPAGRDIGFDGLGDPGRVAR 180

Qy 181 DAVAFKALFWNNVHVRVMPQGFATIRANGALECDGNNPAQMNARIQYKQYCRQL 240
Db 181 DAVAFKALFWNNVHVRVMPQGFATIRANGALECDGNNPAQMNARIQYKQYCRQL 240

Qy 241 GVDPGPNLTC 250
Db 241 GVDPGPNLTC 250

RESULT 13
US-10-692-367-74
; Sequence 74, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-22

Query Match          95.7%; Score 1348; DB 17; Length 250;
Best Local Similarity 95.2%; Pred. No. 5.5e-105;
Matches 238; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-22

Query Match          95.8%; Score 1349; DB 17; Length 256;
Best Local Similarity 93.8%; Pred. No. 4.7e-105;
Matches 240; Conservative 4; Mismatches 6; Indels 6; Gaps 1;

Qy 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQSGGSGGGANVASV 54
Db 1 SMQNCGCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQSGGSGGGANVASV 60

Qy 55 TGSFFNGIKNOAGSGCGKGFYTRSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHE 114
Db 61 TDSFFNGIKNOAGSGCGKGFYTRSAFLSAVKAYPGFAHGSQVQGRKREIAAPFAHATHE 120

Qy 115 TGHFCYISEISKSNAAYCDPTKRWPCAAAGQKYGRGKPLQISWNYNYGPAGRDIGFDGLGD 174
Db 121 TGHFCYINEISKSNAAYCDPTKRWPCAAAGQKYGRGKPLQISWNYNYGPAGRDIGFDGLGD 180

Qy 175 PGRVARDVAVFAKALFWNNVHVRVMPQGFATIRANGALECDGNNPAQMNARIQYK 234
Db 181 PGRVARDVAVFAKALFWNNVHVRVMPQGFATIRANGALECDGNNPAQMNARIQYK 240

Qy 235 QYCRQLGVDPGPNLTC 250
Db 241 QYCRQLGVDPGPNLTC 256

RESULT 14
US-10-692-367-22
; Sequence 22, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; FILE REFERENCE: 549162000320
; CURRENT APPLICATION NUMBER: US/10/692,367
; CURRENT FILING DATE: 2003-10-22
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-22
```

```
Qy 1 SMQCGCOPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGSSGGGANVASVVTGSFFN 60
Db 1 SMQCGCAGLCCSRFGYCGTTDBYCGDGCOSGCRSGGGSSGGGANVASVVTGSFFN 60
Qy 61 GIKQAGSGCEGKNFYTRSAFLSAFKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120
Db 61 GIKQAGSGCEGKNFYTRSAFLSAFKAYPGFAHGSQVQKREIAAPFAHATHETHGFCY 120
Qy 121 ISEISKSNAYCDPTKQWPCAAQKTYGRGPIQISWNNYGPAGRIDGFDGLGDPGRVAR 180
Db 121 ISEISKSNAYCDPTKQWPCAAQKTYGRGPIQISWNNYGPAGRIDGFDGLGDPGRVAR 180
Qy 181 DAVVAFKAALWFMNNVHRVMPQGFATIRAINGALECDGNPAQMNARIGYKCYCROL 240
Db 181 DAVVAFKAALWFMNNVHRVMPQGFATIRAINGALECDGNPAQMNARIGYKCYCROL 240
Qy 241 GVDPGPNLTC 250
Db 241 RVDPGPNLTC 250
```

## RESULT 15

```
US-10-692-367-48
; Sequence 48, Application US/10692367
; Publication No. US20050050595A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Mathias L.
; APPLICANT: True, Thom
; APPLICANT: Simmons, Carl R.
; APPLICANT: Yalpani, Nasser
; TITLE OF INVENTION: Novel compositions with chitinase
; TITLE OF INVENTION: activity
; FILE REFERENCE: 54916200320
; CURRENT APPLICATION NUMBER: US/10/692,367
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 10/389,432
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 10/290,086
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/337,029
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/420,666
; PRIOR FILING DATE: 2002-10-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence produced by shuffling techniques
US-10-692-367-48
```

```
Query Match 95.7%; Score 1348; DB 17; Length 256;
Best Local Similarity 93.8%; Pred. No. 5.7e-105;
Matches 240; Conservative 4; Mismatches 6; Indels 6; Gaps 1;
Qy 1 SMQCGCOPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGSSGGGANVASV 54
Db 1 SMQCGCOPNVCCSKFGYCGTTDEYCGDGCOSGCRSGGGSSGGGANVASV 60
Qy 55 TGSFNGIKQAGSGCEGKNFYTRSAFLSAFKAYPGFAHGSQVQKREIAAPFAHATHE 114
Db 61 TGSFNGIKQAGSGCEGKNFYTRSAFLSAFKAYPGFAHGSQVQKREIAAPFAHATHE 120
Qy 115 TGHCYISETSKSNAYCDPTKQWPCAAQKTYGRGPIQISWNNYGPAGRIDGFDGLD 174
Db 121 TGHPYISETSKSNAYCDPTKQWPCAAQKTYGRGPIQISWNNYGPAGRIDGFDGLD 180
Qy 175 PGRVARDAVAFKAALWFMNNVHRVMPQGFATIRAINGALECDGNPAQMNARIGYK 234
Db 181 PGRVARDAVAFKAALWFMNNVHRVMPQGFATIRAINGALECDGNPAQMNARIGYK 240
```

```
Qy 235 QYCRQLGVDPGPNLTC 250
Db 241 QYCRQLGVDPGPNLTC 256
Search completed: May 24, 2005, 13:12:28
Job time : 90.2505 secs
```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2005, 12:39:31 ; Search time 24.6548 Seconds  
(without alignment)  
975.638 Million cell updates/sec

Title: US-10-692-367-70

Perfect score: 1408

Sequence: 1 SMQNGCQPNVCCSKFGYCG.....GYKQYCRQLGVDPGPNLTC 250

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1314.5	93.4	268	2 B42424	chitinase (EC 3.2.2)
2	1265.5	89.9	280	2 A42424	chitinase (EC 3.2.2)
3	873	62.0	268	2 S25311	chitinase (EC 3.2.2)
4	859	61.0	261	2 S51678	chitinase (EC 3.2.2)
5	834.5	59.3	273	2 T47601	class IV chitinase
6	829.5	58.9	288	2 S46536	chitinase (EC 3.2.2)
7	829	58.9	264	2 A84868	probable endochitini
8	823.5	58.5	270	2 S16579	chitinase (EC 3.2.2)
9	805	57.2	249	2 S57476	chitinase class 4
10	802.5	57.0	229	2 T03405	probable chitinase
11	788.5	56.0	265	2 H84867	probable endochitini
12	783	55.6	276	2 T09131	chitinase (EC 3.2.2)
13	768	54.5	266	2 T14345	chitinase (EC 3.2.2)
14	767	54.5	266	2 T14348	probable chitinase
15	762	54.1	268	2 T14341	probable chitinase
16	754	53.6	268	2 T14344	chitinase (EC 3.2.2)
17	744	52.8	250	1 A44039	chitinase (EC 3.2.2)
18	733.5	52.1	208	2 J80125	chitinase (EC 3.2.2)
19	717	50.9	277	2 G84867	probable endochitini
20	712.5	50.6	281	2 C84868	probable endochitini
21	693.5	49.3	283	2 D84868	probable endochitini
22	691.5	49.1	247	2 S15645	chitinase (EC 3.2.2)
23	682.5	48.5	266	2 S55778	chitinase class IV
24	639	45.4	327	2 T09687	chitinase (EC 3.2.2)
25	627.5	44.6	328	1 S05426	chitinase (EC 3.2.2)
26	621	44.1	324	2 S20981	chitinase (EC 3.2.2)
27	619.5	44.0	323	2 S56694	chitinase (EC 3.2.2)
28	611.5	43.4	324	2 T03614	chitinase (EC 3.2.2)
29	611.5	43.4	329	2 S08627	chitinase (EC 3.2.2)

#### RESULT 1

B42424

chitinase (EC 3.2.1.14) precursor - maize (fragment)

C;Species: Zea mays (maize)

C;Date: 12-Mar-1993 #sequence\_revision 03-Feb-1994 #text\_change 10-Jul-1998

C;Accession: B42424

R;Huynh, Q.K.; Hironaka, C.M.; Levine, E.B.; Smith, C.E.; Borgmeyer, J.R.; Shah, D.M.

J. Biol. Chem. 267, 6635-6640, 1992

A;Title: Antifungal proteins from plants. Purification, molecular cloning, and antifunga

A;Reference number: A42424; MUID:92202208; PMID:1551872

A;Accession: B42424

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-268 <HUY>

A;Cross-references: GB:M84165

A;Note: The authors translated the codon AAG for residue 104 as Asn, GGC for residue 105

0 as Ile, CMA for residue 231 as Asn and CGC for residue 232 as Gly

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;20-55/Domain: hevein chitin-binding domain homology <HCB>

F;70-268/Domain: plant chitinase homology <PCH>

Query Match 93.4%; Score 1314.5; DB 2; Length 268;

Best Local Similarity 93.6%; Pred. No. 1.4e-95;

Matches 233; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 3 QNCGCPNVCCSKFGYCGTGTDEYCGDCGCGPCRSQ-GGGSSGGGANVASVVTGSPFNG 61

Db 20 QNCGCPNVCCSKFGYCGTGTDEYCGDCGCGPCRSQ-GGGSSGGGANVASVVTGSPFNG 79

QY 62 IKNQAGSGCEGKNFYTRSAFLSAVKYPGFAHGGSQVQGRKRIAAFAFAHATHETGHFCYI 121

Db 80 IKNQAGSGCEGKNFYTRSAFLSAVKYPGFAHGGSQVQGRKRIAAFAFAHATHETGHFCYI 139

QY 122 SEISKSNAYCDPTKQWPCAAQKYRGPIQISWNTNYGPAGRDIGPDGLDGPGRVARD 181

Db 140 SEINKSNAYCDPTKQWPCAAQKYRGPIQISWNTNYGPAGRDIGPDGLDGPGRVARD 199

QY 182 AVAFKALWFMNNVHRVMPQGFATITNGALECDGNNPAQWNRARIGYKQYCROLG 241

Db 200 AVAFKALWFMNNVHRVMPQGFATITNGALECDGNNPAQWNRARIGYKQYCROLG 259

QY 242 VDPGPNLTC 250

Db 260 VDPGPNLTC 268

#### RESULT 2

A42424

chitinase (EC 3.2.1.14) A - maize

C;Species: Zea mays (maize)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Mar-1999

C;Accession: A42424; A42260  
R;Huynh, Q.K.; Hironaka, C.M.; Levine, E.B.; Smith, C.E.; Borgmeyer, J.R.; Shah, D.M.  
J. Biol. Chem. 267, 6635-6640, 1992  
A;Title: Antifungal proteins from plants. Purification, molecular cloning, and antifungal activity.  
A;Reference number: A42424; MUID:92202208; PMID:1551872  
A;Accession: A42424  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-280 <HUY>  
A;Experimental source: seed  
A;Note: sequence inconsistent with nucleotide translation  
R;Verbarg, J.G.; Smith, C.E.; Lisek, C.A.; Huynh, Q.K.  
J. Biol. Chem. 267, 3886-3893, 1992  
A;Title: Identification of an essential tyrosine residue in the catalytic site of a chitinase from *Aspergillus fumigatus*.  
A;Reference number: A42260; MUID:92156129; PMID:1740436  
A;Accession: A42260  
A;Molecule type: protein  
A;Residues: 180-195 <VER>  
A;Note: the residue designated 'X' was determined to be derivatized tyrosine; therefore, the residue is not shown.  
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;26-61/Domain: hevein chitin-binding domain homology <HCB>  
F;82-280/Domain: plant chitinase homology <PCH>  
F;188/Active site: Tyr #status predicted

Query Match 89.9%; Score 1265.5; DB 2; Length 280;  
Best Local Similarity 86.7%; Pred. No. 9.7e-92;  
Matches 221; Conservative 13; Mismatches 14; Indels 7; Gaps 1;

Qy 3 QNCGQPNVCCSKFGYCGTDTBYCGDQCGQSPCRSGGGSGG-----GGANVASVVT 55  
Db 26 QNCGQPNVCCSKFGYCGTDTBYCGDQCGQSPCRSGGGSGG-----GGANVASVVT 85

Qy 56 GSFFNGIKNAGSGGEGNFFYTRSAFLSAVKAYPGFAHGGQVQKRIIAFFAHATHET 115  
Db 86 DAFENGIKNAGSGGEGNFFYTRSAFLSAVKAYPGFAHGGQVQKRIIAFFAHATHET 145

Qy 116 GHFCYISISKSNAYCDPTKQWPCAAQKYYGRPLQISWNNYGPAGRDIGDGLGDP 175  
Db 146 GHFCYISISKSNAYCDPTKQWPCAAQKYYGRPLQISWNNYGPAGRDIGDGLGDP 205

Qy 176 GRVADAVVAFKAALWFNNVHVRVMPQGFATIRAINGALCEDGNNPAQNNARIGYYKQ 235  
Db 206 NEVADAVVAFKAALWFNNVHVRVMPQGFATIRAINGALCEDGNNPAQNNARIGYYKQ 265

Qy 236 YCQLGVDPGNLTC 250  
Db 266 YCQLGVDPGNLTC 280

RESULT 3  
S25311  
chitinase (EC 3.2.1.14) precursor - rape  
C;Species: Brassica napus (rape)  
C;Date: 26-Feb-1998 #sequence\_revision 26-Feb-1998 #text\_change 09-Jul-2004  
C;Accession: S25311  
R;Raemussen, U.; Bojsen, K.; Collinge, D.B.  
Plant Mol. Biol. 20, 277-287, 1992  
A;Title: Cloning and characterization of a pathogen-induced chitinase in *Brassica napus*.  
A;Reference number: S25311; MUID:93004480; PMID:1391771  
A;Accession: S25311  
A;Molecule type: mRNA  
A;Residues: 1-268 <RAS>  
A;Cross-references: UNIPROT:Q06209; EMBL:X61488; NID:917798; PIDN:CAA43708.1; PID:g17799  
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-268/Product: chitinase #status predicted <MAT>  
F;25-60/Domain: hevein chitin-binding domain homology <HCB>  
F;74-268/Domain: plant chitinase homology <PCH>

Query Match 62.0%; Score 873; DB 2; Length 268;  
Best Local Similarity 61.4%; Pred. No. 4.3e-61;  
Matches 153; Conservative 33; Mismatches 57; Indels 6; Gaps 3;

Qy 3 QNCGQPNVCCSKFGYCGTDTBYCGDQCGQSPCRSGGGSGG-----GGANVASVVTGSPFNGI 62  
Db 25 QNCGCAPNLCCSQFGYCGTDTBYCGDQCGQSPCRSGGGSGG-----GGANVASVVTGSPFNGI 84

Qy 63 KNOAGSGGEGNFFYTRSAFLSAVKAYPGFAHGGQVQKRIIAFFAHATHETGHFCYIS 122  
Db 85 INQAGGCGAGNFFYTRSAFLSAVKAYPGFAHGGQVQKRIIAFFAHATHETGHFCYIS 140

Qy 123 EIS-KSNAYCDPTKQWPCAAQKYYGRPLQISWNNYGPAGRDIGDGLGDPGRVARD 181  
Db 141 EINGASRDYCDENNRPYCAPGKGYGRGPIQLSWNNYGPAGRDIGDGLGDPGRVARD 200

Qy 182 AVAVAFKAALWFNNVHVRVMPQGFATIRAINGALCEDGNNPAQNNARIGYYKQYCHQLG 241  
Db 201 PTVAFTGLWFMNVRVLPVNLQGFATIRAINGALCEDGNNPAQNNARIRYYRDYCGQLG 259

Qy 242 VDPGNLTC 250  
Db 260 VDPGNLTC 268

RESULT 4  
S51678  
chitinase (EC 3.2.1.14) class I - European elder (fragment)  
N;Alternate names: pathogenesis-related protein PR-3 type  
C;Species: Sambucus nigra (European elder)  
C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S51678  
R;Coupe, S.A.; Taylor, J.E.; Roberts, J.A.  
submitted to the EMBL Data Library, December 1994  
A;Description: Characterisation of mRNAs that encode pathogenesis-related proteins that  
A;Reference number: S51645  
A;Accession: S51678  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <COU>  
A;Cross-references: UNIPROT:Q43150; EMBL:Z46948; NID:9603881; PIDN:CAA87072.1; PID:g6038  
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;16-51/Domain: hevein chitin-binding domain homology <HCB>  
F;61-261/Domain: plant chitinase homology <PCH>

Query Match 61.0%; Score 859; DB 2; Length 261;  
Best Local Similarity 60.5%; Pred. No. 5.2e-60;  
Matches 153; Conservative 31; Mismatches 61; Indels 8; Gaps 4;

Qy 1 SMQNCQPNVCCSKFGYCGTDTBYCGDQCGQSPCRSGGGSGG-----GGANVASVVTGSPFN 60  
Db 14 SGQNCQCAPNLCCSQFGYCGTDTBYCGDQCGQSPCRSGGGSGG-----GGANVASVVTGSPFN 69

Qy 61 GIKNAGSGGEGNFFYTRSAFLSAVKAYPGFAHGGQVQKRIIAFFAHATHETGHFCY 120  
Db 70 GLISPNG-GCAGRGFYTRDAFLRAASFPYPAFGTGTGSDRRRREIAAFAHTSHETGRFCY 128

Qy 121 ISEIS-KSNAYCDPTKQWPCAAQKYYGRPLQISWNNYGPAGRDIGDGLGDPGRVA 179  
Db 129 REEINGASRDYCDENNRPYCAPGKGYGRGPIQLSWNNYGPAGRDIGDGLGDPGRVA 188

Qy 180 RDAVAVAFKAALWFNNVHVRVMPQGFATIRAINGALCEDGNNPAQNNARIGYYKQY 237  
Db 189 RDPVISFRASLWFMNVRVLPVNLQGFATIRAINGALCEDGNNPAQNNARIRYYRDYCGQLG 248

Qy 238 RQLGVDPGNLTC 250  
Db 249 NQLSVPPGGNLC 261

RESULT 5  
T47601



```
class IV chitinase (CHIV) - Arabidopsis thaliana
N:Alternate names: protein T12E18.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47601
R:Blocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M. Mewes,
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224469
A:Accession: T47601
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <BL0>
A:Cross-references: UNIPROT:O9M2U5; EMBL:AL132971
A:Experimental source: cultivar Columbia; BAC clone T12E18
C:Genetics:
A:Map position: 3
A:Introns: 139/1
A:Note: T12E18.110
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

Query Match 59.3%; Score 834.5; DB 2; Length 273;
Best Local Similarity 60.2%; Pred. No. 4.4e-58;
Matches 150; Conservative 23; Mismatches 71; Indels 5; Gaps 2;

Qy 3 QNCGQPNVCCSKFGYCGTDEYCGDGCQSGPCRSGGGSGGGGANNVAVVTGSPFNGI 62
Db 29 QNCGSSBLCCSFQFCGNTSDYCGVCGQGPCFA-----PPANGVSVAEIVTQEFFNGI 84

Qy 63 KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVQVKREIAAFFAHATHETGHFCYIS 122
Db 85 ISQAASSCAGNRFYSRGAFLEALDSYSRFRGVSTDDSRREIAAFFAHVTHETGHFCYIE 144

Qy 123 EI-SKSNAYCDPTKRWPCAAGQKYGRGPIQISWNNYGPAGRDIGFDGLDGFGRVARD 181
Db 145 EIDGASKDYCDENATQYPCNENKGYGRGPIQLSWNFYGPAGTAIGFDGLNAPETVATD 204

Qy 192 AVAFKAALWFWMNNVHRVMPQGGATIRANGALECDGNPAQMNARIGYKQYCRQLG 241
Db 205 PVISPKTALWYTNRVQPVISQFGATIRANGALECDGANTATVQARVRYTTCRQLG 264

Qy 242 VDPGNLTC 250
Db 265 VDPGNLTC 273

RESULT 6
S46536
chitinase (EC 3.2.1.14) - beet
C:Species: Beta vulgaris (beet)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S46536
R:Nielsen, K.K.; Bojlsen, K.; Roepstorff, P.; Mikkelsen, J.D.
Plant Mol. Biol. 25, 241-257, 1994
A:Title: A hydroxyproline-containing class IV chitinase of sugar beet is glycosylated w
A:Reference number: S46536; MUID:94289648; PMID:8018873
A:Accession: S46536
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-288 <NIB>
A:Cross-references: UNIPROT:P42820; EMBL:L25826; NID:g510277; PID:AAA32916.1; PID:g5102
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:28-64/Domain: hevein chitin-binding domain homology <HCB>
F:89-288/Domain: plant chitinase homology <PCH>

Query Match 58.9%; Score 829.5; DB 2; Length 288;
Best Local Similarity 59.3%; Pred. No. 1.1e-57;
Matches 156; Conservative 30; Mismatches 60; Indels 17; Gaps 5;

Qy 3 QNCGQPNVCCSKFGYCGTDEYCGDGCQSGPCRSGGGSGGGGANNVAVVTGSPFNGI 62
Db 28 QNCGCAPNLCCSNFQFCGTGTGYCGVGNQCGQSGPCGGTPTTPTTPTTGTGGGGSSV 87
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Qy 51 ASVVTGSPFNGIKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVQVKREIAAFPAH 110
Db 88 SDIVSQAFFDGIQGAASCPGRKNFYTRAAPFLSAVD--PKFNEGSSDDNKRETAAPFAH 145

Qy 111 ATHTGHFCYISEI--SKSNAYCDPTK-RQWPCAAGQKYGRGPIQISWNNYGPAGRDI 167
Db 146 ISHETTLNLCHIEERDGDVDAYCDQDKAAQYPCAAGKYYGRGPLQLSWNNYALAGQAI 205

Qy 168 GFDGLDGFGRVARDVAVFAALWFWMNNVHRVMPQGGATIRANGALECDGNPAQMN 227
Db 206 GFDGLGNPEKATDVNTSFKAAWFMWMTNVHVSVMNQGFGATTKAINGALECNGQDOAN 265

Qy 228 ARIGYKQYCRQLGVDGPNLTC 250
Db 266 DRIOFYKKYCADFGVAPGDNLTC 288

RESULT 7
A84868
probable endochitinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: A84868
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
nuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84868
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: UNIPROT:O24658; GB:AR002093; NID:g2281111; PID:AAB64047.1; GSPDB:GN
C:Genetics:
A:Gene: At2g43590
A:Map position: 2
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1

Query Match 58.9%; Score 829; DB 2; Length 264;
Best Local Similarity 59.4%; Pred. No. 1.2e-57;
Matches 148; Conservative 33; Mismatches 58; Indels 10; Gaps 5;

Qy 3 QNCGQPNVCCSKFGYCGTDEYCGDGCQSGPCRSGGGSGGGGANNVAVVTGSPFNGI 62
Db 25 QNCGCAPNLCCSFQYCGTDDAYCGVGRSGPCCR--SGTPTGG--SVGSIIVTQGFNNI 80

Qy 63. KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGVQVKREIAAFFAHATHETGHFCYIS 122
Db 81 INQAGNCGAGKRFYTRDSFVNAAATTFNFANSVT----RREIATWFAHTHETGHFCYIE 136

Qy 123 EIS-KSNAYCDPTKRWPCAAGQKYGRGPIQISWNNYGPAGRDIGFDGLDGFGRVARD 181
Db 137 EINGATNYCOSSNTQYPCAPGKYGRGPIQLSWNNYGPAGQSLGLDLRLQPELVGSN 196

Qy 182 AVAFKAALWFWMNNVHRVMPQGGATIRANGALECDGNPAQMNARIGYKQYCRQLG 241
Db 197 PTVAFTGLMFWMNSVRPVLNQGGATIRANG-MECNGNSGAVNARIGYRDYCGQLG 255

Qy 242 VDPGNLTC 250
Db 256 VDPGNLSC 264

RESULT 8
S16579
chitinase (EC 3.2.1.14) precursor - kidney bean
C:Species: Phaseolus vulgaris (kidney bean)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S16579
R:Margis-Pinheiro, M.; Metz-Boutigue, M.H.; Awade, A.; de Tapia, M.; le Ret, M.; Burkard
Plant Mol. Biol. 17, 243-253, 1991
A:Title: Isolation of a complementary DNA encoding the bean PR4 chitinase: an acidic en
```

A;Reference number: S16579; MUID:91322521; PMID:1863776

A;Accession: S16579

A;Molecule type: mRNA

A;Residues: 1-270 <MAB>

A;Cross-references: UNIPROT:P27054; EMBL:X57187

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;24-59/Domain: hevein chitin-binding domain homology <HCB>

F;70-270/Domain: plant chitinase homology <PCH>

Query Match 58.5%; Score 823.5; DB 2; Length 270;

Best Local Similarity 59.7%; Pred. No. 3.2e-56;

Matches 151; Conservative 28; Mismatches 67; Indels 7; Gaps 4;

Qy 1 SMQNGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGSSGGGGANV-ASVVTGSPF 59

Db 22 SAQNGCGAEGJCCSQYGYCGTGEDYCGTGCGQCGPCTTASPPPSN----NVNADILITADFL 77

Qy 60 NGIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKRIAAFFAHATHETGHFC 119

Db 78 NGIIDQADSGCAGKNFYTRDAFLSALNSYTDGFRVGSDDSKRIIAAFAHFTTHETGHFC 137

Qy 120 YISEI-SKSNAYCDPTK-RQWPCAGQKYGRGPLOISWNNYNYGPAGRIDGFDGLGDPGR 177

Db 138 YIEEDGASKDYCDDEESIAQYPCSSKGYGHRGPIQLSNFNYGPAGSNFDFGLGAPET 197

Qy 178 VARDAAVAFKAALWFMMNNVHRVMPQGFATIRAINGALECDGNPAQMNARIQYKQYC 237

Db 198 VSNDDVVSFKTALWYMOHVRPVINOQFGAIIRAINGALECDGANPTTVQARVNYTYEYC 257

Qy 238 RQLGVDPGPNLTC 250

Db 258 RQLGVATGDNLTTC 270

#### RESULT 9

RS7476

chitinase class 4 - cowpea (fragment)

C;Species: Vigna unguiculata (cowpea)

C;Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 09-Jul-2004

C;Accession: S57476

R;Vivo, L.F.T.; Broughton, W.; Krause, A.

submitted to the EMBL Data Library, June 1995

A;Reference number: S57468

A;Accession: S57476

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-249 <VOL>

A;Cross-references: UNIPROT:Q43686; EMBL:X88803; NID:9871767; PIDN:CAA61281.1; PID:98717

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl

F;4-39/Domain: hevein chitin-binding domain homology <HCB>

F;50-249/Domain: plant chitinase homology <PCH>

Query Match 57.2%; Score 805; DB 2; Length 249;

Best Local Similarity 59.5%; Pred. No. 8.2e-56;

Matches 150; Conservative 27; Mismatches 69; Indels 6; Gaps 4;

Qy 1 SMQNGCQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGSSGGGGANVASVVTGSPFN 60

Db 2 SAQNGCGAEGJCCSQYGYCGTGEEYCGTGCGQCGPCTSS---SSSIENNWNVADIIVTDAPFN 58

Qy 61 GIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKRIIAAFAHATHETGHFCY 120

Db 59 GIIDQADSGCVKSFYARDAFLSALDSYTDGFRVGSDDSKRIIAAFAHFTTHETGHFCY 118

Qy 121 ISEI-SKSNAYCDPTK-RQWPCAGQKYGRGPLOISWNNYNYGPAGRIDGFDGLGDPGRV 178

Db 119 IEEIDGASKDYCDDEESIAQYPCSS-SRGYTVVPVQLSNFNYGPAGANNPFDGLGPETV 177

Qy 179 ARDAVAVFKAALWFMMNNVHRVMPQGFATIRAINGALECDGNPAQMNARIQYKQYCR 238

Db 178 SNDDVVSFKTALWYMOHVRPVINOQFGAATIRAINQLECDGANPSTVQARVNYTYEYCR 237

Qy 239 QLGVDPGPNLTC 250

Db 238 QLGVDTCGNLTTC 249

#### RESULT 10

T03405

probable chitinase (BC 3.2.1.14) IIB - rice

C;Species: Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004

C;Accession: T03405

R;Truong, N.; Itoh, Y.

submitted to the EMBL Data Library, April 1997

A;Description: Nucleotide sequence of rice class II chitinase cDNA.

A;Reference number: Z14936

A;Accession: T03405

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-229 <TRU>

A;Cross-references: UNIPROT:O04138; EMBL:AB003194

A;Experimental source: cv. Nipponbare

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl

C;Keywords: Glycosidase; hydrolase; polysaccharide degradation

F;30-229/Domain: plant chitinase homology <PCH>

Query Match 57.0%; Score 802.5; DB 2; Length 229;

Best Local Similarity 68.3%; Pred. No. 1.2e-55;

Matches 140; Conservative 27; Mismatches 37; Indels 1; Gaps 1;

Qy 47 GANVASVVTGSPFNGIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGGSQVQGRKRIAA 106

Db 25 GVSVESVVTTEAFFNGIKNAPNGCAGKSFYTRQSFNLNARSYSFGFANDRTDSDSKREIAA 84

Qy 107 FEAHATHETGHFCYISEISKSNA-YCDPTKRWPCAGQKYGRGPLOISWNNYNYGPAGR 165

Db 85 FFAHVTHETGHMCYINEINGANNMDYCDKSNKQPCQPKKYGRGPLOISWNNYNYGPAGK 144

Qy 166 DIGFDGLGDPGRVARDAAVAFKAALWFMMNNVHRVMPQGFATIRAINGALECDGNPPAQ 225

Db 145 NIGFDGLRDPDKVAQDPTISFKTALWFMMNNVHQVMSQSGFATIRAINGALECKGNKPGA 204

Qy 226 MNARIGYKQYCRQLGVDPGPNLTC 250

Db 205 VNARVNYKYDCRQFGVSGPNLYC 229

#### RESULT 11

H84867

probable endochitinase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: H84867

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84867

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-265 <STO>

A;Cross-references: UNIPROT:O24598; GB:AB002093; NID:g2281112; PIDN:AB64048.1; GSPDB:GN

C;Genetics:

A;Gene: At2g43580

A;Map position: 2

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl

Query Match 56.0%; Score 788.5; DB 2; Length 265;

Best Local Similarity 57.0%; Pred. No. 1.7e-54;

Matches 142; Conservative 34; Mismatches 64; Indels 9; Gaps 4;

Qy 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSQGGSSGGGGANVASVVTGSPFNGI 62

[illegible]

RESULT 12.  
T09131  
chitinase (EC 3.2.1.14) - white spruce  
C:Species: Picea glauca (white spruce)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T09131  
R:Dong, J.Z.; Dunstan, D.I.  
submitted to the EMBL Data Library, January 1996  
A:Description: Developmental regulation of a gene encoding chitinase during somatic embryo  
A:Reference number: Z16579  
A:Accession: T09131  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-276 <DON>  
A:Cross-references: UNIPROT:Q40838; EMBL:L42467; NID:g1161164; PID:g1161165  
A:Genetics:  
A:Gene: chi  
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl  
C:Keywords: Glycosidase; hydrolase; polysaccharide degradation  
F:27-62/Domain: hevein chitin-binding domain homology <HCB>

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RESULT 13
T14345
chitinase (EC 3.2.1.14) EP3-3/E7, class IV - carrot
C:Species: Daucus carota (carrot)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14345
R:Kraigh, K.; De Vries, S.C.

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submitted to the EMBL Data Library, March 1996  
A/Reference number: Z17995  
A/Accession: T14345  
A/Status: preliminary; translated from GB/EMBL/DBDJ  
A/Molecule type: mRNA  
A/Residues: 1-266 <RA>  
A/Cross-references: UNIPROT:Q96410; EMBL:U52847; NID:gl549333; PID:gl549333  
A/Experimental source: strain sg/66 trophy  
C/Genetics:  
A/Gene: EP3  
C/Function:  
A/Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl  
A/Pathway: polysaccharide degradation  
C/Superfamily: lectin-related plant chitinase; hevein chitin-binding domain  
C/Keywords: glycosidase; hydrolase; polysaccharide degradation  
F/21-56/Domain: hevein chitin-binding domain homology <HCB>  
F/69-266/Domain: plant chitinase homology <PCH>

RESULT 14  
T14348  
probable chitinase (EC 3.2.1.14) EP3B/E6, class IV - carrot  
C;Species: Daucus carota (Carrot)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T14348  
R;Kragh, K.; De Vries, S.C.  
submitted to the EMBL Data Library, March 1996  
A;Reference number: Z17995  
A;Accession: T14348  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-266 <RA>  
A;Cross-references: UNIPROT:Q96411; EMBL:U52848; NID:gl549334; PID:gl549335  
A;Experimental source: strain sg766 trophy  
C;Genetics:  
A;Note: EP3  
C;Function:  
A;Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl  
A;Pathway: polysaccharide degradation  
C;Superfamily: lectin-related plant chitinase; hevvin chitin-binding domain  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;21-56/Domain: hevvin chitin-binding domain homology <HCB>  
F;69-466/Domain: plant chitinase homology <PCH>

1 SMONCGCOPNVCCSKFGYCGTTDEYCGDGCOSGPCRSGGGSGGGANVASVVTGSFFN 60

Db	19	SAQNCNCTAGLCCSRKHYCGTTSDYCGEGCQAGPC-TNTAPTGGGNGVSVADIVTDDFFN	77
Qy	61	GIKNQAGSGCGKKNFYTSAFLSAVKAYPGFAHGSGVQGXREIAAFPAHAHATHETGHFCY	120
Db	78	GIISQATGDCDGKKNFYTSAFLSALNALQSYSSFGTSGSADDSKREIAAFPAHAHATHETGYFCH	137
Qy	121	ISETIS-KSNAYCDPTKROWPCAAQKYYGRGFLQISWNNYNGPACRDIGFDGLGDPGRVA	179
Db	138	KEETNGRDKNYCE-SKAGYPCNVNKKYFGRGFLQITWNNYIDAGNSNDFDGLNPDIVA	196
Qy	180	RDVAVFAKALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNAIGYYKQYCRQ	239
Db	199	SDAVVSFKTALWYWKVQSVTSQGFATIRAIN-SIECNGGSPDAVNSRVSLNSYCSK	255
Qy	240	LGVDPGPNLTC	250
Db	256	FGVAPGDNQRC	266
RESULT 15			
T14341			
probable chitinase (EC 3.2.1.14) EP3-1/H5, class IV - carrot (fragment)			
C;Species: Daucus carota (carrot)			
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004			
C;Accession: T14341			
R;Kragh, K.; Toonen, M.A.J.; Bucherna, N.; Lo Schiavo, P.; Hendriks, T.; Meijer, E.A.; K			
Plant Mol. Biol. 31, 631-645, 1996			
A;Title: Characterization of carrot chitinases able to rescue the temperature-sensitive			
A;Reference number: Z17992; MUID:96382431; PMID:8790295			
A;Accession: T14341			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-268 <KRA>			
A;Cross-references: UNIPROT:Q96408; EMBL:U52845; NID:gl549328; PIDN:AAC49435.1; PID:gl54			
A;Experimental source: strain sg766 trophy			
C;Genetics:			
A;Note: EP3			
C;Function:			
A;Description: catalyzes the hydrolysis of the beta-1,4-linkages of N-acetyl-D-glucosami			
A;Pathway: polysaccharide degradation			
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl			
C;Keywords: glycosidase; hydrolase; polysaccharide degradation			
Query Match 54.1%; Score 762; DB 2; Length 268;			
Best Local Similarity 55.4%; Pred. No. 2e-52;			
Matches 139; Conservative 33; Mismatches 75; Indels 4; Gaps 4;			
Qy	1	SMQNGCQPNVCCSKFYCGTTDEYCGDGCGPCRCGGSGGGGANVASVVTGSPFN	60
Db	21	SAQNCNCAAGLCCSKYGYCGTTSDYCGEGCQAGPC-TNSAPSGGNAVSVADIVTDDFFN	79
Qy	61	GIKNQAGSGCGKKNFYTSAFLSAVKAYPGFAHGSGVQGXREIAAFPAHAHATHETGHFCY	120
Db	80	GIISQATGDCDGKKNFYTSAFLSALNALQSYSSFGTSGSADDSKREIAAFPAHAHATHETGYFCH	139
Qy	121	ISETIS-KSNAYCDPTKROWPCAAQKYYGRGFLQISWNNYNGPACRDIGFDGLGDPGRVA	179
Db	140	KEETSGRDHNYCQST-AEYPCNPVNVYFGRGFLQITWNNYIDAGNSNDFDGLNPDIVA	198
Qy	180	RDVAVFAKALWFNNVHVRVMPQGFATIRAINGALECDGNNPAQMNAIGYYKQYCRQ	239
Db	199	SDAVVSFKTALWYWKVQSVTSQGFATIRAIN-SIECNGGSPDAVNSRVSLNSYCSK	257
Qy	240	LGVDPGPNLTC	250
Db	258	FGVAPGDNQGC	268

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2005, 12:21:21 ; Search time 112.919 Seconds  
(without alignments)  
1133.730 Million cell updates/sec

Title: US-10-692-367-70  
Perfect score: 1408  
Sequence: 1 SMQNCQPNVCCSKFGYCG.....GYKQYKQLGVDPGNLTC 250

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1351	96.0	279	2 Q6JBP8	Q6jbp8 zea mays (s
2	1345.5	95.6	280	2 Q6JBQ0	Q6jbp0 zea mays (s
3	1345.5	95.6	286	2 Q6JBQ4	Q6jbp4 zea mays (s
4	1338.5	95.1	286	2 Q6JBP3	Q6jbp3 zea diplo
5	1336.5	94.9	278	2 Q6JBP7	Q6jbp7 zea diplo
6	1336.5	94.9	284	2 Q6JBQ9	Q6jbp9 zea mays (s
7	1335.5	94.9	278	2 Q6JBP2	Q6jbp2 zea diplo
8	1335.5	94.9	278	2 Q6JBP5	Q6jbp5 zea diplo
9	1335.5	94.9	280	2 Q6JBP9	Q6jbp9 zea mays (s
10	1335.5	94.9	280	2 Q6JBQ2	Q6jbp2 zea mays (s
11	1335.5	94.9	280	2 Q6JBQ8	Q6jbp8 zea mays (s
12	1332.5	94.6	282	2 Q6JBQ6	Q6jbp6 zea mays (s
13	1331.5	94.6	280	2 Q6JBQ7	Q6jbp7 zea mays (s
14	1329.5	94.4	282	2 Q6JBQ3	Q6jbp3 zea mays (s
15	1329	94.1	281	2 Q6JBQ1	Q6jbp1 zea mays (s
16	1325	94.1	281	2 Q6JBQ5	Q6jbp5 zea mays (s
17	1323	94.0	279	2 Q6JBQ4	Q6jbp4 zea mays (m
18	1314.5	93.4	269	1 CHIA_MAIZE	P29023 zea mays (m
19	1301	92.4	282	2 Q6JBR2	Q6jbr2 tripsacum d
20	1279	90.8	277	2 Q6JBK3	Q6jbk3 zea mays (s
21	1278	90.8	274	2 Q6JBK1	Q6jbk1 zea diplo
22	1277	90.7	276	2 Q6JBK0	Q6jbk0 zea diplo
23	1273.5	90.4	276	2 Q6JBL2	Q6jbl2 zea mays (s
24	1272.5	90.4	280	2 Q6JBK9	Q6jbk9 zea mays (s
25	1271	90.3	278	2 Q6JBK4	Q6jbk4 zea mays (s
26	1270.5	90.2	276	2 Q6JBL1	Q6jbl1 zea mays (s
27	1269	90.1	277	2 Q6JBK6	Q6jbk6 zea mays (s
28	1268.5	90.1	274	2 Q6JBL4	Q6jbl4 zea mays (s
29	1266.5	90.0	278	2 Q6JBL5	Q6jbl5 zea mays (s
30	1265.5	89.9	280	2 Q6JBK8	Q6jbk8 zea mays (s
31	1264	89.8	279	2 Q6JBL0	Q6jbl0 zea mays (s

32	1263.5	89.7	276	2 Q6JBK7	Q6jbk7 zea mays (s
33	1263.5	89.7	278	2 Q6JBL3	Q6jbl3 zea mays (s
34	1258.5	89.4	280	1 CHIA_MAIZE	P29022 zea mays (m
35	1224	86.9	261	2 Q94EL5	Q94el5 saccharum o
36	1211	86.0	277	2 Q6JBL6	Q6jbl6 tripsacum d
37	1175.5	83.5	261	2 Q94EL3	Q94el3 sorghum hal
38	1135	80.6	262	2 Q93WT2	Q93wt2 sorghum bic
39	1130	80.3	262	2 Q94L15	Q94l15 sorghum bic
40	1129	80.2	272	2 Q93WT1	Q93wt1 sorghum bic
41	1127	80.0	262	2 Q94EL4	Q94el4 sorghum aru
42	1011.5	71.8	288	2 Q7Y120	Q7y120 oryza sativ
43	974	69.2	285	2 Q7XU64	Q7xu64 oryza sativ
44	942	66.9	264	2 Q7XAU6	Q7xau6 vitis vinif
45	926	65.8	264	2 Q24531	Q24531 vitis vinif

#### ALIGNMENTS

RESULT 1  
Q6JBP8 PRELIMINARY; PRT; 279 AA.  
AC Q6JBP8; AC Q6JBP8; 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE Chitinase.  
GN Name=chiB;  
OS Zea mays (subsp. parviglumis) (Balsas teosinte).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=76912;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;  
RA Tiffin P.;  
RT "Comparative evolutionary histories of chitinase genes in the genus  
ze and family poaceae.";  
RL Genetics 167:1331-1340(2004).  
DR EMBL; AY532735; AAT40004.1; -.  
DR EMBL; AY532723; AAT39992.1; -.  
DR HSSP; P10969; 1KTV.  
DR GO; GO:0008061; F:chitin binding; IEA.  
DR GO; GO:0004568; F:chitinase activity; IEA.  
DR GO; GO:0016998; P:cell wall catabolism; IEA.  
DR GO; GO:0006032; P:chitin catabolism; IEA.  
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
DR InterPro; IPR002086; Aldehyd dehydrog.  
DR InterPro; IPR001002; Chitin\_Binding\_1.  
DR InterPro; IPR000726; Glyco\_Hydro\_19.  
DR Pfam; PF00182; Glyco\_hydro\_19; 1.  
DR PRINTS; PR00451; CHITINBINDING.  
DR ProDom; PD000609; Chitin binding\_1; 1.  
DR ProDom; PD354900; Glyco\_Hydro\_19; 1.  
DR SMART; SM00270; ChtdB1; 1.  
DR PROSITE; PS00687; ALDEHYDE DEHYDR\_GLU; UNKNOWN\_1.  
DR PROSITE; PS00773; CHITINASE\_19\_1; 1.  
DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
DR PROSITE; PS00026; CHIT\_BIND\_1; 1.  
DR PROSITE; PS50941; CHIT\_BIND\_2; 1.  
KW Chitin-binding.  
SQ SEQUENCE 279 AA; 28925 MW; 8F38B91DE3B48BE6 CRC64;

Query Match 96.0%; Score 1351; DB 2; Length 279;  
Best Local Similarity 96.0%; Pred. No. 4,7e-102;  
Matches 238; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 QNCQCPNVCCSKFGYCGTTDEYCGDQCQSGPCRSGGSGGGGANVASVVTGSPFNGI 62  
Db 32 QNCQCPNVCCSKFGYCGTTDEYCGDQCQSGPCRSGGSGGGGANVASVVTGSPFNGI 91  
QY 63 KNQAGSCGCKNFYTRSAFLSAVKAYPGFAGGSGVQVKREIAAPFAHATHETGHCFCYIS 122

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|:||||| 92 KSQAGSGCKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGFCYIS 151
|:||||| 123 ELSKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 182
|:||||| 152 EINKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 211
|:||||| 183 VVAFKAALWFWMNNVHRVMPQGFATIRAINGALCEDGNNPAQMNARIQYKQYCRQLGV 242
|:||||| 212 VVAFKAALWFWMNSVHGVPQGFATIRAINGALCEDGNNPAQMNARIQYKQYCRQLGV 271
|:||||| 243 DPGPNLTC 250
|:||||| 272 DPGPNLTC 279

RESULT 2
Q6JBQ0 PRELIMINARY; PRT; 280 AA.
AC Q6JBQ0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Baleas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532733; AAT40002.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0006032; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChitinBD1; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00026; CHIT_BIND_1_2; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 280 AA; 28993 MW; 7E6E2DA395C32FDB CRC64;

Query Match 95.6%; Score 1345.5; DB 2; Length 280;
Best Local Similarity 96.0%; Pred. No. 1.3e-101;
Matches 239; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 3 QNCGQPNVCCSKFGYCGTTDEYCGDCGSCGCRS-GGGSGGGGANVASVVTGSPFNG 61
|:||||| 32 QNCGQPNVCCSKFGYCGTTDEYCGDCGSCGCRS-GGGSGGGGANVASVVTGSPFNG 91
|:||||| 62 IKNQAGSGCKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGFCYI 121
|:||||| 92 IKNQAGSGCKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGFCYI 151
|:||||| 122 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 181
|:||||| 152 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 211
|:||||| 182 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 241
|:||||| 211 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 271
|:||||| 242 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 271
|:||||| 271 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 271

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|:||||| 152 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 211
|:||||| 182 AVAFKAALWFWMNNVHRVMPQGFATIRAINGALCEDGNNPAQMNARIQYKQYCRQLG 241
|:||||| 212 AVAFKAALWFWMNSVHGVPQGFATIRAINGALCEDGNNPAQMNARIQYKQYCRQLG 271
|:||||| 242 VDPGNLTC 250
|:||||| 272 VDPGNLTC 280

RESULT 3
Q6JBQ4 PRELIMINARY; PRT; 283 AA.
AC Q6JBQ4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Baleas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532729; AAT39998.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0006032; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChitinBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00026; CHIT_BIND_1_2; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 283 AA; 29405 MW; 551581B126791A58 CRC64;

Query Match 95.6%; Score 1345.5; DB 2; Length 283;
Best Local Similarity 96.0%; Pred. No. 1.3e-101;
Matches 239; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 3 QNCGQPNVCCSKFGYCGTTDEYCGDCGSCGCRS-GGGSGGGGANVASVVTGSPFNG 61
|:||||| 35 QNCGQPNVCCSKFGYCGTTDEYCGDCGSCGCRS-GGGSGGGGANVASVVTGSPFNG 94
|:||||| 62 IKNQAGSGCKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGFCYI 121
|:||||| 95 IKNQAGSGCKNFYTRSAFLSAVKAYPGFAHGGSOVQKREIAAFPAHATHETHGFCYI 154
|:||||| 122 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 181
|:||||| 155 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 214
|:||||| 182 AVAFKAALWFWMNNVHRVMPQGFATIRAINGALCEDGNNPAQMNARIQYKQYCRQLG 241
|:||||| 214 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 271
|:||||| 241 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 271
|:||||| 271 SEISKSNAYCDPTKRWPCAAQKYYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 271

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||||| 215 AVAFKALWFMWNSVHGVPQFGATTRAINGALECGGNPAQNNARVYTRQICRLG 274
||||| 242 VDPGNLTC 250
||||| 275 VDPGNLTC 283

RESULT 4
Q6JBP3
ID Q6JBP3 PRELIMINARY; PRT; 286 AA.
AC Q6JBP3;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Chitinase.
GN Name=chiB;
OS Zea diploperennis (Diploperennial teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4576;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532740; AAT40009.1; -.
DR HSP; P10969; IK7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR01002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD00609; Chitin binding_1; 1.
DR InterPro; IPR000726; Glyco_hydro_19; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD00609; Chitin binding_1; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 286 AA; 29352 MW; 7577FEE94C0773A CRC64;

Query Match 95.1%; Score 1338.5; DB 2; Length 286;
Best Local Similarity 93.3%; Pred. No. 5e-101;
Matches 238; Conservative 6; Mismatches 4; Indels 7; Gaps 1;

QY 3 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGG-----SSGGGANVASVVT 55
DB 32 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGSGGGGSGGGGANVASVVT 91

QY 56 GSPFNGIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSGSQVKREIAFAFAHATHET 115
DB 92 GSFNGIKNAGSGCGEKNFYTRSAFLSAVKAYPGFAHGSGSQVKREIAFAFAHATHET 151

QY 116 GHFCYISIKSNAYCDPTKQWPCAGQKYGRGFLQISWNYNGPAGRIDGPDGLGDP 175
DB 152 GHFCYISIKSNAYCDPTKQWPCAGQKYGRGFLQISWNYNGPAGRAIGPDGLGDP 211

QY 176 GRVARDVAVPAKALWFMWNNVHRVMPQFGATIRAINGALECGDGNPAQNNARIGYYKQ 235
DB 212 GRVARDVAVPAKALWFMWNSVHGVPQFGATTRAINGALECGGNPAQNNARVYTRQ 271

QY 236 YCRQLGVDPGNLTC 250
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||||| 272 YCRQLGVDPGNLTC 286

RESULT 5
Q6JBP7
ID Q6JBP7 PRELIMINARY; PRT; 278 AA.
AC Q6JBP7;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Chitinase.
GN Name=chiB;
OS Zea diploperennis (Diploperennial teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4576;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532736; AAT40005.1; -.
DR HSP; P10969; IK7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR01002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD00609; Chitin binding_1; 1.
DR InterPro; IPR000726; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 278 AA; 28838 MW; 8D65AB2FCED91585 CRC64;

Query Match 94.9%; Score 1336.5; DB 2; Length 278;
Best Local Similarity 95.6%; Pred. No. 7e-101;
Matches 237; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 3 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGSGGGGANVASVVTGFFNGI 62
DB 32 QNCQCPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGSGGGGSGGGGANVASVVTGFFNGI 90

QY 63 KNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGSQVKREIAFAFAHATHETGHFCYIS 122
DB 91 KSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGSQVKREIAFAFAHATHETGHFCYIS 150

QY 123 EISKSNAAYCDPTKQWPCAGQKYGRGFLQISWNYNGPAGRIDGPDGLGDPGRVARD 182
DB 151 EINKSNAAYCDPTKQWPCAGQKYGRGFLQISWNYNGPAGRAIGPDGLGDPGRVARD 210

QY 183 VVAFKALWFMWNNVHRVMPQFGATIRAINGALECGDGNPAQNNARIGYYKQYCRQLGV 242
DB 211 VVAFKALWFMWNSVHGVPQFGATTRAINGALECGGNPAQNNARVYTRQICRLGV 270

QY 243 DPGNLTC 250
DB 271 DPGNLTC 278
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RESULT 6
Q6JBQ9
ID Q6JBQ9 PRELIMINARY; PRT; 284 AA.
AC Q6JBQ9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532724; AAT39993.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR SMART; SM00451; CHITINBINDING.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR PRINTS; PR00451; Chitin-binding.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 284 AA; 29256 MW; B210EB7C204A6567 CRC64;

Query Match 94.9%; Score 1336.5; DB 2; Length 284;
Best Local Similarity 93.7%; Pred. No. 7.2e-101;
Matches 237; Conservative 7; Mismatches 4; Indels 5; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDCGCGSPCRSGGGG-----SSGGGGANVASVVTGS 57
Db 32 QNCGQPNVCCSKFGYCGTTDEYCGDCGCGSPCRSGGGGGSSSSGGGGANVASVVTGS 91

QY 58 PFNGIKNAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGH 117
Db 92 PFNGIKNAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGH 151

QY 118 FCIYSEISKSNAYCDPTKRWPCAAQKYGRGPIQISWNNYGPAGRDIGFDGLGDPGR 177
Db 152 FCIYSEINKSNAYCDPSKRWPCAAQKYGRGPIQISWNNYGPAGKAIGFDGLGDPGR 211

QY 178 VARDAAVAFKAALWFMMNVRHVRMPQGFATIRAINGALECDGNPNARIGYKQYC 237
Db 212 VARDAAVAFKAALWFMMNSVHGVPQGFATIRAINGALECGGNPNARVGYRQYC 271

QY 238 RQLGVDPGNLTC 250
Db 272 RQLGVDPGNLTC 284

RESULT 7
Q6JB2
ID Q6JB2 PRELIMINARY; PRT; 278 AA.
AC Q6JB2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Chitinase.

DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea diploperennis (Diploperennial teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4576;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532741; AAT40010.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00451; Chitin-binding.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS50941; CHIT_BIND_1_2; 1.
KW Chitin-binding.
SQ SEQUENCE 278 AA; 28865 MW; 23A117EDFAB8F908 CRC64;

Query Match 94.9%; Score 1335.5; DB 2; Length 278;
Best Local Similarity 95.6%; Pred. No. 8.5e-101;
Matches 237; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDCGCGSPCRSGGGGGGGGGANVASVVTGSFFNGI 62
Db 32 QNCGQPNVCCSKFGYCGTTDEYCGDCGCGSPCRS-GGGSSGGGGANVASVVTGSFFNGI 90

QY 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGHFCYIS 122
Db 91 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAAFFAHATHETGHFCYIS 150

QY 123 EISKSNAYCDPTKRWPCAAQKYGRGPIQISWNNYGPAGRDIGFDGLGDPGRVARD 182
Db 151 EINKSNAYCDPSKRWPCAAQKYGRGPIQISWNNYGPAGRAIGFDGLGDPGRVARD 210

QY 183 VVAFKAALWFMMNVRHVRMPQGFATIRAINGALECDGNPNARIGYKQYCROLGV 242
Db 211 VVAFKAALWFMMNSVHGVPQGFATIRAINGALECGGNPNARVGYRQYCRQLGV 270

QY 243 DPGNLTLC 250
Db 271 DPGNLTLC 278

RESULT 8
Q6JB5
ID Q6JB5 PRELIMINARY; PRT; 278 AA.
AC Q6JB5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Chitinase.

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GN Name=chiB;
OS Zea diploperennis (Diploperennial teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4576;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RT Zea and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532738; AAT40007.1; -.
DR EMBL; AY532739; AAT40008.1; -.
DR EMBL; AY532742; AAT40011.1; -.
DR EMBL; AY532737; AAT40006.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0001698; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin binding_1; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD000609; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE 19_1; 1.
DR PROSITE; PS00774; CHITINASE 19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
DR Chitin-binding.
KW Chitin-binding.
SQ SEQUENCE 278 AA; 29024 MW; 6DDA23E340CA0610 CRC64;

Query Match 94.9%; Score 1335.5; DB 2; Length 278;
Best Local Similarity 95.6%; Pred. No. 8.5e-101;
Matches 237; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSFFNGI 62
DB 32 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSFFNGI 90

QY 63 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAHATHETGHFCYIS 122
DB 91 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAHATHETGHFCYIS 150

QY 123 EISKSNAYCDPTKRWPCAAQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARD 182
DB 151 EINKSNAYCDPSKRWPCAAQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDPGRVARD 210

QY 183 VVAFKAALWFWMNNVHRVMPQGFATIRAINALECDGNNPAQMNARIYYKYQYCRQLGV 242
DB 211 VVAFKAALWFWMNSVHGVVPGFGATIRAINALECGGNNPAQMNARVGYTRYQYCRQLGV 270

QY 243 DPGPNLTC 250
DB 271 DPGPNLTC 278

RESULT 9
Q6JBP9 PRELIMINARY; PRT; 280 AA.
AC Q6JBP9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Chitinase.
GN Name=chiB;

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OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
RT Zea and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532734; AAT40003.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0001698; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:response to pest, pathogen or parasite; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD000609; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE 19_1; 1.
DR PROSITE; PS00774; CHITINASE 19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_1_1; 1.
DR PROSITE; PS00941; CHIT_BIND_1_2; 1.
DR Chitin-binding.
KW Chitin-binding.
SQ SEQUENCE 280 AA; 29009 MW; 64BB647946D9F05F CRC64;

Query Match 94.9%; Score 1335.5; DB 2; Length 280;
Best Local Similarity 95.2%; Pred. No. 8.5e-101;
Matches 237; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSFFNG 61
DB 32 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSFFNG 91

QY 62 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAHATHETGHFCYI 121
DB 92 KNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSQVQKREIAFAHATHETGHFCYI 151

QY 122 SEISKSNAYCDPTKRWPCAAQKYYGRGPLQISWNYNYGPAGRDIGFDGLGDPGRVARD 181
DB 152 SEINKSNAYCDPSKRWPCAAQKYYGRGPLQISWNYNYGPAGRAIGFDGLGDPGRVARD 211

QY 182 AVVAFKAALWFWMNNVHRVMPQGFATIRAINALECDGNNPAQMNARIYYKYQYCRQLG 241
DB 212 AVVAFKAALWFWMNSVHGVVPGFGATIRAINALECGGNNPAQMNARVGYTRYQYCRQLG 271

QY 242 VDPGNLTC 250
DB 272 VDPGNLTC 280

RESULT 10
Q6JBQ2 PRELIMINARY; PRT; 280 AA.
AC Q6JBQ2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

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OX NCBI\_TaxID=76912;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15280246; DOI=10.1534/genetics.104.026856;  
 RA Tiffin P.;  
 RT "Comparative evolutionary histories of chitinase genes in the genus  
 RT zea and family poaceae";  
 RL Genetics 167:1331-1340(2004).  
 DR EMBL; AY532731; AAT4000.1; -.  
 DR HSSP; P10969; 1KTV.  
 DR GO; GO:0008061; F:chitin binding; IEA.  
 DR GO; GO:0004568; F:chitinase activity; IEA.  
 DR GO; GO:0016998; P:cell wall catabolism; IEA.  
 DR GO; GO:0006032; P:chitin catabolism; IEA.  
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
 DR InterPro; IPR002086; Aldehyd dehydrog.  
 DR InterPro; IPR001002; Chitin binding\_1.  
 DR Pfam; PF00182; Glyco\_hydro\_19; 1.  
 DR PRINTS; PR00451; CHITINBINDING.  
 DR ProDom; PD000609; Chitin binding\_1; 1.  
 DR ProDom; PD000609; Chitin binding\_1; 1.  
 DR SMART; SM00270; ChtBD1; 1.  
 DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN\_1.  
 DR PROSITE; PS00773; CHITINASE\_19\_1; 1.  
 DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
 DR PROSITE; PS00026; CHIT\_BIND\_1\_1; 1.  
 DR PROSITE; PS50941; CHIT\_BIND\_1\_2; 1.  
 KW Chitin-binding.  
 SQ SEQUENCE 280 AA; 28963 MW; 60FA61748883998 CRC64;  
  
 Query Match 94.9%; Score 1335.5; DB 2; Length 280;  
 Best Local Similarity 95.2%; Pred. No. 8.5e-101;  
 Matches 237; Conservative 5; Mismatches 6; Indels 1; Gaps 1;  
  
 QY 3 QNCGQPNVCCSKFYCGTDTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSPFNG 61  
 DB |||||  
 QY 32 QNCGQPNVCCSKFYCGTDTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSPFNG 91  
 DB |||||  
 QY 62 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSVQVQKREIAFAFAHATHETGHFCYI 121  
 DB |||||  
 QY 92 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSVQVQKREIAFAFAHATHETGHFCYI 151  
 DB |||||  
 QY 122 SEISKSNAVCPTKRWPCAGQKYGRGLQISWNYNYPAGRDIGFDGLGDPGRVARD 181  
 DB |||||  
 QY 152 SEINKSNAYCDPTKQWPCAGQKYGRGLQISWNYNYPAGRDIGFDGLGDPGRVARD 211  
 DB |||||  
 QY 182 AVAFKAALWFWMNNVHRVMPQGFATIRAINGALECDGNPAQNNARIQYKYCRQLG 241  
 DB |||||  
 QY 212 AVAFKAALWFWMNSVHGVVPGQGFATIRAINGALECDGNPAQNNARVGYRYQYCRQLG 271  
 DB |||||  
 QY 242 VDPGNLTC 250  
 DB |||||  
 QY 272 VDPGNLTC 280  
 DB |||||  
  
 RESULT 11  
 Q6JB08 PRELIMINARY; PRT; 280 AA.  
 ID Q6JB08  
 AC Q6JB08; (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE Chitinase.  
 GN Name=chiB;  
 OS Zea mays (subsp. parviglumis) (Balsas teosinte).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=76912;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15280246; DOI=10.1534/genetics.104.026856;

RA Tiffin P.;  
 RT "Comparative evolutionary histories of chitinase genes in the genus  
 RT zea and family poaceae";  
 RL Genetics 167:1331-1340(2004).  
 DR EMBL; AY532725; AAT39994.1; -.  
 DR HSSP; P10969; 1KTV.  
 DR GO; GO:0008061; F:chitin binding; IEA.  
 DR GO; GO:0004568; F:chitinase activity; IEA.  
 DR GO; GO:0016998; P:cell wall catabolism; IEA.  
 DR GO; GO:0006032; P:chitin catabolism; IEA.  
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
 DR InterPro; IPR002086; Aldehyd dehydrog.  
 DR InterPro; IPR001002; Chitin binding\_1.  
 DR Pfam; PF00182; Glyco\_hydro\_19; 1.  
 DR PRINTS; PR00451; CHITINBINDING.  
 DR ProDom; PD000609; Chitin binding\_1; 1.  
 DR ProDom; PD000609; Chitin binding\_1; 1.  
 DR SMART; SM00270; ChtBD1; 1.  
 DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN\_1.  
 DR PROSITE; PS00773; CHITINASE\_19\_1; 1.  
 DR PROSITE; PS00774; CHITINASE\_19\_2; 1.  
 DR PROSITE; PS00026; CHIT\_BIND\_1\_1; 1.  
 DR PROSITE; PS50941; CHIT\_BIND\_1\_2; 1.  
 KW Chitin-binding.  
 SQ SEQUENCE 280 AA; 28922 MW; 7FCE9A0996867FCA CRC64;  
  
 Query Match 94.9%; Score 1335.5; DB 2; Length 280;  
 Best Local Similarity 95.2%; Pred. No. 8.5e-101;  
 Matches 237; Conservative 6; Mismatches 5; Indels 1; Gaps 1;  
  
 QY 3 QNCGQPNVCCSKFYCGTDTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSPFNG 61  
 DB |||||  
 QY 32 QNCGQPNVCCSKFYCGTDTDEYCGDGCQSGPCRS-GGGSSGGGGANVASVVTGSPFNG 91  
 DB |||||  
 QY 62 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSVQVQKREIAFAFAHATHETGHFCYI 121  
 DB |||||  
 QY 92 IKNOAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSVQVQKREIAFAFAHATHETGHFCYI 151  
 DB |||||  
 QY 122 SEISKSNAVCPTKRWPCAGQKYGRGLQISWNYNYPAGRDIGFDGLGDPGRVARD 181  
 DB |||||  
 QY 152 SEINKSNAYCDPTKQWPCAGQKYGRGLQISWNYNYPAGRDIGFDGLGDPGRVARD 211  
 DB |||||  
 QY 182 AVAFKAALWFWMNNVHRVMPQGFATIRAINGALECDGNPAQNNARIQYKYCRQLG 241  
 DB |||||  
 QY 212 AVAFKAALWFWMNSVHGVVPGQGFATIRAINGALECDGNPAQNNARVGYRYQYCRQLG 271  
 DB |||||  
 QY 242 VDPGNLTC 250  
 DB |||||  
 QY 272 VDPGNLTC 280  
 DB |||||  
  
 RESULT 12  
 Q6JB06 PRELIMINARY; PRT; 282 AA.  
 ID Q6JB06  
 AC Q6JB06; (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE Chitinase.  
 GN Name=chiB;  
 OS Zea mays (subsp. parviglumis) (Balsas teosinte).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=76912;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=15280246; DOI=10.1534/genetics.104.026856;  
 RA Tiffin P.;  
 RT "Comparative evolutionary histories of chitinase genes in the genus  
 RT zea and family poaceae";  
 RL Genetics 167:1331-1340(2004).

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DR EMBL; AY532727; AAT39996.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0004568; P:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19_1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD00609; Chitin binding_1; 1.
DR InterPro; IPR00726; Glyco_hydro_19_1.
DR Pfam; PF00182; Glyco_hydro_19_1.
DR SMART; SM00270; ChtBD1; 1.
DR ProDom; PD00609; Glyco_hydro_19_1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_I_1; 1.
DR PROSITE; PS00026; CHIT_BIND_I_2; 1.
DR PROSITE; PS00941; CHIT_BIND_I_2; 1.
KW Chitin-binding.
SQ SEQUENCE 282 AA; 29133 MW; FBB060F48CA67945 CRC64;

Query Match          94.6%; Score 1332.5; DB 2; Length 282;
Best Local Similarity 94.8%; Pred. No. 1.5e-100;
Matches 236; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 61
DB 34 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 93

QY 62 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGSQVQKREIAAFPAHAHETHGHFCYI 121
DB 94 IKSQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGSQVQKREIAAFPAHAHETHGHFCYI 153

QY 122 SEIKSNAYCDPTKQWPCAAQKQYGRGLQISWNYNYPAGRDIGDGLDGPGRVARD 181
DB 154 SEIKSNAYCDPSKQWPCAAQKQYGRGLQISWNYNYPAGRDIGDGLDGPGRVARD 213

QY 182 AVVAFKALWFMNNVHVRMPQGFATIRANGALECDGNPAQNNARIGYYKQYCRQLG 241
DB 214 AVVAFKALWFMNVSVHGVVPGFGATTIRANGALECCGNNPAQNNARVGYRYQYCRQLG 273

QY 242 VDPGNLTC 250
DB 274 VDPGNLTC 282

RESULT 13
Q6JBQ7 ID Q6JBQ7 PRELIMINARY; PRT; 280 AA.
AC Q6JBQ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532726; AAT39995.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0004568; P:chitinase activity; IEA.
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DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR Pfam; PF00182; Glyco_hydro_19_1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD00609; Chitin binding_1; 1.
DR InterPro; IPR00726; Glyco_hydro_19_1.
DR SMART; SM00270; ChtBD1; 1.
DR ProDom; PD00609; Glyco_hydro_19_1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_I_1; 1.
DR PROSITE; PS00026; CHIT_BIND_I_2; 1.
KW Chitin-binding.
SQ SEQUENCE 280 AA; 28965 MW; 47102378A9B6799D CRC64;

Query Match          94.6%; Score 1331.5; DB 2; Length 280;
Best Local Similarity 94.8%; Pred. No. 1.8e-100;
Matches 236; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 61
DB 32 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 91

QY 62 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGSQVQKREIAAFPAHAHETHGHFCYI 121
DB 92 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGSGSQVQKREIAAFPAHAHETHGHFCYI 151

QY 122 SEIKSNAYCDPTKQWPCAAQKQYGRGLQISWNYNYPAGRDIGDGLDGPGRVARD 181
DB 152 SEIKSNAYCDPSKQWPCAAQKQYGRGLQISWNYNYPAGRDIGDGLDGPGRVARD 211

QY 182 AVVAFKALWFMNNVHVRMPQGFATIRANGALECDGNPAQNNARIGYYKQYCRQLG 241
DB 212 AVVAFKALWFMNVSVHGVVPGFGATTIRANGALECCGNNPAQNNARVGYRYQYCRQLG 271

QY 242 VDPGNLTC 250
DB 272 VDPGNLTC 280

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AC Q6JBQ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chiB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532730; AAT39999.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0004568; P:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
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DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_I_1; 1.
DR PROSITE; PS00941; CHIT_BIND_I_2; 1.
KW Chitin-binding.
SQ SEQUENCE 282 AA; 29147 MW; 4E10632A4F979D20 CRC64;

Query Match          94.4%; Score 1329.5; DB 2; Length 282;
Best Local Similarity 94.8%; Pred. No. 2.6e-100;
Matches 236; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 3 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRS-GGGSGSGGGGANVASVVTGSPFNG 61
DB 34 QNCGQPNVCCSKFGYCGTTDEYCGDGCQSGPCRSGGGGGGGGGANVASVVTSSPFNG 93

QY 62 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATHETGHFCYI 121
DB 94 IKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATHETGHFCYI 153

QY 122 SEISKSNAVCPTKQWPCAAQGYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 181
DB 154 SEISKSNAVCPTKQWPCAAQGYGRGLQISWNNYGPAGRDIGFDGLGDPGRVARD 213

QY 182 AVVAFAKALWFMMNVRHVMPPQGFATIRAINGALCEDGNNPAQMNARIGYKQYCRQLG 241
DB 214 AVVAFAKALWFMMNVRHVMPPQGFATIRAINGALCEDGNNPAQMNARIGYKQYCRQLG 273

QY 242 VDPGPNLTC 250
DB 274 VDPGPNLTC 282

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## RESULT 15

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chitinase.
GN Name=chIB;
OS Zea mays (subsp. parviglumis) (Balsas teosinte).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15280246; DOI=10.1534/genetics.104.026856;
RA Tiffin P.;
RT "Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae.";
RL Genetics 167:1331-1340(2004).
DR EMBL; AY532722; AAT39991.1; -.
DR HSSP; P10969; 1K7V.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0004568; F:chitinase activity; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0006032; P:chitin catabolism; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR001002; Chitin binding_1.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.

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DR ProDom; PD000609; Chitin binding_1; 1.
DR ProDom; PD354900; Glyco_hydro_19; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHIT_BIND_I_1; 1.
DR PROSITE; PS00941; CHIT_BIND_I_2; 1.
KW Chitin-binding.
SQ SEQUENCE 281 AA; 28979 MW; C23523FE12D986A6 CRC64;

Query Match          94.4%; Score 1329; DB 2; Length 281;
Best Local Similarity 94.4%; Pred. No. 2.9e-100;
Matches 236; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

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QY 61 GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATHETGHFCY 120
DB 92 GIKNQAGSGCEGKNFYTRSAFLSAVKAYPGFAHGGSQVQKREIAAFPAHATHETGHFCY 151

QY 121 ISEISKSNAVCPTKQWPCAAQGYGRGLQISWNNYGPAGRDIGFDGLGDPGRVAR 180
DB 152 ISEISKSNAVCPTKQWPCAAQGYGRGLQISWNNYGPAGRDIGFDGLGDPGRVAR 211

QY 181 DAVVAFAKALWFMMNVRHVMPPQGFATIRAINGALCEDGNNPAQMNARIGYKQYCRQL 240
DB 212 DAVVAFAKALWFMMNVRHVMPPQGFATIRAINGALCEDGNNPAQMNARIGYKQYCRQL 271

QY 241 GVDPGPNLTC 250
DB 272 GVDPGPNLTC 281

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Search completed: May 24, 2005, 12:54:17  
Job time : 113.919 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 15:37:22 ; Search time 2973.37 Seconds  
(without alignments)  
4074.095 Million cell updates/sec

Title: US-10-692-367-70  
Perfect score: 1408  
Sequence: 1 SMQNCQPNVCCSKFVCG.....GYKQYCRQLGVDPGNLTC 250

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgm2\_1/USPTO.spool-US10692367/runat\_20052005\_172254\_20002/app\_query.fasta\_1.846  
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-USER=US10692367 @CGN 1\_1\_3055 @runat\_20052005\_172254\_20002 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*

1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_ats:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1351	96.0	1094	6 AR321624	AR321624 Sequence
2	1314.5	93.4	810	8 MZECHTB	M84165 Zea mays ch
3	1312.5	93.2	1121	8 AY532735	AY532735 Zea mays
4	1306.5	92.8	1127	8 AY532733	AY532733 Zea mays

5	1299	92.3	1081	8 AY532737	AY532737 Zea diplo
6	1299	92.3	1081	8 AY532738	AY532738 Zea diplo
7	1299	92.3	1081	8 AY532742	AY532742 Zea diplo
8	1299	92.3	1127	8 AY532723	AY532723 Zea mays
9	1298	92.2	1114	8 AY532725	AY532725 Zea mays
10	1294	91.9	1123	8 AY532729	AY532729 Zea mays
11	1293.5	91.9	1133	8 AY532727	AY532727 Zea mays
12	1292.5	91.8	1123	8 AY532726	AY532726 Zea mays
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14	1286	91.3	1126	8 AY532732	AY532732 Zea mays
15	1285	91.3	1138	8 AY532724	AY532724 Zea mays
16	1284.5	91.2	1122	8 AY532736	AY532736 Zea diplo
17	1281.5	91.0	1140	8 AY532731	AY532731 Zea mays
18	1279.5	90.9	1080	8 AY532739	AY532739 Zea diplo
19	1278	90.8	1134	8 AY532734	AY532734 Zea mays
20	1277.5	90.7	1111	8 AY532741	AY532741 Zea diplo
21	1271	90.3	1127	8 AY532730	AY532730 Zea mays
22	1270.5	90.2	1130	8 AY532722	AY532722 Zea mays
23	1262	89.6	1138	8 AY532728	AY532728 Zea mays
24	1258.5	89.4	843	8 MZECHTB	M84164 Zea mays ch
25	1243.5	88.3	1104	8 AY532782	AY532782 Zea diplo
26	1242.5	88.2	985	8 AY532721	AY532721 Tripsacum
27	1242.5	88.2	1107	8 AY532781	AY532781 Zea diplo
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31	1242.5	88.2	1110	8 AY532786	AY532786 Zea diplo
32	1242.5	88.2	1110	8 AY532787	AY532787 Zea diplo
33	1242.5	88.2	1110	8 AY532788	AY532788 Zea diplo
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36	1234	87.6	1104	8 AY532772	AY532772 Zea mays
37	1233	87.6	1115	8 AY532768	AY532768 Zea mays
38	1232	87.5	1120	8 AY532769	AY532769 Zea mays
39	1230	87.4	1101	8 AY532770	AY532770 Zea mays
40	1227	87.1	1127	8 AY532776	AY532776 Zea mays
41	1217.5	86.5	1094	8 AY532778	AY532778 Zea mays
42	1217.5	86.5	1094	8 AY532779	AY532779 Zea mays
43	1216.5	86.4	1132	8 AY532774	AY532774 Zea mays
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ALIGNMENTS

RESULT 1  
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LOCUS AR321624 1094 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1 from patent US 6563020.  
ACCESSION AR321624  
VERSION AR321624.1 GI:33706864  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1. (bases 1 to 1094)  
AUTHORS Simmons,C.R. and Yalpani,N.  
TITLE Maize chitinases and their use in enhancing disease resistance in crop plants  
JOURNAL Patent: US 6563020-A 1 13-MAY-2003;  
FEATURES Location/Qualifiers  
source 1. .1094  
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ORIGIN

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Percent Similarity: 95.97% Mismatches: 4  
Best Local Similarity: 95.95% Indels: 0  
Query Match: 6 Gaps: 0  
DB:

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Qy	42	SerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGly	61
Db	181	GGCAGTGTGCGGTGTGCGACGTGGCTAGCGTCTGACAGCTCTTCTTCAACGGC	240
Qy	62	IleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPhe	81
Db	241	ATCAAGAACCCAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGCTC	300
Qy	82	LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlySerGlnValGlnGlyLys	101
Db	301	CTGAGCGCGCTCAAGGGCTACCCAGGGCTCGCCCATGCGGGTGCAGAGTGCAAGGCAAG	360
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Db	361	CGCGAGATCGCGCTTCTTTCGGCGACGCCACGACGAGACCGGGCATTTCTGCTACATC	420
Qy	122	SerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAla	141
Db	421	AGCGAGATCAACAAGCAACGCTACTGCGACCCGACCAAGAGGAGTGGCGCTCGGCC	480
Qy	142	AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly	161
Db	481	GCGGGGCAGAAGTACTACGGGCGCGCGCTGCGAGATCTCGTGGAACTACAACTACGGG	540
Qy	162	ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp	181
Db	541	CCCCCGGGAGGGCCATCGGCTTCGAGGGCTCGGGGACCCCGGACAGGTGGCGCGGAC	600
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		PUBMED	1551872
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		ORIGIN	
		Alignment Scores:	
		Pred. No.:	3.1e-92 Length: 810
		Score:	1314.50 Matches: 233
		Percent Similarity:	95.98% Conservative: 6
		Best Local Similarity:	93.57% Mismatches: 9
		Query Match:	93.36% Indels: 1
		DB:	8 Gaps: 1
		US-10-692-367-70 (1-250) x MZCHITB (1-810)	
Qy	3	GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr	22
Db	61	CAGACTCGCGCTGCCAGCCAAACGCTCTGTCGACGAACTTCGGTACTCGGCACGACC	120
Qy	23	AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGly----	41
Db	121	GACGAGTACTGTGCGCAGCGGTGCAGTCGCGCGCCGTCGCGCCGCGGCGCGGC	180
Qy	42	SerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGly	61
Db	181	GGCAGTGTGCGGTGTGCGACGTGGCTAGCGTCTGACAGCTCTTCTTCAACGGC	240
Qy	62	IleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPhe	81
Db	241	ATCAAGAACCCAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGCTC	300
Qy	82	LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlySerGlnValGlnGlyLys	101
Db	301	CTGAGCGCGCTCAAGGGCTACCCAGGGCTCGCCCATGCGGGTGCAGAGTGCAAGGCAAG	360
Qy	102	ArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIle	121
Db	361	CGCGAGATCGCGCTTCTTTCGGCGACGCCACGACGAGACCGGGCATTTCTGCTACATC	420
Qy	122	SerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAla	141
Db	421	AGCGAGATCAACAAGCAACGCTACTGCGACCCGACCAAGAGGAGTGGCGCTCGGCC	480
Qy	142	AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly	161
Db	481	GCGGGGCAGAAGTACTACGGGCGCGCGCTGCGAGATCTCGTGGAACTACAACTACGGG	540
Qy	162	ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp	181
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Qy 182 AlaValValAlaPheLysAlaAlaLeuTTPheTTPMetAenValHisArgValMet 201
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Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAseGlyAen 221
Db 661 CCGCAGGGTTCGGCGCCACACACGAGGCCATGCAACGCGCCCTCGAGTGGCGGGGAC 720
Qy 222 AsnProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
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Qy 242 ValAspProGlyProAenLeuThrCys 250
Db 781 GTCGACCCGGGGCCAACTCACCTGC 807

RESULT 3
AY532735
LOCUS
DEFINITION
Zea mays subsp. parviglumis isolate p15 chitinase (chiB) gene,
complete cds.
ACCESSION
AY532735
VERSION
AY532735.1 GI:48093251
KEYWORDS
Zea mays subsp. parviglumis
SOURCE
Zea mays subsp. parviglumis
ORGANISM
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1121)
Tiffin, P.
Comparative evolutionary histories of chitinase genes in the genus
zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
15280246
REFERENCE
2 (bases 1 to 1121)
Tiffin, P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
FEATURES
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/translations="MAKAGAPRVSAAOLVTLGLSLICAVAGPAAQNCOPNVCCSK
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DPTKRWPCAAQYGRGLQISWNYNYPAGRAIGFDGLGDPGRVARDVAVFKAA
LWFMNSVHGVFPQGFATTRAINGALECGGNPNQAMNARVGYTRYQYCRQLGVDPGPN
LTC"

ORIGIN
Alignment Scores:
Pred. No.: 6.2e-92 Length: 1121
Score: 1312.50 Matches: 237
Percent Similarity: 84.08% Conservative: 6
Best Local Similarity: 82.01% Mismatches: 5
Query Match: 93.22% Indels: 41

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Db 107 CAGNACTGGCGCTGCCAGCCAAACGATATGTCAGCANGTTTGGCTACTGGGCAACGCC 166
Qy 23 AsnGluTyrCysGlyAseGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlySer 42
Db 167 GACGAGTACTCGCGCAGCGGTCACGTCCGGGCGCTGCGCGCTCGGCGCGCGCGCAGC 226
Qy 43 SerGlyGlyGlyGlyAlaAenValAlaSerValValThrGlySerPheAenGlyLle 62
Db 227 AGTGGCGCGGTGGTGGAAACGGTGGCTAGCGTCTCACCGGCTCTCTTCTTCAACGGGATC 286
Qy 63 LysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPheLeu 82
Db 287 AAGAGCCAGCCGCGGAGCGGTCGAGGGCAAGAACTTCTACACCCGAGCGCTTCTCTG 346
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 347 AGCGCGCTCAAGGCGTACCCAGCGCTTCCGCCATCGCGGTCGACAGGTGCAGGGCAAGCGC 406
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHis 117
Db 407 GAGATCGCGCCCTTCTTTCGCGCACGCCACACGAGACCGGGCGGTAAGTTGGCTCGCTCT 466
Qy 117 ----- 117
Db 467 TCAGCGCGCGCAGGTCTTTTGATTTTAATTGACCCATCATGCTCATCAATTTATTT 526
Qy 118 -----PheCysTyrIle 121
Db 527 ATTATTTTGGAAAAATTTTCGCTGCTGTGTGTGTGCACGGCGAGATTTCTGTACATC 586
Qy 122 SerGluIleSerLysSerAenAlaTyrCysAspProThrLysArgGlnTTPProCysAla 141
Db 587 AGCGAGATCAACAGAGCAACGCTACTGCGACCCGACCAAGAGGAGTGGCGCTCGGCC 646
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTTPAenTyrAsnTyrGly 161
Db 647 CGCGGCGCAGNAGTACTACGGCGCGCGCCCTGCGATCTCTGGAACTACACTACGGG 706
Qy 162 ProAlaGlyArgAsePleGlyPheAseGlyLeuGlyAseProGlyArgValAlaAArgAse 181
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Qy 182 AlaValValAlaPheLysAlaAlaLeuTTPheTTPMetAenAenValHisArgValMet 201
Db 767 GCGTGGTGGCGTTCAGGCGCGCGCTCTGGTTCGGATGAACAGCGTGCACGGGGTGGTG 826
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAseGlyAen 221
Db 827 CCGCAGGGTTCGGCGCCACACACGAGGCCATCAACGGCGCCCTCGAGTGGGCGGGAC 886
Qy 222 AsnProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 887 AACCCCGCCAGATGAACGCGCGTCTGGTACTACAGGAGTACTCTCCGCGACTCGCGC 946
Qy 242 ValAspProGlyProAenLeuThrCys 250
Db 947 GTCGACCCGGGGCCAACTCACCTGC 973

RESULT 4
AY532733
LOCUS
DEFINITION
Zea mays subsp. parviglumis isolate p12 chitinase (chiB) gene,
complete cds.
ACCESSION
AY532733
VERSION
AY532733.1 GI:48093247
KEYWORDS
Zea mays subsp. parviglumis

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ORGANISM
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1127)
Tiffin,P.
REFERENCE
AUTHORS
TITLE
Comparative evolutionary histories of chitinase genes in the genus
Zea and family poaceae
JOURNAL
GENETICS 167 (3), 1331-1340 (2004)
PUBMED
15280246
2 (bases 1 to 1127)
Tiffin,P.
REFERENCE
AUTHORS
TITLE
Direct Submission
JOURNAL
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
FEATURES
Location/Qualifiers
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/isolate="p12"
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NLTC"
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Pred. No.: 1.8e-91 Length: 1127
Score: 1306.50 Matches: 238
Percent Similarity: 83.51% Conservative: 5
Best Local Similarity: 81.79% Mismatches: 5
Query Match: 92.79% Indels: 43
DB: 8 Gaps: 2
US-10-692-367-70 (1-250) x AY532733 (1-1127)
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Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerCysGlyProCysArgSer---GlyGlyGly 41
Db 167 GACGAGTACTCGCGCGACGGGTGCCAGTCGCGGCCCTGCGCGCGCGCGCGCGCG 226
Qy 42 SerSerGlyGlyGlyGlyAlaAasnValAlaSerValValThrGlySerPhePheAasnGly 61
Db 227 AGCAGTGGCGCGGTGGTGGCAACGTGGTAGCTCTGTCACCGGCTCTTCTTCAACGGC 286
Qy 62 IleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPhe 81
Db 287 ATCAAGAACCAAGCGCGGAGCGGTGGCGAGGCGCAAGAACTTCTACACCGGAGCGCTTC 346
Qy 82 LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101
Db 347 CTGAGCGCGGTCAGAGCGGTACCCAGGCTTCGCCCATGCGGGGTGCGAGGTGACGGCAAG 406
Qy 102 ArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHis----- 117

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Db 407 CGCGAGATCGCGCCTCTTCTTGGCGCACGCGCACGCGAGACCGGCGTAAGCTGGCTCTA 466
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Qy 118 -----PheCys 119
Db 527 TCAATTTTTTTTTTGGAAAATTTTCGCTGCTGTGTCTGTGTCCACGGGCAGATTCTCTGC 586
Qy 120 TyrIleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpPro 139
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Qy 140 CysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAasnTyrAsn 159
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Db 707 TACGGCGCGCGGGAGGGCCATCGGTTCCAGCGGCTCGGGGACCCCGGCGAGGGTGGCG 766
Qy 180 ArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAenValHisArg 199
Db 767 CGGAGCGCGTGGTGGCTTCAAGGCGGCGCTCTGGTTCTGTGATGAACACGCTGCACGGG 826
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Db 827 GTGGTGGCGGAGGGTTCGGCGCCACCCAGGGGCCATCAACGGCGCCCTCGAGTGGCGG 886
Qy 220 GlyAasnProAlaGlnMetAasnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGln 239
Db 887 GGGACACACCCCGCCCGAGATGAACGGCGGCTCGCTACTACAGGCAGTACTCGCGCCAG 946
Qy 240 LeuGlyValAspProGlyProAasnLeuThrCys 250
Db 947 CTCGGCGTCGACCGCGGCGCCACCTCACCTCGC 979
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AY532737 1081 bp DNA linear PLN 29-JUL-2004
LOCUS
DEFINITION
Zea diploperennis isolate d2 chitinase (chiB) gene, complete cds.
ACCESSION
AY532737
VERSION
AY532737.1 GI:48093255
KEYWORDS
Zea diploperennis
SOURCE
Zea diploperennis
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1081)
Tiffin,P.
REFERENCE
AUTHORS
TITLE
Comparative evolutionary histories of chitinase genes in the genus
Zea and family poaceae
JOURNAL
GENETICS 167 (3), 1331-1340 (2004)
PUBMED
15280246
2 (bases 1 to 1081)
Tiffin,P.
REFERENCE
AUTHORS
TITLE
Direct Submission
JOURNAL
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
FEATURES
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TC"

ORIGIN
Alignment Scores:
Pred. No.: 6,51e-91 Length: 1081
Score: 1299.00 Matches: 236
Percent Similarity: 84.91% Conservative: 6
Best Local Similarity: 82.81% Mismatches: 5
Query Match: 92.26% Indels: 38
DB: 8 Gaps: 2

US-10-692-367-70 (1-250) x AY532737 (1-1081)

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Db 107 CAGAACTCGCGCTGCCAGCCAAACGCTGCTGTCAGCAAGTTTCGGCTACTCGCGCACGACC 166
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 167 GACGAGTACTCGCGGACGCGGTGTCAGTTCGGGCCCGTCCGCTCG---GGCGCGCGGAGC 223
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGlyIle 62
Db 224 AGTGGCGGCTGTGCGAAGCTGGCTAGCGTGTGCTACCGGCTCTCTTCTTCAACGGCATC 283
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyIysAsnPheTyrThrArgSerAlaPheLeu 82
Db 284 AAGAACAAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCCGCGAGCGGCTTCCTG 343
Qy 83 SerAlaValIysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 344 AGCCCGTCAAGCGTACCAGGCTTCGCCATCGCGGGTTCGACGGTGCAGGGCAAGCGC 403
Qy 103 GluIleAlaAlaPheAlaHisAlaThrHisGluThrGlyHis----- 117
Db 404 GAGATCGCGCTTCTTCGCGCACGCCACGACGAGACCGGGCGGTAAAGTTGGCTCGGTCT 463
Qy 117 ----- 117
Db 464 TCCGCGCGCGCAGGTTCTTTGATTTTGTACCCATCATGCTGATCAATTTTTTTTTTTT 523
Qy 118 -----PheCysTyrIleSerGluIleSer 125
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Db 764 TTCAGGCGGCGCTCTGTTCTGATGATGACAGCGTGCAGGGGTGGTGGCGGAGGTTTC 823

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226 MetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGly 245
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246 ProAsnLeuThrCys 250
944 CCCAACCTCACTGC 958

RESULT 6
LOCUS AY532738 1081 bp DNA linear PLN 29-JUL-2004
DEFINITION Zea diploperennis isolate d4 chitinase (chiB) gene, complete cds.
ACCESSION AY532738
VERSION AY532738.1 GI:48093257
KEYWORDS
SOURCE Zea diploperennis
ORGANISM Zea diploperennis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1081)
AUTHORS Tiffn,P.
TITLE Comparative evolutionary histories of chitinase genes in the genus
ze and family poaceae
JOURNAL Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE 2 (bases 1 to 1081)
AUTHORS Tiffn,P.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
FEATURES
Location/Qualifiers
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Db      584 AAGAGCAACGGCTACTTGCACCAAGCAAGAGGAGGAGTGGCGGTGCGCGCGGGCGAGAG 643
Qy      146 TyTyrGlyArgGlyProLeuGlnIleSerTrpAenTyrAenTyrGlyProAlaGlyArg 165
Db      644 TACTACGGCGCGCGCGCTGCAGATCTCGTGGAACTACAACTACGGGCGCGCGGGGAGG 703
Qy      166 AspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValAla 185
Db      704 GCCATCGGCTTCGACGGGCTCGGGAGCCCCGGCAGGGTGGCGCGGAGCGGTGGTGGCG 763
Qy      186 PheLysAlaAlaLeuTrpPheTrpMetAenAenValHisArgValMetProGlnGlyPhe 205
Db      764 TTCAAGCGCGGCGCTCTGGTCTTGGATGAACAGCGTCGACGGGGTGGTGGCGCGAGGTTT 823
Qy      206 GlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAspGlyAenAenProAlaGln 225
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Qy      226 MetAenAlaArgIleGlyTyrTrpLysGlnTyrCysArgGlnLeuGlyValAspProGly 245
Db      884 ATGAAAGCGGCGGTGGGCTACTACAGGCACTATGCGCGCCAGCTCGGGTTCGACCCCGGG 943
Qy      246 ProAenLeuThrCys 250
Db      944 CCCAACCTCACCTGC 958

RESULT 8
AY532723
LOCUS      1127 bp DNA linear PLN 29-JUL-2004
DEFINITION Zea mays subsp. parviglumis isolate p2 chitinase (chiB) gene,
            complete cds.
ACCESSION  AY532723
VERSION     AY532723.1 GI:48093227
KEYWORDS   Zea mays subsp. parviglumis
SOURCE      Zea mays subsp. parviglumis
ORGANISM    Zea mays subsp. parviglumis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 1127)
AUTHORS     Tiffin,P.
TITLE       Comparative evolutionary histories of chitinase genes in the genus
            zea and family poaceae
JOURNAL     Genetics 167 (3), 1331-1340 (2004)
PUBMED      15280246
REFERENCE   2 (bases 1 to 1127)
AUTHORS     Tiffin,P.
TITLE       Direct Submission
JOURNAL     Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
            1445 Gortner Ave., St. Paul, MN 55108-1095, USA
FEATURES   source
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DPTKRWPCAAAGOKYTRGRLQISWNYNYAGRAIGFDGLGDPGRVARDAVAFKAA
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LTC"

ORIGIN
Alignment Scores:
Pred. No.:      6.8e-91      Length:      1127
Score:          1299.00      Matches:    237
Percent Similarity: 83.51%    Conservative: 6
Best Local Similarity: 81.44%  Mismatches: 5
Query Match:     92.26%      Indels:     43
DB:              8          Gaps:       1

US-10-692-367-70 (1-250) x AY532723 (1-1127)

Qy      3  GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db      107 CAGAACTGCGGGCTGCCAGGCCAAACGATATGCTGCAGCAAGTTTGGCTACTCGGGCAGCACC 166
Qy      23  AspGlnTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db      167 GACAGTACTTCGGCGGACGGGTGCCAGTCCGGCCCGCTCGGGCGGGCGGGCAGC 226
Qy      43  SerGlyGlyGlyGlyAlaAenValAenSerValValThrGlySerPheAenGlyIle 62
Db      227 AGTGGGGCGGTGGTGGCAAGTGGCTAGCGTGTCAACCGGCTCTTCTTCAACGGGCATC 286
Qy      63  LysAenGlnAlaGlySerGlyCysGlnGlyLysAenPheTyrThrArgSerAlaPheLeu 82
Db      287 AAGAGCCAGGCGGGAGCGGGTGCAGGGGCAAGAACTTCTACACCGGAGCGGCTTCTGTG 346
Qy      83  SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db      347 AGCGCGGTCAAGGGGTACCCAGGCTTCGCCCATGGCGGGTGCAGGGTGCAGGGCAAGCGC 406
Qy      103 GluIleAlaAlaPhePheAlaHisAlaThrHisGlu----- 114
Db      407 GAGATCGCGCCCTTCTTGGCGCACGCCACGACGACGAGACCGGGCGTAAGCTGGCTCTATCT 466
Qy      114 ----- 114
Db      467 ATTAACCTCGCTCTTCAGCGCGCGCAGGTCTTTTGATTTTTCACCATCATGCTGATCA 526
Qy      115 -----ThrGlyHis-PheCysTy 120
Db      527 ATTTTTCGAAATTTTCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 586
Qy      120 rIleSerGluIleSerLysSerAenAlaTyrCysAspProThrLysArgGlnTrpProCys 140
Db      587 CATCAGCGAGATCAACAAGAGAACGCTACTCGGACCCGACCAAGAGGAGTGGCGGTG 646
Qy      140 sAlaAlaGlyGlnLysTyrTrpGlyArgGlyProLeuGlnIleSerTrpAenTyrAenTy 160
Db      647 CGCGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 706
Qy      160 rGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAa 180
Db      707 CGGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 766
Qy      180 gAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAenAenValHisArgVa 200
Db      767 GGACGGCGGTGGTGGCTTCAAGGGCGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 826
Qy      200 lMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAspG 220
Db      827 GGTGCGCGAGGGTTCGGCGCCACACGAGGGCGCATCAACGGGGCGGCTCGAGTGGCGCGG 886
Qy      220 YAenAenProAlaGlnMetAenAlaArgIleGlyTyrTrpLysGlnTyrCysArgGlnLe 240

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Db      887 GAACAACCCGCCAGATGAACGCGCGTGGCTACTACAGGCACTACTCGCCAGCT 946
Qy      240 uGlyValAspProGlyProGlyLeuThrCys 250
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RESULT 9
AY532725
LOCUS   1114 bp DNA linear PLN 29-JUL-2004
DEFINITION
Zea mays subsp. parviglumis isolate p3b chitinase (chiB) gene,
complete cds.
ACCESSION
AY532725
VERSION
AY532725.1 GI:48093231
KEYWORDS
ORGANISM
Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 1114)
Tiffin,P.
COMPARATIVE evolutionary histories of chitinase genes in the genus
zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
PUBMED
15280246
REFERENCE
2 (bases 1 to 1114)
Tiffin,P.
Direct Submission
Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
1445 Gortner Ave., St. Paul, MN 55108-1095, USA
LOCATION/Qualifiers
1. 1114
/organism="Zea mays subsp. parviglumis"
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/isolate="p3b"
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/db_xref="taxon:76912"
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/protein_id="AAT39994.1"
/db_xref="GI:48093232"
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CDFSKRQWPCAGQKTYGRGPLQISWNINYPAGRAIGFDGLDGPGRVARDVAVFA
ALMFWMNSVHGVVPGFGATRAINGALECGNNPAQMNARVGYRQYCRQLGVDFGP
NLTC"

gene
mRNA
CDS

ORIGIN
Alignment Scores:
Pred. No.: 8.02e-91 Length: 1114
Score: 1298.00 Matches: 236
Percent Similarity: 84.03% Conservative: 6
Best Local Similarity: 81.94% Mismatches: 6
Query Match: 92.19% Indels: 40
DB: 8 Gaps: 2

US-10-692-367-70 (1-250) x AY532725 (1-1114)

Qy      3 GlnAenCysGlyCysGlnProAenValCysCysSerLySphGlyTyrCysGlyThrThr 22
Db      107 CAGAACTGGGCTGCCAGCCAAACGCTCTGCTGACAGCAAGTTCCGCTACTCGGCACGACC 166
Qy      23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSer---GlyGlyGlyGly 41

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Db      167 GACGAGTACTGCGCGCAGCGGTCCTCAGTCCGGGCCCTCGCGCTCGCGCGCGCGCGGC 226
Qy      42 SerSerGlyGlyGlyGlyAlaAenValAlaSerValValThrGlySerPhePheAenGly 61
Db      227 AGCAGTGGCGCGGTGGTGGCAACGTGGCTAGGCTGTCACCGGCTCTTCTTTCACGCGC 286
Qy      62 IleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPhe 81
Db      287 ATCAAGAACCCAGCGCGGAGCGGTCGAGGCGCAAGAACTTCTACACCCGCGAGCGCGTTC 346
Qy      82 LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101
Db      347 CTGAGCGCGCTCAAGCGCTTCCAGGCTTCGCCCATGGCGGGTCGGCGGTCGACGGGCAAG 406
Qy      102 ArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHis----- 117
Db      407 CGCGAGATCGCCGCTTCTTTCGGCGCAGCCACGACGAGACCAGGCGGTAAAGTTGGCTCGG 466
Qy      117 ----- 117
Db      467 TCTTCGCGCGCGCAGGTTCTTTGTATTTTGTACCCATCATGCTGATCAATTTCTTTT 526
Qy      118 -----PheCysTyrLleSer 122
Db      527 TTTTGTGAAATTCGCTGCTGTGTGTGTGTCACGGGCAGATTTCTGCTACATCAGC 586
Qy      123 GluIleSerLysSerAenAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAla 142
Db      587 GAGATCAACAGAGCAACGCTACTGCGACCCGACGAGGAGGAGTGGCGTGGCGCGCG 646
Qy      143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAenTyrAenTyrGlyPro 162
Db      647 GGGCAGAGTACTACGGCGCGCGCTGTCAGATCTCGTGGAACTACAACTACGGGCCC 706
Qy      163 AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla 182
Db      707 GCGGAGGAGGCCATCGGCTTCGACGGGCTCGGGGACCCCGGAGGGTGGCGCGGAGCGCC 766
Qy      183 ValValAlaPheLysAlaAlaLeuTyrPheTyrMetAenValHisArgValMetPro 202
Db      767 GTGGTGGGCTTCAAGGCGCGGCTCTGGTCTGGATGAACAGCGTGCACGGGGTGGTCCG 826
Qy      203 GlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAspGlyAenAen 222
Db      827 CAGGGGTTTCGGCGCCACCAAGGCGCATCAAGGCGCGCTCGAGTGGCGGCGGAAACAAC 886
Qy      223 ProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyVal 242
Db      887 CCCGCCAGATGAACGCGCGCTCGGCTACTACAGGCACTACTGCGCGGAGTCTCGCGGTC 946
Qy      243 AspProGlyProAenLeuThrCys 250
Db      947 GACCCGGGCGCCAACTCAGCTGC 970

RESULT 10
AY532729
LOCUS   1123 bp DNA linear PLN 29-JUL-2004
DEFINITION
Zea mays subsp. parviglumis isolate p6 chitinase (chiB) gene,
complete cds.
ACCESSION
AY532729
VERSION
AY532729.1 GI:48093239
KEYWORDS
SOURCE
ORGANISM
Zea mays subsp. parviglumis
Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 1123)
Tiffin,P.
COMPARATIVE evolutionary histories of chitinase genes in the genus
zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
PUBMED
15280246

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REFERENCE
AUTHORS      Tiffin, P.
TITLE        Direct Submission
JOURNAL      Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
              1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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              /db_xref="taxon:76912"
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              NAYCDPTKRWQCAAGQKYYGRGLQISWNYNTPGPRAGI GFDGLGDPGRVARDVVA
              FKALWFWMNSVHGVPQGFATRAINGALECGGNPAQMNARVGYRYQYCRQLGVD
              PGPNLTC"

  gene
  mRNA
  CDS

ORIGIN
Alignment Scores:
Pred. No.:      1.64e-90      Length:      1123
Score:          1294.00      Matches:      238
Percent Similarity: 83.51%      Conservative: 5
Best Local Similarity: 81.79%      Mismatches: 5
Query Match:     91.90%      Indels:      43
DB:              8          Gaps:          2

US-10-692-367-70 (1-250) x AY532729 (1-1123)

Qy      3  GlnAenCyGlyCysGlnProAasnValCysCySerLySphGlyTyrCysGlyThrThr 22
Db      110 CAGAACTCGCGCTGCCAGCCAAAGCTGTGTCGAGCAAGTTTCGGCTACTCGCGCAGCAC 169
Qy      23  AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlyGlyGly 41
Db      170 GACGAGTACTCGCGGACGGGTGCAGTCGGGCCCGTGCCTCGCGCGCGCGCGGCGGCGAGC 229
Qy      42  SerSerGlyGlyGlyGlyAlaAasnValAlaSerValThrGlySerPhePheAasnGly 61
Db      230 AGCAGTGGCGCGGTGGTGGCAAGCTGCTAGCGTGCCTCAGCGGCTCTTCTTCAACGGC 289
Qy      62  IleLyAenGlnAlaGlySerGlyCysGluClyLyAenPheTyrThrArgSerAlaPhe 81
Db      290 ATCAAGAACCAAGCGCGAGCGGTGCGAGGCAAGAACTTCTACACCCGAGCGCGTTC 349
Qy      82  LeuSerAlaValLyAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101
Db      350 CTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGCGCGGTGCGAGGTGCAGGGCGAG 409
Qy      102 ArgGluLeuAlaAlaPhePheAlaHisAlaThrHisGlu----- 114
Db      410 CGCGAGATCGCGCGCTTCTTCGCGCAGCCACGACGAGACCGGCGGCTAAAGTTGGCTCGG 469
Qy      114 ----- 114
Db      470 TCTTCCGCGCGCGAGGTTCTTTGATTTTAAATTGACCCATCATGCTGATCAATTTT 529
Qy      115 -----ThrGlyHis-PheCysTyr 120
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Qy      120 rIleSerGluIleSerLySerAenAlaTyrCysAspProThrLyAargGlnTrrProCy 140
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Qy      140 sAlaAlaGlyGlnLySerTyrGlyArgGlyProLeuGlnIleSerTrrPheAenTyrAenTy 160
Db      650 CGCGCGCGGCGAGAGTACTACGGCGCGCGCGCTCGAGATCTCTGTGGAACTACAACCTA 709
Qy      160 rGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAar 180
Db      710 CGGCGCGCGCGGAGGCCCATCGGCTTCGAGCGGCTCGGGAGCCCGCGCAGGTGGCGCG 769
Qy      180 gAspAlaValAlaPheLyAlaLeuTrrPheTrrPheTrrPheTrrPheTrrPheTrrPheTrr 200
Db      770 GGACGCGCGTGGTGGTCAAGCGCGCGCTCTGGTTCTGGATGAACAGCGGTGCAACGGGT 829
Qy      200 lMetProGlnGlyPheGlyAlaThrIleArgAlaIleAasnGlyAlaLeuGlyCysAspGly 220
Db      830 GGTGCCCGAGGGTTTCGGCGCCACCCAGGCGCATCAAGCGGCGCTCTCGAGTGGCGCGG 889
Qy      220 YasnAasnProAlaGlnMetAenAlaArgIleGlyTyrLySglnTyrCysArgGlnLe 240
Db      890 GAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGGCGAGTACTGCGCGCAGCT 949
Qy      240 uGlyValAspProGlyProAasnLeuThrCys 250
Db      950 CGGCGTGCACCGCGCGGCCAACCTCACCTGC 980

RESULT 11
LOCUS      AY532727                      1133 bp      DNA      linear      PLN 29-JUL-2004
DEFINITION Zea mays subsp. parviglumis isolate p5 chitinase (chIB) gene,
complete cds.
ACCESSION  AY532727
VERSION    AY532727.1  GI:48093235
KEYWORDS
SOURCE     Zea mays subsp. parviglumis
            Zea mays subsp. parviglumis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1. (bases 1 to 1133)
            Tiffin, P.
            Comparative evolutionary histories of chitinase genes in the genus
            Zea and family poaceae
            Genetics 167 (3), 1331-1340 (2004)
PUBMED    15280246
REFERENCE  2. (bases 1 to 1133)
            Tiffin, P.
            Direct Submission
            Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
            1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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AYCDPSKRWPCAGAKYIGRGPLQISWNYNYPAGRAIGFDGLGDPGRVARDVAVAF
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GPNLTC"

ORIGIN
Alignment Scores:
Pred. No.: 1,81e-90 Length: 1133
Score: 1293.50 Matches: 235
Percent Similarity: 83.16% Conservative: 7
Best Local Similarity: 80.76% Mismatches: 6
Query Match: 91.87% Indels: 43
DB: 8 Gaps: 2

US-10-692-367-70 (1-250) x AY532727 (1-1133)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThr 22
Db 113 CAGAACTCGGCTGCCAGCCAAAGCTCTGCTGCAGCAAGTTCCGCTACTCGGCACGACC 172
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSer---GlyGlyGly 41
Db 173 GACGAGTACTCGCGCGACGGGTGCGAGTCCGGCGCGCTGCGCGCTCGGGCGCGCGCGGC 232
Qy 42 SerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGly 61
Db 233 GGCAGTGGTGGCGGTGTGTGCGAAGTGGCTAGGCTGCTACCGGCTCTCTTCTTCAACGGC 292
Qy 62 IleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPhe 81
Db 293 ATCAAGACCGAGCGCGGAGGGGTGCGAGGCGAGAACTTCTACACCGCGAGCGGCTC 352
Qy 82 LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101
Db 353 CTGAGCGCGTCAAGCGGTACCCAGGGTTCGCCCATGCGCGGTGCGAGGTGCGAGGCGAAG 412
Qy 102 ArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHis----- 117
Db 413 CGCGAGATCGCGCGCTTCTTCGCGCACGCCACGACGAGACCGCGCGCGTAAGTTGGTCCG 472
Qy 117 ----- 117
Db 473 GCCTTCGCGCGCCACAGGTTCTTTGATTTTAAATTTGACCATCATGCTGATCAATTT 532
Qy 118 -----PheCys 119
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Qy 120 TyrIleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrPro 139
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Qy 140 CysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsn 159
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Db 713 TACGGGCGCGCGGAGGGCCATCGGCTTCGACGGGCTCGGGGACCCCGCGAGGGTGGCG 772
Qy 180 ArgAspAlaValValAlaPheLysAlaAlaLeuTyrPheTrpMetAsnAsnValHisArg 199
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953 CTGCGGCTCGACCCCGGGCCCACTCACTGCG 985

RESULT 12
AY532726 1123 bp DNA linear PLN 29-JUL-2004
LOCUS Zea mays subsp. parviglumis isolate p4 chitinase (chiB) gene,
DEFINITION complete cds.
ACCESSION AY532726
VERSION AY532726.1 GI:48093233
KEYWORDS
SOURCE Zea mays subsp. parviglumis
ORGANISM Zea mays subsp. parviglumis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1123)
Tiffin,P.
Comparative evolutionary histories of chitinase genes in the genus
Zea and family poaceae
Genetics 167 (3), 1331-1340 (2004)
PUBMED 15280246
REFERENCE 2 (bases 1 to 1123)
Tiffin,P.
Direct Submission
AUTHORS
TITLE Submitted (23-JAN-2004) Plant Biology, University of Minnesota,
JOURNAL 1445 Gortner Ave., St. Paul, MN 55108-1095, USA
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Location/Qualifiers
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NLTC"

ORIGIN
Alignment Scores:
Pred. No.: 2,14e-90 Length: 1123
Score: 1292.50 Matches: 235
Percent Similarity: 82.82% Conservative: 6
Best Local Similarity: 80.76% Mismatches: 7
Query Match: 91.80% Indels: 43
DB: 8 Gaps: 2

US-10-692-367-70 (1-250) x AY532726 (1-1123)
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Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThr 22
Db 107 CAGAACTCGGCTGCCAGCCAAAGCTCTGCTGCAGCAAGTTCCGCTACTCGGCACGACC 165
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSer---GlyGlyGly 41
Db 167 GACGAGTACTCGCGCGAGTGCAGTCCAGTCCGGCGCGCTCGCGCGCGCGCGCGG 226
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QY 42 SerSerGlyGlyGlyAlaAenValaSerValThrGlySerPheAenGly 61  
 Db 227 GGCAGTGGTGGGTGGTGGAACTGGCTAGCGTCTGACCAAGCTCTTCAACGGC 286

QY 62 IleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPhe 81  
 Db 287 ATCAAGAACCCAGCGCGGAGGGTGGAGGCAAGAACTTCTACACCGGAGCGCTTC 346

QY 82 LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101  
 Db 347 CTGAGCCCGCTCAAGGGGTACCCAGGGTTCGCCCATGGCGGTGCAGAGTGCAGGGCAAG 406

QY 102 ArgGluLeuAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHis----- 117  
 Db 407 CGCAGATCGCGCTCTTTCGCCGACGCCAGCAGAGACCGGGCGCTAAGTGGCTCTTA 466

QY 117 ----- 117

Db 467 TCTATTAACTCGCTCTTCAGCGCGGCAGGTTCTTTGATTTTGTACCCCATCATGCTGA 526

QY 118 -----PheCys 119  
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QY 120 TyrIleSerGluIleSerLysSerAenAlaTyrCysAspProThrLysArgGlnTyrPro 139  
 Db 587 TACATCAGCGAGATCAACAAGAGAACGCTTCTGCGACCCGAGCAAGAGGCGAGTGGCCG 646

QY 140 CysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAenTyrAen 159  
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QY 160 TyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAla 179  
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QY 180 ArgAspAlaValAlaAlaPheLysAlaAlaLeuTyrPheTyrMetAenAenValHisArg 199  
 Db 767 CGGACGCCCTGGTGGCGTTCAGAGCGCGCTCTGCTTCTGAGTGAACACGCGTGCACGG 826

QY 200 ValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAsp 219  
 Db 827 GTGGTGGCGGAGGGTTCGGCGCCACCACCGGGCCATCAACGGCGCCCTCGAGTGGCG 886

QY 220 GlyAenAenProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGln 239  
 Db 887 GGGAAACAACCCGCCAGATGAACCGCGGCTCGGCTACTACAGGCAGTACTCGCGCCAG 946

QY 240 LeuGlyValAspProGlyProAenLeuThrCys 250  
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RESULT 13  
 LOCUS AY532740 1128 bp DNA linear PLN 29-JUL-2004  
 DEFINITION Zea diploperennis isolate d6 chitinase (chiB) gene, complete cds.  
 ACCESSION AY532740  
 VERSION AY532740.1 GI:48093261  
 KEYWORDS  
 SOURCE Zea diploperennis  
 ORGANISM Zea diploperennis  
 BUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;  
 SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES; POACEAE; PACCAD  
 CLADE; PANICOIDEAE; ANDROPOGONEAE; ZEA.  
 1 (bases 1 to 1128)  
 Tiffin, P.  
 Comparative evolutionary histories of chitinase genes in the genus  
 zea and family poaceae  
 Genetics 167 (3), 1331-1340 (2004)  
 15280246  
 2 (bases 1 to 1128)  
 Tiffin, P.  
 Direct Submission

JOURNAL Submitted (23-JAN-2004) Plant Biology, University of Minnesota,  
 1445 Gortner Ave., St. Paul, MN 55108-1095, USA  
 FEATURES Location/Qualifiers  
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 /organism="Zea diploperennis"  
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 GSGCEKNFTVRSAPLSAVKAYPGFAHGSQVCKREIAAFPAHAHETGHFCV ISRI  
 NKSNAYCDPSKQWPCAAQKYYGRCPLQISNNYNGPAGRAIGFDGLDGPGRVADA  
 VVAFKAALWFNWSVHGVTVPQSFQATRAINGALECGNNPAQNNARVGYRYQYCRQL  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 5 21e-90 Length: 1128  
 Score: 1207.50 Matches: 237  
 Percent Similarity: 82.09% Conservative: 6  
 Best Local Similarity: 80.07% Mismatches: 5  
 Query Match: 91.44% Indels: 48  
 DB: 8 Gaps: 2

US-10-692-367-70 (1-250) x AY532740 (1-1128)  
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 Db 107 CAGAACCTGGCTGCGCAGCNAACGCTCTGTCGACGAACTTCGGCTACTCGCGCAGCACC 166  
 QY 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGly 41  
 Db 167 GACGAGTACTGCGGCGACCGGTGCCAGTCCGGCCCGCTCGCGCGCGCGCGCGG 226  
 QY 42 -----SerSerGlyGlyGlyGlyAlaAenValAlaSerValValThr 55  
 Db 227 GCGCGCGCGCGCGCGCAGCAGCAGTGGCGCGGTGGTCCGACCTGGCTAGCTGCTCACC 286  
 QY 56 GlySerPheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAenPhe 75  
 Db 287 GGCCTCTTCTCAACGGCATCAAGAACCGCGCGGCGGTGCGAGGCGGCAAGAACTTC 346  
 QY 76 TyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGly 95  
 Db 347 TACACCGGAGTGGCTTCTGAGCGCGCTCAAGCGGTACCCAGGCTTCGCCCATGGCGGG 406  
 QY 96 SerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGlu 114  
 Db 407 TCGAGGTGCGAGGCAAGCGGAGATCGCGGCTTTCTTCGCGCACCCACGACGAGACC 466  
 QY 114 ----- 114  
 Db 467 GGGCGTAAGTGGCTCGGTCTTCGCGCGCGCAGGTTCTTTGATTTTAAATTTGACCCA 526  
 QY 115 -----Thr 115  
 Db 527 TCATGCTGATCAAAATTTATTTTTTTTGGAAAAATTTTTCGCTGCTGCTGTGTGTGACG 586  
 QY 116 GlyHis-PheCysTyrIleSerGluIleSerLysSerAenAlaTyrCysAspProThrLys 135  
 Db 587 GGCAGATTCTGCTACATCAGCGAGATCAACAAGAGCAACGCGCTACTCGGACCCGAGCAA 646





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 15:33:17 ; Search time 370.316 Seconds  
(without alignment)  
3996.417 Million cell updates/sec

Title: US-10-692-367-70

Perfect score: 1408

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Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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6: geneseqn2002as:\*  
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9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1408	100.0	753	13 ADS92685	Adg92685 Chitinase
2	1377	97.8	753	13 ADS92667	Adg92667 Chitinase
3	1372	97.4	753	13 ADS92697	Adg92697 Chitinase
4	1366	97.0	753	13 ADS92683	Adg92683 Chitinase
5	1363	96.8	753	13 ADS92693	Adg92693 Chitinase

6	1360	96.6	753	13 ADS92671	Adg92671 Chitinase
7	1358	96.4	753	13 ADS92659	Adg92659 Chitinase
8	1357.5	96.4	774	13 ADS92687	Adg92687 Chitinase
9	1351	96.0	753	13 ADS92665	Adg92665 Chitinase
10	1351	96.0	1094	3 AAA96222	Aaa96222 cDNA enco
11	1350	95.9	753	13 ADS92669	Adg92669 Chitinase
12	1348	95.7	753	13 ADS92637	Adg92637 Chitinase
13	1348	95.7	771	13 ADS92663	Adg92663 Chitinase
14	1345	95.5	771	13 ADS92689	Adg92689 Chitinase
15	1344	95.5	771	13 ADS92675	Adg92675 Chitinase
16	1342	95.3	771	13 ADS92677	Adg92677 Chitinase
17	1341	95.2	753	13 ADS92651	Adg92651 Chitinase
18	1336.5	94.9	750	13 ADS92695	Adg92695 Chitinase
19	1335.5	94.9	774	13 ADS92681	Adg92681 Chitinase
20	1335	94.8	771	13 ADS92699	Adg92699 Chitinase
21	1328.5	94.4	774	13 ADS92645	Adg92645 Chitinase
22	1328.5	94.4	774	13 ADS92649	Adg92649 Chitinase
23	1325.5	94.1	780	13 ADS92655	Adg92655 Chitinase
24	1324.5	94.1	780	13 ADS92691	Adg92691 Chitinase
25	1323	94.0	753	13 ADS92673	Adg92673 Chitinase
26	1322.5	93.9	774	13 ADS92661	Adg92661 Chitinase
27	1321.5	93.9	774	13 ADS92679	Adg92679 Chitinase
28	1319	93.7	753	13 ADS92647	Adg92647 Chitinase
29	1318.5	93.6	774	13 ADS92627	Adg92627 Chitinase
30	1312	93.2	753	13 ADS92643	Adg92643 Chitinase
31	1309.5	93.0	774	13 ADS92653	Adg92653 Chitinase
32	1300.5	92.4	774	13 ADS92639	Adg92639 Chitinase
33	1285	91.3	771	13 ADS92657	Adg92657 Chitinase
34	1283.5	91.2	774	13 ADS92623	Adg92623 Chitinase
35	1271.5	90.3	840	11 ADJ12126	Adj12126 Maize cDN
36	1255	89.1	765	13 ADS92641	Adg92641 Chitinase
37	1253	89.0	777	13 ADS92631	Adg92631 Chitinase
38	1245	88.4	777	13 ADS92619	Adg92619 Chitinase
39	1244.5	88.4	756	13 ADS92629	Adg92629 Chitinase
40	1242.5	88.2	756	13 ADS92621	Adg92621 Chitinase
41	1236.5	87.8	756	13 ADS92625	Adg92625 Chitinase
42	1011.5	71.8	843	8 ADA70140	Ada70140 Rice gene
43	1011.5	71.8	843	11 ADJ11575	Adj11575 Rice cDNA
c 44	1011.5	71.8	906	11 ADJ11773	Adj11773 Rice cDNA
c 45	1011.5	71.8	909	11 ADJ11435	Adj11435 Rice cDNA

#### ALIGNMENTS

RESULT 1  
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ID ADS92685 standard; DNA; 753 BP.  
XX  
AC ADS92685;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
Chitinase variant polynucleotide #32.  
DE  
Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
(VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Muller ML, True T, Simmons CR, Yalpani N;

```
XX WPI; 2004-365417/34.
DR P-PSDB; ADS92666.
XX
PT New chitinase polynucleotides and polypeptides, useful in producing
FT plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 4; SEQ ID NO 69; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC polynucleotide of the invention. The nematode is from the genus
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 141 A; 245 C; 261 G; 106 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,31e-117 Length: 753
Score: 1408.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92666 (1-753)

QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTGGCGTGCAGCAAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60

QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
DB 61 ACAACCGACGAGTACTGGCGGCAGCGGTGCCAGTCCGCGCCGCTCGCGCGCGGC 120

QY 41 GlySerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsn 60
DB 121 GGCACGAGTGGCGCGGTGGTGCAGAACGTGGTACGGTCCGTCACCGGCTCTCTTCAAC 180

QY 61 GlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80
DB 181 GCATCAAGAACCGCGCGGAGCGGTGCGAGGCGCAAGACTTCTACACCGGAGCGG 240

QY 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100
DB 241 TTCCTGAGCGCGTCAAGCGGTACCGAGGCTTCGCCCATGGCGGTCAACGGTGCAGGCG 300

QY 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
DB 301 AAGCCGAGATCGCCGCTTCTTCGCGCAGCGCACGACGAGACCGGGCATTTCTGTATAC 360

QY 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140
DB 361 ATCAGCGAGATCAGCAAGCAAGCAACCGCTTACGAGACCGCGGACGAGCGGTGCGGTC 420

QY 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyr 160
DB 421 GCGCGCGGCGCAGAACTACTACGGCGCGCGCGCTGTCAGATCTCGTGAACCTACAACTAC 480

QY 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
DB 481 GGGCCCGCGGGGAGGAGCATCGGCTTCACGCGGCTTCGGGGACCGCGGCGGCGGCGG 540

QY 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200
DB 541 GACGCGGTGGTGGCTTCAAGCGCGCGCTCTGGTTCTGGATGAACAACTGCACCGGTG 600

QY 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220
DB 1 TCGATGCAGAACTGGCGTGCAGCAAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60
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DB 601 ATGCGCGAGGCTTCGGCGCCACCACCATCAGGCGCCATCAACGCGCGCTCGAGTGCAGCGG 660
QY 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240
DB 661 AACAAACCCCGCCAGATGAACGCGCATCGGCTACTACAAGCAGTACTGCGCGCAGCTC 720
QY 241 GlyValAspProGlyProAsnLeuThrCys 250
DB 721 GCGCTGCGACCCAGGCGCCCAACCTCACTTGC 750

RESULT 2
ADS92667
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XX
AC ADS92667;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polynucleotide #23.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PI (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
WPI; 2004-365417/34.
DR P-PSDB; ADS92668.
XX
New chitinase polynucleotides and polypeptides, useful in producing
plants with enhanced resistance against a fungus or a nematode.
XX
Claim 4; SEQ ID NO 51; 197pp; English.
XX
The invention relates to chitinase polypeptides and the polynucleotides
encoding them. A method of enhancing plant resistance to a fungus or
nematode comprises introducing into a plant a recombinant expression
cassette comprising a promoter operably linked to a chitinase
polynucleotide of the invention. The plant is maize or soybean. The
fungus is from the genus Fusarium. The nematode is from the genus
Heterodera. The polynucleotides and polypeptides are useful in enhancing
plant resistance to a fungus or nematode. This sequence represents a
chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 135 A; 245 C; 265 G; 108 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.2e-114 Length: 753
Score: 1377.00 Matches: 243
Percent Similarity: 98.80% Conservative: 4
Best Local Similarity: 97.20% Mismatches: 3
Query Match: 97.80% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92667 (1-753)

QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTGGCGTGCAGCAAAAGTATGCTGCAGCAAGTTTCGGCTACTGCGGC 60
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Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACGACCGACGAGTACTGCGCGGACGGGTGCGAGTCCGGCCCGTCCGCTCGGGCGGCG 120  
Qy 41 GlySerSerGlyGlyGlyValAsnValAlaSerValValThrGlySerPhePheAen 60  
Db 121 GCGACGAGTGGCGGGTGGTGGCGAACGTGCTAGCTGCTGACCGGCTCTCTTTCAAC 180  
Qy 61 GlyTleYsAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80  
Db 181 GGCATCAAGACCGAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGG 240  
Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlySerGlnValGlnGly 100  
Db 241 TTCTCTAGCGCGGTCAAGCGGTACCCAGGCTTCGCCCATGCGGGTCCAGGTGCGAGGCG 300  
Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120  
Db 301 AAGCGCGAGATCGCGGCTCTTCGCGCATGTGACGACAGAGACCGGGCATTTCTGCTAC 360  
Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140  
Db 361 ATCAGCGAGATCAACAGGACGACGCTACTGCGACCGCGGCGGCACTGCGCGTGC 420  
Qy 141 AlaAlaGlyGlnLysTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160  
Db 421 GCCCGCGGCGAAGTACTACGGCGCGCGCGCTGCTGCGAGATCTGCTGGAACCTACACTAC 480  
Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180  
Db 481 GGGCGCGGCGGAGGCGCATCGCTTCACCGGCTCGGGGACCGCGGCGGCGGCGG 540  
Qy 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200  
Db 541 GACGCGGTGGTGGCGTTCAAGCGCGGCTCTGTTCTGATGACCAAGCTGACCGTGTG 600  
Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220  
Db 601 ATGCGCGAGGCTTCGGCGGCCACCATCAGGCGCATCAACGGCGGCTCGAGTGGCGGG 660  
Qy 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240  
Db 661 AACAAACCGCGCGCGAGATCAAGCGCGCTCGCTACTACAGGAGTACTGCGCGGCGGCTC 720  
Qy 241 GlyValAspProGlyProAsnLeuThrCys 250  
Db 721 GCGGTGCGACCGGCGGCGCACTCACTTGC 750

## RESULT 3

ADS92697

ID ADS92697 standard; DNA; 753 BP.

XX AC ADS92697;

XX DT 02-DEC-2004 (first entry)

XX DE Chitinase variant polynucleotide #38.

XX KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

XX OS Heterodera.

XX PN Synthetic.

XX WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

XX PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;  
PI

XX WPI; 2004-365417/34.

DR P-PSDB; ADS92698.

XX New chitinase polynucleotides and polypeptides, useful in producing  
plants with enhanced resistance against a fungus or a nematode.

XX Claim 4; SEQ ID NO 81; 197pp; English.

XX The invention relates to chitinase polypeptides and the polynucleotides  
encoding them. A method of enhancing plant resistance to a fungus or  
nematode comprising introducing into a plant a recombinant expression  
cassette comprising a promoter operably linked to a chitinase  
polynucleotide of the invention. The plant is maize or soybean. The  
fungus is from the genus Fusarium. The nematode is from the genus  
Heterodera. The polynucleotides and polypeptides are useful in enhancing  
plant resistance to a fungus or nematode. This sequence represents a  
chitinase variant polynucleotide of the invention.

XX Sequence 753 BP; 140 A; 240 C; 263 G; 110 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8.98e-114 Length: 753

Score: 1378.00 Matches: 243

Percent Similarity: 98.40% Conservative: 3

Best Local Similarity: 97.20% Mismatches: 4

Query Match: 97.44% Indels: 0

DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92697 (1-753)

Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20

Db 1 TCGATGCAGAACTGCGGCTGCCAGCAACATATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40

Db 61 ACGACCGACGAGTACTGCGGCGACGGGTGCGAGTTCGGGCGCGCTGCGACTCGGGGCGGCG 120

Qy 41 GlySerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAen 60

Db 121 GGCAGCAGTGGCGGCGTGGTGGCAATGTGGTAATGTGGTCAACCGACGCTTCTTCAAC 180

Qy 61 GlyTleYsAsnGlnAlaGlySerGlyCysGluClyLysAsnPheTyrThrArgSerAla 80

Db 181 GGCATCAAGAACCCAGCGCGGAGCGGTGCGAGGCGCAAGAACTTCTACACCGGAGCGCG 240

Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100

Db 241 TTCTCTAGCGCGGTCAAGGCGTACCCAGGCTTCGCCCATGCGGGGTGCGAGTGCAGGCG 300

Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120

Db 301 AAGCGCGAGATTGCGGCTTCTTCGCGCATGCCACGACGACGAGACCGGCACTTCTGCTAC 360

Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140

Db 361 ATCAGCGAGATCAACAGAGCAACGCTTACTGCGACCGCGGCGGCGGCAAGAGCGAGTGC 420

Qy 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160

Db 421 GCCCGCGGCGAAGTACTACGGGCGGCGCGCTGCGAGATCTCTGTTGGAATCTACACTAC 480

Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180

Db 481 GGGCGCGGCGGAGGCGCATCGGCTTCAGCGGCTTCGGGACCGCGGCGGCGGCGGCGG 540

Qy 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200

Db 541 GACCGCTGGTGGCTTCAAGCGCGCTCTGGTTCTGGATGAACAACGTCACCGTGTG 600  
Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220  
Db 601 ATCCCGCAGGGTTCGGTGGCCACCATCCGGGCCATCAACGGCGCTCGAGTGGCGCGG 660  
Qy 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240  
Db 661 AACACCCCGCCAGATGACGCGCGCATCGGCTACTACAGCAGTACTGCGCCGAGCTC 720  
Qy 241 GlyValAspProGlyProAsnLeuThrCys 250  
Db 721 GCGCTGACCCAGGGCCCAACCTCACTTGC 750

## RESULT 4

ADSS92683  
ID ADS92683 standard; DNA; 765 BP.

AC  
XX  
XX

DT 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #31.

DE Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

XX Synthetic.

XX WO2004037194-A2.

XX PD 06-MAY-2004.

XX PF 22-OCT-2003; 2003WO-US033588.

XX PR 22-OCT-2002; 2002US-0420666P.

PR 06-NOV-2002; 2002US-00290086.

XX PR 14-MAR-2003; 2003US-00389432.

XX PA (VERD-) VERDIA INC.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Muller ML, True T, Simmons CR, Yalpani N;

XX DR P-PSDB; ADS92684.

XX DR WPI; 2004-365417/34.

XX DR P-PSDB; ADS92684.

XX PS Claim 4; SEQ ID NO 67; 197pp; English.

CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

XX SQ Sequence 765 BP; 144 A; 248 C; 267 G; 106 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3.16e-113 Length: 765  
Score: 1366.00 Matches: 243  
Percent Similarity: 96.85% Conservative: 3  
Best Local Similarity: 95.67% Mismatches: 4  
Query Match: 97.02% Indels: 4  
DB: 13 Gaps: 1

US-10-692-367-70 (1-250) x ADS92683 (1-765)  
Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
Db 1 TCATATGACAACTCGGCTGCCAGCAAACTATGCTGCAGCAAGTTTCGGTACTGCGGC 60  
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
Db 61 ACAACCGACGAGTACTGCGCGACGGGTGCCAGTCCGGCCCGCTCCGCTCGGGCGCGGC 120  
Qy 41 GlySerSerGlyGly-----GlyGlyAlaAsnValAlaSerValValThrGly 56  
Db 121 GCGCGCGCGAGCGCGCGGAGGAGGTGGTGGCAACGGTGGCTAGCGTCTGTCACCGGC 180  
Qy 57 SerPhePheAsnGlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyr 76  
Db 181 TCCTTCTTCAACGGCATCAGAACAGCGCGGAGCGGGTGCAGAGGCAAGAACTTCTAC 240  
Qy 77 ThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySer 96  
Db 241 ACCCGAGCGCGTTCCTGAGCGCGTCAAGCGGTACCCAGGCTTCGCCCATGCGGGTCA 300  
Qy 97 GlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGly 116  
Db 301 CAGGTGACGAGCAAGCGCGAGATTGCCGCTTCTTCGCGCAACGCCACGACGACCGGG 360  
Qy 117 HisPheCysTyrIleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArg 136  
Db 361 CATTTCTGTACATCAGCGAGATCAACAGAGCAACGCCCTACTCGGACCCGACCAAGAG 420  
Qy 137 GlnTrpProCysAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrp 156  
Db 421 CAGTGGCGTGGCGCGCGGCGAGAGTACTACGCGCGCGCGCTCGAGATCTCGTGG 480  
Qy 157 AsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGly 176  
Db 481 AACTACAACTACGCGCGCGCGCGGAGGCCCATCGCTTCGACCGGCTCGGGAGACCCCAAC 540  
Qy 177 ArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsn 196  
Db 541 AGGTTGGCGCAGGACGCGCTGGTGGCTTCAAGGGGGGCGCTCTGGTTCTGGATGAACAAC 600  
Qy 197 ValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeu 216  
Db 601 GTGCACCGTGTGATGCGCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCGCTC 660  
Qy 217 GluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyr 236  
Db 661 GAGTGACGCGGAAACAACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGAGTAC 720  
Qy 237 CysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250  
Db 721 TGCCGCCAGCTCGGCGTCCGACCCAGGGCCCAACCTCACTTGC 762

## RESULT 5

ADSS92693

ID ADS92693 standard; DNA; 753 BP.

XX  
XX  
XX

DT 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #36.

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

XX Synthetic.

XX WO2004037194-A2.

XX PD 06-MAY-2004.

XX

```

PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR P-PSDB; ADS92671.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 77; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 142 A; 244 C; 262 G; 105 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,76e-113 Length: 753
Score: 1363.00 Matches: 240
Percent Similarity: 98.00% Conservative: 5
Best Local Similarity: 96.00% Mismatches: 5
Query Match: 96.80% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92693 (1-753)

QY 1 SerMetGlnAsnGlyCysGlnProAsnValCysSerLysPheGlyTyrCysGly 20
DB 1 TCGATGCAGAACTGCGGTGTCAGCAACAGTATGCTGCAGCAAGTTTCGGTACTGCGGC 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
DB 61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTGGGCCCGTGCCTCGGGCGGGCG 120
QY 41 GlySerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsn 60
DB 121 GCGACGACGTGGCGGGTGGTGTGAACGTGGCCAGCATCGTGACCGGCTCCTTCTTCAAC 180
QY 61 GlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80
DB 181 GGCATCAAGAACCGCGCGGAGCGGGTCCGAGGGCAAGAACTTCTACCCCGGAGCGCG 240
QY 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100
DB 241 TTCTGTAGCGCGTCAAGCGGTACCCAGCGTTCGCCCATGCGCGGACGAGGTGGAGGCG 300
QY 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
DB 301 AAGCCGAGATGTCGCGCTTCTTCGCGACGCGCACGACGAGCGCGGCATTTCTGTCTAC 360
QY 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCys 140
DB 361 ATCAGCGAGATCAGCAGAGCAACCCCTACTGCGACCCGACCAAGAGCAGTGGCGGTGC 420
QY 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyr 160
DB 421 GCCGGGGGCGAGAGTACTACGAGCGCGCGCTGCGAGATCTCGTGGAACTACAACTAC 480

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QY 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
DB 481 GGGCCCCGGGGAGGCCATCGGCTTCGACGGGTGCGGGACCCCAACAGAGGTGGCGGG 540
QY 181 AspAlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgVal 200
DB 541 GACGCGGTGGTGGGTTCAAGGCGCGCTCTGGTCTTGGATGAACAGCGTGCACCGTGTG 600
QY 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGlyCysAspGly 220
DB 601 ATGCGCGAGGGCTTCGGCGCCACCATCAGGCGCCATCAACGGCGCCTCGAGTGGCGGG 660
QY 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240
DB 661 AACAAACCGCGCCAGATGAAGCGCGCATCGGCTACTACAGAGCATGCTGCCCGCAGCTC 720
QY 241 GlyValAspProGlyProAsnLeuThrCys 250
DB 721 GGCCTCGACCCAGGGGCCCACTCACTTGC 750

RESULT 6
ADS92671
ID ADS92671 standard; DNA; 753 BP.
XX
AC ADS92671;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polynucleotide #25.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
XX (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
DR P-PSDB; ADS92672.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 55; 197pp; English.
XX
CC The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
XX
SQ Sequence 753 BP; 144 A; 245 C; 255 G; 109 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.07e-112 Length: 753
Score: 1360.00 Matches: 240

```

Percent Similarity: 97.20% Conservatives: 3  
 Best Local Similarity: 96.00% Mismatches: 7  
 Query Match: 96.59% Indels: 0  
 DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92671 (1-753)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 Db 1 TCGATGCAGAACTCGGGTGCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40  
 Db 61 ACAACGACGAGTACTCGCGGCACCGGTGCCAGTCCGCGCGGTGCCACTCGCGCGCGGT 120

Qy 41 GlySerSerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePhean 60  
 Db 121 GCGCGCGTGGCGCGGTGGTGGCAACGTGCTAGCTGCTGACCGGTCTCTTTCAAC 180

Qy 61 GlyLeLysAenGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80  
 Db 181 GGCATCAGAACCCAGCGCGGGTGGCGAGGCGAGAACTTCTACACCGCGAGCGG 240

Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100  
 Db 241 TTCTGTAGCGCGGTCAAGCGGTACCCAGGCTTGGCCCATGGCGGTCAACGGTGCAGGGC 300

Qy 101 LysArgGluLeAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120  
 Db 301 AAGCGCGAGATGCGCGCTCTTTCGCGCATGTACGACACGAGACCGGCGCATTTCTGTAC 360

Qy 121 IleSerGluLysSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140  
 Db 361 ATCAGGAGATCAACAAGACGACCGCTTCTGCGACCCGACCAAGAGCGAGTGGCGGTG 420

Qy 141 AlaAlaGlyGlnLysTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160  
 Db 421 GCGCGCGGCGAGAGTACTACGGCGCGCGCGCTGTCAGATCTCTGGAACTACAACTAC 480

Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180  
 Db 481 GGGCGCGCGGAGGAGCATCGCTTCAACGGGCTCGCCGACCCCAACAGGGTGGCGGAG 540

Qy 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200  
 Db 541 GACGCGGTGGTGGCTTCAAGCGCGGTCTGTGTTCTGATGAACAACGTGCACCGTGTG 600

Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220  
 Db 601 ATGCGCGAGGCTTGGCGGCCACCATCAGGCGCATCAACGGCGCGCTCGAGTGGCGGG 660

Qy 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240  
 Db 661 AACAAACCCCGCCAGATGAACGGCGCATCGGCTACTCAAGAGAGTACTGCGCGCGAGCTC 720

Qy 241 GlyValAspProGlyProAsnLeuThrCys 250  
 Db 721 GCGGTGAGACCCAGGCGCCCACTCACTTGC 750

## RESULT 7

ADS92659

ID ADS92659 standard, DNA; 753 BP.

XX AC

XX AD

XX 02-DEC-2004 (first entry)

XX DT

XX Chitinase variant polynucleotide #19.

XX DE

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;

XX KW

XX Heterodera.

XX OS

XX Synthetic.

XX WO2004037194-A2.  
 FN 06-MAY-2004.  
 PD 22-OCT-2003; 2003WO-US033588.  
 PF 22-OCT-2002; 2002US-0420666P.  
 XX 06-NOV-2002; 2002US-00290086.  
 PR 14-MAR-2003; 2003US-00389432.  
 XX (VERD-) VERDIA INC.  
 PA (PTON-) PIONEER HI-BRED INT INC.  
 XX Muller ML, True T, Simmons CR, Yalpani N;  
 PI WPI, 2004-365417/34.  
 XX P-PSDB; ADS92660.  
 DR New chitinase polynucleotides and polypeptides, useful in producing  
 PT plants with enhanced resistance against a fungus or a nematode.  
 XX Claim 4; SEQ ID NO 43; 197pp; English.  
 PS The invention relates to chitinase polypeptides and the polynucleotides  
 CC encoding them. A method of enhancing plant resistance to a fungus or  
 CC nematode comprises introducing into a plant a recombinant expression  
 CC cassette comprising a promoter operably linked to a chitinase  
 CC polynucleotide of the invention. The plant is maize or soybean. The  
 CC fungus is from the genus *Fusarium*. The nematode is from the genus  
 CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
 CC plant resistance to a fungus or nematode. This sequence represents a  
 CC chitinase variant polynucleotide of the invention.  
 XX SQ Sequence 753 BP; 139 A; 243 C; 262 G; 109 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.62e-112 Length: 753  
 Score: 1358.00 Matches: 239  
 Percent Similarity: 98.00% Conservative: 6  
 Best Local Similarity: 95.60% Mismatches: 5  
 Query Match: 96.45% Indels: 0  
 DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92659 (1-753)

Qy 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
 Db 1 TCGATGCAGAACTCGGGTGCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60

Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40  
 Db 61 ACGACCGACGAGTACTCGCGGCAGCGGTGCAGTCCGCGCGCGTCCGCTCGGGCGGCG 120

Qy 41 GlySerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsn 60  
 Db 121 GGCAGCAGTGGCGCGGTGGTGGCAACGTGCTAATGTGGTCAACGACGCGGTCTTCAAC 180

Qy 61 GlyLeLysAenGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80  
 Db 181 GGCATCAAGAACCCAGCGCGGAGCGGTGGCGAGGCGCAAGAACTTCTACACCGGAGCGG 240

Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100  
 Db 241 TTCTGTAGCGCGGTCAAGCGGTACCCAGGCTTGGCCCATGGCGGTCCGAGTCCGAGCGG 300

Qy 101 LysArgGluLeAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120  
 Db 301 AAGCGCGAGATGCGCGCTCTTTCGCGCATGTACGACACGAGACCGGCGCATTTCTGTAC 360

Qy 121 IleSerGluLysSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140  
 Db 361 ATCAGCGAGATCAACAAGAGCAACGCTTCTGCGACCCCGACCAAGAGCGAGTGGCGGTG 420

```
QY 141 AlalaGlyGlnLysTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyr 160
Db 421 GCCCGGGGAGAGTACTACGGCGCGCGCGCTGCAGATCTCGTGAACCTACAACTAC 480
QY 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
Db 481 GGGCCCGGGGAGGGCCATCGGCTTCAGCGGGCTCGGGGACCCCGGAGGGTGGCGGG 540
QY 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnValHisArgVal 200
Db 541 GACGCGGTGGTGGCTTCAAGCGCGGCTCTGGTTCTGGATCAACAACGTCACCGTGTG 600
QY 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGly 220
Db 601 ATGCGCAGGGGCTTCGGCGGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTGGCGGG 660
QY 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240
Db 661 AACACCCCGCCAGATGACGGCGCGCTCGGCTACTACAGCAGTACTGCGCGCAGCTC 720
QY 241 GlyValAspProGlyProAsnLeuThrCys 250
Db 721 GCGGTGAGCCAGGGGCCCAACCTCACTTGC 750
```

## RESULT 8

AD592687  
ID AD592687 standard; DNA; 774 BP.

AC AD592687;

DT 02-DEC-2004 (first entry)

DE Chitinase variant polynucleotide #33.

KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.

XX Synthetic.

OS WO2004037194-A2.

XX 06-MAY-2004.

XX 22-OCT-2003; 2003WO-US033588.

XX 22-OCT-2002; 2002US-0420666P.

PR 06-NOV-2002; 2002US-00290086.

PR 14-MAR-2003; 2003US-00389432.

XX (VERD-) VERDIA INC.

PA (PION-) PIONEER HI-BRED INT INC.

XX Muller ML, True T, Simmons CR, Yalpani N;

XX WPI; 2004-365417/34.

DR P-PSDB; AD592688.

XX Claim 4; SEQ ID NO 71; 197pp; English.

CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.

SQ Sequence 774 BP; 142 A; 249 C; 278 G; 105 T; 0 U; 0 Other;

## Alignment Scores:

Pred. NO.: 1.85e-112 Length: 774  
Score: 1357.50 Matches: 242  
Percent Similarity: 95.72% Conservative: 4  
Best Local Similarity: 94.16% Mismatches: 4  
Query Match: 96.41% Indels: 7  
DB: 13 Gaps: 1

US-10-692-367-70 (1-250) x AD592687 (1-774)

```
QY 1 SerMetGlnAnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGGCTGCCAGCAAACTATGCTGCAGCAAGTTCCGGCTACTCGCGC 60
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db 61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCCGGCCGCTGCCGCTCGGGCGGGT 120
QY 41 GlySerSerGlyGly-----GlyGlyAlaAsnValAlaSerVal 53
Db 121 GCGCGCGCGCGCGCGCGAGCGCGGAGGCAGTGGCGGTGGCGAACTGGCTAATGTG 180
QY 54 ValThrGlySerPhePheAsnGlyIleIysAsnGlnAlaGlySerGlyCysGluGlyLys 73
Db 181 GTCACCGACGCGTCTTCAACGGCATCAAGGACGAGCCGGAGCGGGTGGAGGGCAAG 240
QY 74 AsnPheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHis 93
Db 241 AACTTCTACACCGGAGCGGCTTCTGAGCGCGCTCAAGGGCTACCCAGGGTTCGCCCAT 300
QY 94 GlyGlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHis 113
Db 301 GCGCGGTCAACAGTGCAGGCGAAGCGGAGATCGCGCTTCTTCGCGCACGCCACGCGAC 360
QY 114 GluThrGlyHisPheCysTyrIleSerGluIleSerLysSerAsnAlaTyrCysAspPro 133
Db 361 GAGACCGGGCATTTCTGCTACATCAGCGAGATCAACAAGAGCAACGCTACTTGGCAGCCG 420
QY 134 ThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGln 153
Db 421 ACCAAGAGGACAGTGGCGCTGCGCGCGGGGAGAGTACTACGGGCGGGCCGCTGCAG 480
QY 154 IleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGly 173
Db 481 ATCTCGTGAACCTACAACTACGGCGCGCGGGAGGCGCATCGGCTTCGAGCGGCTCGGG 540
QY 174 AspProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrp 193
Db 541 GACCCCGGCGGGTGGCGCGGAGCGCGGTGGCGGTTCAGAGCGCGCGCTCTGGTTCTGG 600
QY 194 MetAsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsn 213
Db 601 ATGAACAACGTGCACCGCTGTGATGTCGCGCAGGGCTTCGGCGCCACCATCAGGGCCATCAAC 660
QY 214 GlyAlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyr 233
Db 661 GCGCGCTCGAGTGCAGCGGAACAACCCCGCCAGATGAACGCGCGCATCGGCTACTAC 720
QY 234 LysGlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250
Db 721 AAGCAGTACTCCGCCAGCTCGCGGTGCAGCCAGGGGCCCAACCTCACTTGC 771
```

## RESULT 9

AD592665  
ID AD592665 standard; DNA; 753 BP.

XX AD592665;

XX 02-DEC-2004 (first entry)

XX Chitinase variant polynucleotide #22.

```

XX Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
XX Synthetic.
XX
XX WO2004037194-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033588.
XX
XX 22-OCT-2002; 2002US-0420666P.
XX
XX 06-NOV-2002; 2002US-00290086.
XX
XX 14-MAR-2003; 2003US-00389432.
XX
XX (VERD-) VERDIA INC.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Muller ML, True T, Simmons CR, Yalpani N;
XX
XX WPI; 2004-365417/34.
XX
XX P-PSDB; ADS92666.
XX
XX New chitinase polynucleotides and polypeptides, useful in producing
XX plants with enhanced resistance against a fungus or a nematode.
XX
XX Claim 4; SEQ ID NO 49; 197pp; English.
XX
XX The invention relates to chitinase polypeptides and the polynucleotides
XX encoding them. A method of enhancing plant resistance to a fungus or
XX nematode comprises introducing into a plant a recombinant expression
XX cassette comprising a promoter operably linked to a chitinase
XX polynucleotide of the invention. The plant is maize or soybean. The
XX fungus is from the genus Fusarium. The nematode is from the genus
XX Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX plant resistance to a fungus or nematode. This sequence represents a
XX chitinase variant polynucleotide of the invention.
XX
XX SQ Sequence 753 BP; 138 A; 238 C; 270 G; 107 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.86e-112 Length: 753
Score: 1351.00 Matches: 237
Percent Similarity: 97.20% Conservative: 6
Best Local Similarity: 94.80% Mismatches: 7
Query Match: 95.95% Indels: 0
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92665 (1-753)

QY 1 SerMetGlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAAGAACTGCGGCTGCCAGCAACATATGCTGTCAGCAAGATTGGCTACTGCGGC 60
QY 21 ThrThrAepGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCGACGAGTACTGCGGCGACGGGTGCCAGTCGGGCCCGCTGCGGCTGCGGCGGCGGC 120
QY 41 GlySerSerGlyGlyGlyGlyAlaAenValAlaSerValValThrGlySerPhePheAen 60
Db 121 GGCAGCAGTGGCGGCGGTGTGAACGTGCCAGCATCGTGACCGGCTCTCTTCTTCAAC 180
QY 61 GlyTleLysAenGlnAlaGlySerGlyCysGlnGlyLysAenPheTyrThrArgSerAla 80
Db 181 GGCATCAAGAACACCGGCGGAGCGGTGCCAGGCGCAAGAACTTCTACACCGGAGCGGC 240
QY 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100
Db 241 TTCCTGAGCGCGGTCAAGCGGTACCCAGGCTTCCGCCATGCGGCGGAGGTGGAGGCG 300
QY 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120

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Db 301 AAGCGCAGATCGCGCGCTTCTTCGCGCATGTCCAGCATGAGACCGGSCATTTCTGCTAC 360
QY 121 IleSerGluIleSerLysSerAsnAlaTyrCysAepProThrLysArgGlnTyrProCys 140
Db 361 ATCAGCGAGATCAGAAAGAGCAACGCTTACTTGCACCGCCAGCAAGAGCAGTGGCCGTC 420
QY 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyr 160
Db 421 GCCGGGGGCAAGAGTACTACGGCGCGCGCCGCTGCGAGATCTCGTGGAACTACAACCTAC 480
QY 161 GlyProAlaGlyArgAepIleGlyPheAepGlyLeuGlyAepProGlyArgValAlaArg 180
Db 481 GGGCCCGCGGAGGCGCATCGGCTTTCGACGGGCTCGGGGACCCCGGCGAGGTGGCGCGG 540
QY 181 AspAlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHisArgVal 200
Db 541 GACGCTGTGGTGGCGTTCAAGCGCGCGCTCTGGTTCGGATGAACAGCGTGCACGGGTG 600
QY 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAepGly 220
Db 601 GCGCGCAGGGGTTGCGGCGCCACCATCAGGGCCATCAACGGCGACTCGAGTGGCGGCGG 660
QY 221 AsnAenProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeu 240
Db 661 AACCAACCGCGCCAGATGAACGCGCGCTCGGCTACTACAGCAGTACTGCCACAGCTC 720
QY 241 GlyValAepProGlyProAenLeuThrCys 250
Db 721 GCGCTGCAACCGCGGCGCAACCTCACTTGC 750

RESULT 10
AAA96222
ID AAA96222 standard; cDNA; 1094 BP.
XX
XX AC AAA96222;
XX
XX DT 08-FEB-2001 (first entry)
XX
XX DE cDNA encoding a maize chitinase polypeptide designated ZmCh2.
XX
XX KW Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase family 18;
XX pathogen control; disease resistance; molecular marker; ss.
XX
XX OS Zea mays.
XX
XX FH Key Location/Qualifiers
XX CDS 51..896
XX FT /*tag= a
XX FT /product= "chitinase"
XX
XX PN WO200056908-A2.
XX
XX PD 28-SEP-2000.
XX
XX PF 09-MAR-2000; 2000WO-US006121.
XX
XX PR 24-MAR-1999; 99US-0125915P.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Simmons CR, Yalpani N;
XX
XX P-PSDB; AAB18894.
XX
XX WPI; 2000-628269/60.
XX
XX New maize chitinase genes encoding seven chitinases of glucosyl hydrolase
XX family 19 are useful for enhancing disease resistance in crop plants by
XX modulating its expression in plants.
XX
XX PS Claim 1; Page 64-65; 96pp; English.
XX
XX CC The present sequence encodes a chitinase polypeptide. The specification
XX describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896,

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CC AAB18999, and AAB18902-05), and glucosyl hydrolase family 18 chitinases  
CC (AAB18995, AAB18997-98 and AAB18900-01). The level of chitinase in plants  
CC can be modulated to enhance disease resistance in crop plants and for  
CC control of pathogens. The chitinase polynucleotides are also useful as  
CC molecular markers for genotype in a plant, and for sequence shuffling.  
XX  
SQ Sequence 1094 BP; 226 A; 339 C; 368 G; 161 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.08e-111 Length: 1094  
Score: 1351.00 Matches: 238  
Percent Similarity: 98.39% Conservative: 6  
Best Local Similarity: 95.97% Mismatches: 4  
Query Match: 95.95% Indels: 0  
DB: 3 Gaps: 0

US-10-692-367-70 (1-250) x AAA96222 (1-1094)

QY 3 GlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
DB 150 CAGAACTCGGCTGCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGCACGACC 209  
QY 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
DB 210 GACGAGTACTCGGCGACGGGTGCCAGTCGGGCCGCTCGGCGGGCGGCGGACG 269  
QY 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPheAsnGlyIle 62  
DB 270 AGTGGCGCGGTGGTGGCAAGCTGCTAGCGTCGTACCGGCTCTCTTCAACGGCATC 329  
QY 63 LysAenGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
DB 330 AAGACCGAGCGCGGAGCGGGTGCAGGGCGAAGAACTTCTACCCCGGAGCGGTCCTG 389  
QY 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
DB 390 AGCGCGGTACAGGCTACCCAGGCTTCGCCCATGCGGGTGCAGGTGCAGGCAAGCGC 449  
QY 103 GlulleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
DB 450 GAGATCGCGCGCTTCTCGCGCACGCCACGACGAGACCGGCGCATTTCTGCTACATCAGC 509  
QY 123 GlulleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTTPProCysAlaAla 142  
DB 510 GAGATCAACACAGACAGCCCTACTGCGACCGCACCAAGAGCGCATGTGGCGCGCGC 569  
QY 143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnLysSerTrpAsnTyrAsnTyrGlyPro 162  
DB 570 GGGCAGAGTACTACGGCGCGCGCGCTGCGATCTCTGGACTACACTACGGGCGC 629  
QY 163 AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAraAspAla 182  
DB 630 CGGGGAGGGCCATCGGCTTCAGCGGCTCGGGGACCCCGCGGCGGCGGCGCGC 689  
QY 183 ValValAlaPheLysAlaAlaLeuTyrPheTyrPheTyrMetAsnAsnValHisArgValMetPro 202  
DB 690 GTGGTGGCGTTCAGCGCGCGCTCTGCTTCTGGATGAACAGCGTGCACGGGTGTGCGC 749  
QY 203 GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsn 222  
DB 750 CAGGGGTTCGGCGCACCAACAGGGCCATCAACGGCGCTCTGAGTGGCGGGGAGCAAC 809  
QY 223 ProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyVal 242  
DB 810 CCGCGCCAGATGAACCGCGGCTCGGCTACTACAGGCGAGTACTGCGCGCAGCTCGCGCGC 869  
QY 243 AspProGlyProAsnLeuThrCys 250  
DB 870 GACCCCGGGCGCCCACTCACCTGC 893

RESULT 11

ADS92669

ID ADS92669 standard; DNA; 753 BP.

XX ADS92669;  
AC  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Chitinase variant polynucleotide #24.  
XX  
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;  
KW Heterodera.  
XX  
OS Synthetic.  
XX  
PN WO2004037194-A2.  
XX  
PD 06-MAY-2004.  
XX  
PF 22-OCT-2003; 2003WO-US033588.  
XX  
PR 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-0029086P.  
PR 14-MAR-2003; 2003US-00389432.  
XX  
PA (VERD-) VERDIA INC.  
PA (PION-) PIONEER HI-BRED INT INC.  
PI Muller ML, True T, Simmons CR, Yalpani N;  
XX  
DR WPI; 2004-365417/34.  
DR P-PSDB; ADS92670.  
XX  
PT New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX  
PS Claim 4; SEQ ID NO 53; 197pp; English.  
XX  
CC The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus Fusarium. The nematode is from the genus  
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
SQ Sequence 753 BP; 141 A; 248 C; 254 G; 110 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.44e-112 Length: 753  
Score: 1350.00 Matches: 236  
Percent Similarity: 97.60% Conservative: 8  
Best Local Similarity: 94.40% Mismatches: 6  
Query Match: 95.88% Indels: 0  
DB: 13 Gaps: 0

US-10-692-367-70 (1-250) x ADS92669 (1-753)

QY 1 SerMetGlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
DB 1 TCGATGCAGAACTCGGCTGCAGCCAAACGTATGCTGCAGCAAGTTTGGCTACTGCGGC 60  
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
DB 61 ACGACCCAGCAGTACTGCGCGCGCGGGTGCAGTCGGGCGCGCTGCTCACTCGGGCGGCGC 120  
QY 41 GlySerSerGlyGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsn 60  
DB 121 GGCAGCAGTGGCGCGGGTGGTGGCAAGCTGCTAGCTGCTCAGCGGCTCTTCTTCAAC 180  
QY 61 GlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80  
DB 181 GGCATCAAGAACCGCGCGGGTGCAGGGCAAGAACTTCTACCCCGGAGCGCG 240



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Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlySerGlnValGlnGly 100
Db 241 TTCTGTAGCGCGGTCAAGCGGTACCGAGGCTTCGCCCATGGCGGTGCAGGTCGAGGCG 300
Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
Db 301 AAGCGCGAGATCGCGCGCTTCTTCGCGATGTCTACGCATGAGACCGGCGCATTTCTGTCTAC 360
Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140
Db 361 ATCAGCGAGATCAACAGAGCAACGCCCTACTGCGACCCGACCAAGAGCGATGGCCGTGC 420
Qy 141 AlaAlaGlyGlnLysTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160
Db 421 GCGCGCGGCGAGAGTACTACGGGCGCGCGCTGCGAGCTGTCTGTGAACCTACAACTAC 480
Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
Db 481 GGGCCCGCGCGGAGGAGCATCGGCTTCAACGGGCTCGCGGACCCCAACAGAGGTCGCGCGAG 540
Qy 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200
Db 541 GAGCGCGTGTGCGGCTTCAGTTCGCGGCTCTGTCTGTGATGAACAGCTGCACGCGTGTG 600
Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGlnCysAspGly 220
Db 601 ATGCGCGAGGCTTCGCGCGCCACCATCAGGGCCATCAACGGCGGCTCTGAGTGGCGGCGG 660
Qy 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTrpLysGlnTyrCysArgGlnLeu 240
Db 661 AACAAACCCCGCCAGATGAACGCGCGCTCGGCTACTACAGGCGATGACTGCGCGCGAGTCT 720
Qy 241 GlyValAspProGlyProAsnLeuThrCys 250
Db 721 GCGGTGACCCAGGCGCCCACTCACTTGC 750
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## RESULT 12

```
ID ADS92637
ID ADS92637 standard; DNA; 753 BP.
XX
AC ADS92637;
XX
DT 02-DEC-2004 (first entry)
XX
DE Chitinase variant polynucleotide #8.
XX
KW Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
KW Heterodera.
XX
OS Synthetic.
XX
PN WO2004037194-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033588.
XX
PR 22-OCT-2002; 2002US-0420666P.
PR 06-NOV-2002; 2002US-00290086.
PR 14-MAR-2003; 2003US-00389432.
XX
PA (VERD-) VERDIA INC.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Muller ML, True T, Simmons CR, Yalpani N;
XX
DR WPI; 2004-365417/34.
XX
DR P-PSDB; ADS92638.
XX
PT New chitinase polynucleotides and polypeptides, useful in producing
PT plants with enhanced resistance against a fungus or a nematode.
XX
PS Claim 4; SEQ ID NO 21; 197pp; English.
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XX The invention relates to chitinase polypeptides and the polynucleotides
CC encoding them. A method of enhancing plant resistance to a fungus or
CC nematode comprises introducing into a plant a recombinant expression
CC cassette comprising a promoter operably linked to a chitinase
CC polynucleotide of the invention. The plant is maize or soybean. The
CC fungus is from the genus Fusarium. The nematode is from the genus
CC Heterodera. The polynucleotides and polypeptides are useful in enhancing
CC plant resistance to a fungus or nematode. This sequence represents a
CC chitinase variant polynucleotide of the invention.
```

XX Sequence 753 BP; 132 A; 247 C; 269 G; 105 T; 0 U; 0 Other;

## Alignment Scores:

```
Pred. No.: 1.28e-111 Length: 753
Score: 1348.00 Matches: 238
Percent Similarity: 98.00% Conservatives: 7
Best Local Similarity: 95.20% Mismatches: 5
Query Match: 95.74% Indels: 0
DB: 13 Gaps: 0
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US-10-692-367-70 (1-250) x ADS92637 (1-753)

```
Qy 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20
Db 1 TCGATGCAGAACTCGCGGTGCGGCTCGGGCTGTGCTGCAGCCGCTTCGGGTACTGGGCG 60
Qy 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40
Db 61 ACGACCCAGCAGTACTCGCGCGACGGGTGCGGCTGCGGCGGCTGCGGCGGCGGCG 120
Qy 41 GlySerSerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsn 60
Db 121 GGCAGCAGTGGCGGCTGTGCGAACGTGGTAGCTGCTACCGGCTCTCTTCTTCAAC 180
Qy 61 GlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80
Db 181 GGCATCAAGACCCAGGCGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 240
Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100
Db 241 TTCCTGAGCGCGGTCAAGGCGGTACCCAGGCTTGCCCATGCGGCTGCGAGGTGCAGGCG 300
Qy 101 LysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
Db 301 AAGCGCGAGATCGCGCGCTTCTTCGCGCACGCCACGACGAGACCGGCGCATTTCTGTCTAC 360
Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140
Db 361 ATCAGCGAGATCAACAGAGCAACGCCCTACTGCGACCCGACCAAGAGCGATGGCCGTGC 420
Qy 141 AlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160
Db 421 GCGCGGCGGAGAGTACTACGGGCGGCGGCGGCTGCGAGTCTGCGTGAACCTACACTAC 480
Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
Db 481 GGGCCCGCGGCGGCGCATCGGCTTCGAGCGGCTCGGGCACCCCGCGCGGCGGCGG 540
Qy 181 AspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200
Db 541 GACGCGGTGTGGCGGTTCAAGGCGGCGCTCTGCGTTCGAGTGAACAAACGTCGACCGGTG 600
Qy 201 MetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGlnCysAspGly 220
Db 601 ATGCGCGAGGCTTCGCGGCGCACCATCAGGCGGCGGCTGCGGCGGCGGCTCGAGTGCAC 660
Qy 221 AsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTrpLysGlnTyrCysArgGlnLeu 240
Db 661 AACAAACCCCGCCAGATGAACGCGCGGCTCGGCTACTACAGGCGATGACTGCGGCGAGTCT 720
Qy 241 GlyValAspProGlyProAsnLeuThrCys 250
|||||
```

```

Db      721 CGCGTCGACCCAGGGCCCAACTACCTGCG 750
RESULT 13
ADS92663
ID      ADS92663 standard; DNA; 771 BP.
XX      AC
XX      ADS92663;
XX      AC
DT      02-DEC-2004 (first entry)
XX      Chitinase variant polynucleotide #21.
DE      Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX      Heterodera.
XX      Synthetic.
XX      OS
XX      PN      WO2004037194-A2.
XX      PD      06-MAY-2004.
XX      PF      22-OCT-2003; 2003WO-US033588.
XX      PR      22-OCT-2002; 2002US-0420666P.
XX      PR      06-NOV-2002; 2002US-00290086.
XX      PR      14-MAR-2003; 2003US-00389432.
XX      (VERD-) VERDIA INC.
XX      PA      (PION-) PIONEER HI-BRED INT INC.
XX      PI      Muller ML, True T, Simmons CR, Yalpani N;
XX      DR      WPI; 2004-365417/34.
XX      DR      P-FSDB; ADS92664.
XX      PT      New chitinase polynucleotides and polypeptides, useful in producing
XX      PT      plants with enhanced resistance against a fungus or a nematode.
XX      PS      Claim 4; SEQ ID NO 47; 197pp; English.
XX      CC      The invention relates to chitinase polypeptides and the polynucleotides
XX      CC      encoding them. A method of enhancing plant resistance to a fungus or
XX      CC      nematode comprises introducing into a plant a recombinant expression
XX      CC      cassette comprising a promoter operably linked to a chitinase
XX      CC      polynucleotide of the invention. The plant is maize or soybean. The
XX      CC      fungus is from the genus Fusarium. The nematode is from the genus
XX      CC      Heterodera. The polynucleotides and polypeptides are useful in enhancing
XX      CC      plant resistance to a fungus or nematode. This sequence represents a
XX      CC      chitinase variant polynucleotide of the invention.
XX      SQ      Sequence 771 BP; 137 A; 251 C; 277 G; 106 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,31e-111      Length:      771
Score:      1348.00      Matches:      240
Percent Similarity:      95.31%      Conservative:      4
Best Local Similarity:      93.75%      Mismatches:      6
Query Match:      95.74%      Indels:      6
DB:      13      Gaps:      1

US-10-692-367-70 (1-250) x ADS92663 (1-771)

Qy      1 SerMetGlnAenCysGlyCysGlnProAenValCysSerLysPheGlyTyrCysGly 20
Db      1 TCGATGCAGAACTGCGGGTGCAGCAACATGATGTCGAGCAAGTTCGGCTACTCGGCG 60
Qy      21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGly 40
Db      61 ACGACCGACGAGTACTGCGGGACGGGTGCCAGTCGGGCCCGTGGCGCTCGGGCGGCG 120
Qy      41 GlySerSerGlyGly-----GlyGlyAlaAenValAlaSerValVal 54
Db      121 GCGGCGCGCGCGGAGGCGGCGGCGGAGCGAGTGGCGGTGCAGACGTGGCTAGCGTCGTC 180

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Qy      55 ThrGlySerPheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAen 74
Db      181 ACCGGCTCCTTCTTCAACGGCATCAAGAACCCAGGCCCGGGAGCGGTGCGAGGGCAAGAAC 240
Qy      75 PheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGly 94
Db      241 TTCTACACCCGGAGCGGTCTCTGAGCGCCGCTCAAGGGGTACCCAGGGCTTCCCTCATGGC 300
Qy      95 GlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThHisGlu 114
Db      301 GGGTCACAGGTGCGAGGCAAGCGGAGATCGCCGCTTCTTCGGGCATGTCCGCGCAG 360
Qy      115 ThrGlyHisPheCysTyrIleSerGluIleSerLysSerAenAlaTyrCysAspProThr 134
Db      361 ACCGGGCATTTCCGCTACATCAGCGAGGTCAACAGAGACACGCTTACTGCGACCCGACC 420
Qy      135 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 154
Db      421 AAGAGCGAGTGGCGCTGCGCGCGGGGAGAGTACTACGGCGCGGCCCTGCGAGATC 480
Qy      155 SerTrpAenTyrAenTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAep 174
Db      481 TCGTGGAACTACAACTACGGGCCCGCGGGAGGGCCATCGGCTTTGACGGGCTCGGGGAC 540
Qy      175 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 194
Db      541 CCGCGAGGGTGGCGCGGACGCGCGTGGTGGCGTTCAAGCGCGGCGCTCTGGTTCTGGATG 600
Qy      195 AenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAenGly 214
Db      601 AACAACTGCAACCGTGTGATGCCCGAGGGTTCGGCGCCACCCATCAGGGCCATCAACGGC 660
Qy      215 AlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAenAlaArgIleGlyTyrTrpLys 234
Db      661 GCGCTCGAGTGGCGCGGAAACAACCCCGCCAGATGAACGGCGCGCTCGGCTACTACAGG 720
Qy      235 GlnTyrCysArgGlnLeuGlyValAspProGlyProAenLeuThrCys 250
Db      721 CAGTACTGCGCCAGCTCGCGCTCGACCCAGGGGCCCAACCTCACTTGC 768

RESULT 14
ADS92689
ID      ADS92689 standard; DNA; 771 BP.
XX      AC
XX      ADS92689;
DT      02-DEC-2004 (first entry)
XX      Chitinase variant polynucleotide #34.
XX      Chitinase; gene; ds; plant resistance; fungus; nematode; Fusarium;
XX      Heterodera.
XX      Synthetic.
XX      WO2004037194-A2.
XX      PD      06-MAY-2004.
XX      PF      22-OCT-2003; 2003WO-US033588.
XX      PR      22-OCT-2002; 2002US-0420666P.
XX      PR      06-NOV-2002; 2002US-00290086.
XX      PR      14-MAR-2003; 2003US-00389432.
XX      (VERD-) VERDIA INC.
XX      PA      (PION-) PIONEER HI-BRED INT INC.
XX      PI      Muller ML, True T, Simmons CR, Yalpani N;
XX      DR      WPI; 2004-365417/34.
XX      DR      P-FSDB; ADS92690.

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XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX Claim 4; SEQ ID NO 73; 197pp; English.  
XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX Sequence 771 BP; 140 A; 249 C; 275 G; 107 T; 0 U; 0 Other;  
SQ  
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Pred. No.: 2.44e-111 Length: 771  
Score: 1345.00 Matches: 239  
Percent Similarity: 94.92% Conservative: 4  
Best Local Similarity: 93.36% Mismatches: 7  
Query Match: 95.53% Indels: 6  
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DB 1 TCGATGCAAGAACTGCGGTGCGGCAACAACTGTCGACGAACTTCGGCTACTGCGGC 60  
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40  
DB 61 ACGACGACGAGTACTGCGGCGACGGGTGCGAGTGGCCGCGCGCGCGCGCGCGC 120  
QY 41 GlySerSerGlyGly-----GlyGlyAlaAsnValAlaSerValVal 54  
DB 121 GCGGTGC 180  
QY 55 ThrGlySerPhePheAsnGlyLeuLeuAsnGlnAlaGlySerGlyCysGluGlyValAsn 74  
DB 181 ACCGACTCTTCTTCAACGGCATCAAGAGCCAGCGCGCGCGCGCGCGCGCGCGCGC 240  
QY 75 PheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGly 94  
DB 241 TTCTACACCGCGAGCGGTCTCTGAGCGCGCTCAAGGCGTACCCAGGCTTCGCCATGCG 300  
QY 95 GlySerGlnValGlnGlyArgGluLeuAlaPheAlaHisAlaThrHisGlu 114  
DB 301 GGGTCGCAAGGTGCAAGCGGAGATCGCGCTTCTTCGGCGCATGTCAACGCGAG 360  
QY 115 ThrGlyHisPheCysTyrLysSerGluLeuSerLysSerAsnAlaTyrCysAspProThr 134  
DB 361 ACCGGCATTTCTGCTCATCAACGAGATCAACAGAGCAACGCTCTCTGCGACCCGAC 420  
QY 135 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrGlyArgGlyProLeuGlnIle 154  
DB 421 AAGAGGCGAGTGGC 480  
QY 155 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAsp 174  
DB 481 TCGTGGAACTACAATACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 540  
QY 175 ProGlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTrpPheTrpMet 194  
DB 541 CCGCGAGGTGGC 600  
QY 195 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 214  
DB 601 AACACGTCGACCGGTGTATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 660  
QY 215 AlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLys 234

DB 661 GCCCTCGAGTGCAGCGGAAACAACCGCGCCAGATGAACGCGCATCGGCTACTACAAG 720  
QY 235 GlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250  
DB 721 CAGTACTGCCCGCAGCTCGGGCTGACCCAGGGCCCAACCTCACTTGC 768  
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ID ADS92675 standard; DNA; 771 BP.  
XX ADS92675;  
AC ADS92675;  
XX 02-DEC-2004 (first entry)  
XX Chitinase variant polynucleotide #27.  
XX Chitinase; gene; ds; plant resistance; fungus; nematode; *Fusarium*;  
KW *Heterodera*.  
XX Synthetic.  
XX WO2004037194-A2.  
XX 06-MAY-2004.  
XX 22-OCT-2003; 2003WO-US033588.  
XX 22-OCT-2002; 2002US-0420666P.  
PR 06-NOV-2002; 2002US-00290086.  
PR 14-MAR-2003; 2003US-00389432.  
XX (VERD-) VERDIA INC.  
PA PIONEER HI-BRED INT INC.  
XX Muller ML, True T, Simmons CR, Yalpani N;  
XX WPI; 2004-365417/34.  
DR P-PSDB; ADS92676.  
XX New chitinase polynucleotides and polypeptides, useful in producing  
PT plants with enhanced resistance against a fungus or a nematode.  
XX Claim 4; SEQ ID NO 59; 197pp; English.  
XX The invention relates to chitinase polypeptides and the polynucleotides  
CC encoding them. A method of enhancing plant resistance to a fungus or  
CC nematode comprises introducing into a plant a recombinant expression  
CC cassette comprising a promoter operably linked to a chitinase  
CC polynucleotide of the invention. The plant is maize or soybean. The  
CC fungus is from the genus *Fusarium*. The nematode is from the genus  
CC *Heterodera*. The polynucleotides and polypeptides are useful in enhancing  
CC plant resistance to a fungus or nematode. This sequence represents a  
CC chitinase variant polynucleotide of the invention.  
XX Sequence 771 BP; 139 A; 247 C; 274 G; 111 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 3e-111 Length: 771  
Score: 1344.00 Matches: 238  
Percent Similarity: 94.92% Conservative: 5  
Best Local Similarity: 92.97% Mismatches: 7  
Query Match: 95.45% Indels: 6  
DB: 13 Gaps: 1  
US-10-692-367-70 (1-250) x ADS92675 (1-771)  
QY 1 SerMetGlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGly 20  
DB 1 TCGATGCAAGAACTGCGGTGCGGCAACAACTTCGCTGCGACGAACTTCGCTACTGCGGC 60  
QY 21 ThrThrAspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGly 40

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Db 121 GCGCGCGGTGGCGGCGGAGCGGCGGAGCGAGTGGCGGTGGCAACGTGGCTAAATGTGGTC 180
QY 55 ThrGlySerPhePheAsnGlyIleIysAsnGlnIleGlySerGlyCysGluGlyIysAsn 74
Db 181 ACCGACGGTCTTCAACGGCATCAAGAACCCAGGCCGGAGCGGGTGGAGGGCAAGAAC 240
QY 75 PheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGly 94
Db 241 TTCTACACCCGAGCGCGTCTCTAGCGCGGTCAAGGCGTACCCAGGCTTCGCCCATGSC 300
QY 95 GlySerGlnValGlnGlyIysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGlu 114
Db 301 GGGTCACAGGTGCAGGGCAAGCGCGAGATTGCCGCTTCTTCGCGCATGTCAACGACGAG 360
QY 115 ThrGlyHisPheCysTyrIleSerGluIleSerLysSerAsnAlaTyrCysAspProThr 134
Db 361 ACCGGGCATTCTGCTACATACGCGAGATCAACAAGACGACCTACTGGACCCGACC 420
QY 135 LysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 154
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QY 155 SerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAsp 174
Db 481 TCGTGGAACTACAACTACGCGGCGCGGCGGAGGCGCATCGGCTTCGACGGGCTCGGGAC 540
QY 175 ProGlyArgValAlaArgAspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMet 194
Db 541 CCCGCGAGGGTGGCGGAGCGCGCGTGGTGGCGTTCAAGCGGCGGCGCTCTGGTCTGGATG 600
QY 195 AsnAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGly 214
Db 601 AACAACTGTCACCGTGTGTATGCGCGAGGGCTTCGGGCGCCACCATCAGGGCCCATCAACGCG 660
QY 215 AlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLys 234
Db 661 GCCCTCGAGTGCAGCGGAACAACCCCGCCAGATGAACGCGCGCGCTCGGCTACTACAGG 720
QY 235 GlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250
Db 721 CAGTACTGCCGCGCAGCTCGGCGTCCAGCCAGGGCCCAACCTCACTTGC 768
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Job time : 374.316 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 17:19:13 ; Search time 125.74 Seconds  
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Perfect score: 1408  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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  - 3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq:\*
  - 4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq:\*
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  - 6: /cgm2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	861	61.2	1048	4	US-09-522-714-21
3	830	58.9	1079	1	US-08-181-271A-37
4	830	58.9	1079	1	US-08-449-315-37
5	830	58.9	1079	1	US-08-444-803-37
6	830	58.9	1079	1	US-08-449-043-37
7	830	58.9	1079	1	US-08-456-265A-37
8	830	58.9	1079	1	US-08-455-416-37
9	830	58.9	1079	1	US-08-455-244-37
10	830	58.9	1079	1	US-08-454-876-37
11	830	58.9	1079	2	US-08-457-364-37
12	830	58.9	1079	2	US-08-456-262-37

13	830	58.9	1079	2	US-08-456-240-37	Sequence 37, Appl
14	830	58.9	1079	2	US-08-455-736-37	Sequence 37, Appl
15	830	58.9	1079	2	US-08-971-217-37	Sequence 37, Appl
16	830	58.9	1079	3	US-09-350-600-37	Sequence 37, Appl
17	830	58.9	1079	4	US-09-906-234-37	Sequence 37, Appl
18	825	58.6	1116	4	US-09-522-714-31	Sequence 31, Appl
19	697.5	49.5	881	4	US-09-522-714-29	Sequence 29, Appl
20	621	44.1	943	2	US-08-475-427-15	Sequence 15, Appl
21	621	44.1	943	2	US-07-842-165-15	Sequence 15, Appl
22	620	44.0	1152	1	US-08-047-413-10	Sequence 10, Appl
23	620	44.0	1152	3	US-08-229-050-10	Sequence 10, Appl
24	620	44.0	1152	3	US-08-801-563-10	Sequence 10, Appl
25	592	42.0	1151	1	US-07-704-288C-2	Sequence 2, Appl
26	592	42.0	1151	1	US-08-093-372-1	Sequence 1, Appl
27	592	42.0	1151	1	US-08-379-259-2	Sequence 2, Appl
28	591.5	42.0	1225	1	US-08-286-020-1	Sequence 1, Appl
29	591.5	42.0	1225	1	US-08-603-919-1	Sequence 1, Appl
30	588	41.8	960	4	US-09-534-229C-8	Sequence 8, Appl
31	581	41.3	905	2	US-08-475-427-14	Sequence 14, Appl
32	581	41.3	905	2	US-07-842-165-14	Sequence 14, Appl
33	572.5	40.7	1153	2	US-08-475-427-4	Sequence 4, Appl
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35	572.5	40.7	1153	3	US-08-448-398-6	Sequence 6, Appl
36	572.5	40.7	1163	2	US-08-475-427-12	Sequence 12, Appl
37	572.5	40.7	1163	2	US-07-842-165-12	Sequence 12, Appl
38	572.5	40.7	1863	1	US-08-525-507-16	Sequence 16, Appl
39	572.5	40.7	1863	2	US-08-475-427-9	Sequence 9, Appl
40	572.5	40.7	1863	2	US-07-842-165-9	Sequence 7, Appl
41	549.5	39.0	972	4	US-09-534-229C-7	Sequence 5, Appl
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43	535.5	38.0	1318	3	US-09-125-891-1	Sequence 5, Appl
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45	533.5	37.9	3012	2	US-07-842-165-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-09-522-714-1  
; Sequence 1, Application US/09522714  
; Patent No. 6563020  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Yalpani, Nasser  
; TITLE OF INVENTION: Maize Chitinases and Their Use in  
; FILE REFERENCE: 1100  
; CURRENT APPLICATION NUMBER: US/09/522,714  
; CURRENT FILING DATE: 2000-03-10  
; EARLIER APPLICATION NUMBER: 60/125,915  
; EARLIER FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1094  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (51)...(893)  
US-09-522-714-1

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Pred. No.: 5.77e-138 Length: 1094  
Score: 1351.00 Matches: 238  
Percent Similarity: 98.39% Conservative: 6  
Best Local Similarity: 95.97% Mismatches: 4  
Query Match: 95.95% Indels: 0  
DB: 4 Gaps: -0

US-10-692-367-70 (1-250) x US-09-522-714-1 (1-1094)

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Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 210 GACGAGTACTCGCGGCGAGCGGGTGCAGTTCGGGCGCGTCCGCTCGCGGCGGCGGACG 269
Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyTle 62
Db 270 AGTGGCGGCGGTGGTGGCAAGTGGCTAGCGTGGTGCAGCGGCTCTCTTCAACGGCATC 329
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
Db 330 AAGACCGACGCGCGGAGCGGGTGCAGGCGCAAGAACTTCTACCCGAGCGCGTTCCTG 389
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyArg 102
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Qy 123 GluLeuSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAla 142
Db 510 GAGATCAACAAGAGCAACCGCTACTTGCAGCCCGACCAAGAGCGAGTGGCGCGCGCG 569
Qy 143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGlyPro 162
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Qy 183 ValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHisArgValMetPro 202
Db 690 GTGGTGGCGGTTCAGAGCGCGCTCTGGTTCGTGGATGAACAGCGTGCAGCGGTGGTGGCG 749
Qy 203 GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsn 222
Db 750 CAGGGTTTCGGCGCCGCCACCGAGGCGCATACGCGCGCCCTCGAGTGGCGGGGAGCAAC 809
Qy 223 ProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyVal 242
Db 810 CCGCGCCAGATGAACGCGCGCGTGGCTACTACAGGCGAGTACTGCGCGCAGCTCGCGCTC 869
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Db 870 GACCCCGGGCCCAACCTCACCTGC 893
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## RESULT 2

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; Sequence 21, Application US/09522714
; Patent No. 6563020
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Maize Chitinases and Their Use in
; TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
; FILE REFERENCE: 1100
; CURRENT APPLICATION NUMBER: US/09/522,714
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/125,915
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
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; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
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/ LOCATION: (42)... (854)
US-09-522-714-21
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Pred. No.: 861.00 Matches: 156
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Best Local Similarity: 62.15% Mismatches: 62
Query Match: 61.15% Indels: 8
DB: 4 Gaps: 3
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US-10-692-367-70 (1-250) x US-09-522-714-21 (1-1048)

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Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 177 GAGGACTACTGCGGCGCGGGTGCAGTGGGGCCCTGC-----GACGTG 221
Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyTle 62
Db 222 CCGGAGACCAACAAACGCGTTCGTCGCCAGCATCGTGCAGCGCGCTTCTTCGAGCGCGCTC 281
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
Db 282 CTCGCGCAGCGCGCGCTCGTGGAGGCCAACCGCTTCTACACCGCGAGCGCTTCTCTC 341
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyArg 102
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Db 402 GAGATCGCGCGCTTCTTCGCGCAACCGCAACCGAGACCATAAAGTTCGTGTATCATCAAC 461
Qy 123 GluIle---SerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAla 141
Db 462 GAGATCGAGCGCGCGGAGCAAGAACTACTGCGCGCGGCAACACACGAGTGGCGCGCCAG 521
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGly 161
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Db 582 CCGCGCGGCGAGAGCATCGGCTTCGAGCGGTGGCGGACCCCGAGCGGTGGCGCGGAGC 641
Qy 182 AlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHisArg----- 199
Db 642 GCGGTGCTCGGTTCCGCTCCGCGCTCTGGTACTGGATGAACACGTCGAGCGGCGCATC 701
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Qy 220 GlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGln 239
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## RESULT 3

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US-08-181-271A-37
; Sequence 37, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
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APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/181.271A  
FILING DATE: 13-JAN-94  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
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APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-181-271A-37  
Alignment Scores:  
Pred. No.: 4.84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
Gaps: 5  
US-10-692-367-70 (1-250) x US-08-181-271A-37 (1-1079)  
Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyCysGlyThrThr 22  
Db 93 CAAAACGCGGTTCGGCTCCAAACCTCTGTTCAGTCAGTTCGGTACTGTGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAaspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTGCGGTGTTCGATGCCGATCAGGTCTCTGTAGCA-----GGTAGTGAACC 206  
Qy 43 SerGlyGlyGlyAlaAenValAenValValThrGlySerPheAenGlyIle 62  
Db 207 CCGACCGGAGGG-----TCGGTCGTAGCATGTGACCAAGGTTCTTTAAACAATATT 260  
Qy 63 LysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPheLeu 82  
Db 261 ATCAACCCAGCTGTGTATGTTGCGCGGGGAAAGATTCTACACCGTGACTCTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACGCGCTAATACCTTTCCCACTTTGCCAATCTTGTACC-----AGACGT 368  
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTGCTACCATGTTTGTCTCATTTCACTCAGAGACCGGACATTTCTGTACATAGAA 428  
Qy 123 GluIleSer---LysSerAenAlaTyrCysAaspProThrLysArgGlnTyrProCysAla 141  
Db 429 GAGATTAAACGGGCAACACGTAACCTACTGTCAGAGCAGCAGACACACAATACCCATGTCA 488  
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAenTyrAenTyrGly 161  
Db 489 CCGGGAAGAGGCTACTTCGGTCGTGTCGATCCCACTATCATGGAACATACAACTACCGGA 548  
Qy 162 ProAlaGlyArgAaspIleGlyPheAaspGlyLeuGlyAaspProGlyArgValAlaArgAasp 181  
Db 549 GCGTGTGCTCAAGCTCTCGGTCCTTTCGACCTTCACGACGCGCCGCACTTGTGGGTAGAAC 608  
Qy 182 AlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAenValHisArgValMet 201  
Db 609 CCAACTGTAGCTTTCAGTTCGGGTTTGTGGTTTGGATGATAGCGTAAGCCCGGTTCTG 668  
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGlyCysAaspGlyAen 221  
Db 669 AACCAAGGGTTTGAGGCCACCATTTAGAGCTATTATATGGA---ATGGAATGTAAACGGTGGT 725  
Qy 222 AenProAlaGlnMetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241

Db 726 AATTCGGTGCAGTCAACGCAAGGATTGGATATAGAGACTATTGGGACAGCTTGGT 785  
Qy 242 ValAspProGlyProAsnLeuThrCys 250  
Db 786 GTGACCCCTGGTCTTAACCTTAGTTGC 812

## RESULT 4

US-08-449-315-37  
; Sequence 37, Application US/08449315  
; Patent No. 5650505  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,315  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504

; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-449-315-37

Alignment Scores:  
Pred. No.: 4,84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-449-315-37 (1-1079)

Qy 3 GluAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAAACTGCGGTTCGCTCCAAACCTCTGTTGCAGTCAGTTCGGTTACTGTGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTGCGGTGTTGGATGCCGATCAGTCTCTGTAGA-----GGTAGTGAACC 206  
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyIle 62  
Db 207 CCGACCGGAGGG-----TCGGTCGGTAGCATTGTGACACAAAGGTTTCTTTAACAAATT 260  
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
Db 261 ATCAACCAAGCTGTAATGTTGCGCGGGGAAAGATTCTACACCGTGACTCTTTCTGT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACGCGCTAATACTTTCCCACTTTGCCAATCTCTGTACC-----AGAGGT 368  
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTGCTACCATGTTTGTCTCATTTCACTCACGAGACCGGACATTTCTGCTACATAGAA 428  
Qy 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTTPProCysAla 141  
Db 429 GAGATTAAACGAGCAACACAGTAACTACTGCAAGAGCAGCAACACACAAATACCCATGTGCA 488

Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrGly 161  
Db CGGGAAGAGGCTACTTCGGTCGTGGTCCGATCCCAACTATCATGGAACCTCAACTACCGA 548  
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181  
Db GCGTGTGGTCAAAGTCTCGTCTTGACCTTCTACCCAGCCCGAAGTGTGGGTAGCAAC 608  
Qy 182 AlaValAlaPheGlyAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201  
Db CCAACTGTAGCTTTCAGGTCGGTGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 668  
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAlaGlnLeuGlnCysAspGlyAsn 221  
Db AACCAAGGTTTGGAGCCACCATTAAGAGTATTATATGGA--ATGGAATGTAAACGGTGGT 725  
Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241  
Db AATCCGGTGCAGTCAACGCAAGGATTGGATCTATAGACTATTGTGGACAGCTTGGT 785  
Qy 242 ValAspProGlyProAsnLeuThrCys 250  
Db GTGACCCCTGGTCTTAACCTTAGTTGC 812

## RESULT 5

US-08-444-803-37  
; Sequence 37, Application US/08444803  
; Patent No. 5654414

## GENERAL INFORMATION:

; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Unnes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,803  
; FILING DATE: 19-MAY-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-444-803-37

Alignment Scores:  
Pred. No.: 4,84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-444-803-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db CAAAACTGCGGTTCGGCTCCAAACCTCTGTTGCAGTCAGTTCGGTACTGTTGTTACCGAC 152  
Qy 23 AspGlnTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db GATGCATACCTGCGGTGTGGATGCCGATCAGTCCCTTGTAGA-----GGTAGTGGAAAC 206  
Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGlyTyr 62  
Db CCGACCCGAGGG-----TCGGTCGGTAGCATTTGTGACACAGGTTTCTTTAACTATT 260



Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-449-043-37 (1-1079)

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QY 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrCysGlyThrThr 22
DB 93 CAATACTGGTGGCTCCAAACCTCTGTCAGTCAGTTCGGTTACTGGTACCCGAC 152
QY 23 AspGlyTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
DB 153 GATGCATACCTGGGTGGTGGATGCCGATCAGTCTCTGTAGA-----GGTAGTGAACC 206
QY 43 SerGlyGlyGlyGlyAlaAenValAlaSerValThrGlySerPhePheAenGlyIle 62
DB 207 CCGACCGGAGG-----TCGGTCGGTAGCATTTGTGACACCAAGGTTCTTTAAACAAT 260
QY 63 LysAenGlnAlaGlySerGlyCysGlnGlyLysAenPheTyrThrArgSerAlaPheLeu 82
DB 261 ATCAACCAAGCTGTATGGTTCGCGGGGAAAGATTTACACCCGAGACTCTTTCGTT 320
QY 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
DB 321 AACGCGCTAATACTTTCCCAACTTTCGCAATTCTGTTACC-----AGAGGT 368
QY 103 GluLeuAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
DB 369 GAAATTGCTACCATGTTTGCTCATTTCACTCAGCAGACCGGACATTTCTGCTACATAGAA 428
QY 123 GluIleSer---LysSerAenAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
DB 429 GAGATTACGAGGACCAACGTAACCTACTGCCAGACGACCAACACACAATATCCCATGTGCA 488
QY 142 AlaGlyLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGly 161
DB 489 CCGGGAAGAGCTACTTCGGTTCGGTTCGGTCCGATCCAACTATCATGGAACCTACACTCGGA 548
QY 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
DB 549 CGGTGTGCTCAAGTCTCGGCTTTCGACCTTCTACGCCAGCCGAACTTGTGGTAGCAAC 608
QY 182 AlaValAlaPheLysAlaLeuThrPheTrpMetAenAenValHisArgValMet 201
DB 609 CCAACTGTAGCTTTTCAGTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGT 668
QY 202 ProGlnGlyPheGlyValThrIleArgAlaIleAenGlyAlaLeuGluCysAspGlyAsn 221
DB 669 AACCAAGGTTTGGAGCCACCATAGAGCTATTATATGA---ATGGAATGTACGGTGGT 725
QY 222 AenProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
DB 726 AATTCGGTGCAGTCAACGCAAGGATTGGATCTATATAGAGCTATTGTGGACAGCTTGGT 785
QY 242 ValAspProGlyProAenLeuThrCys 250
DB 786 GTGACCCCTGCTCACTTACCTTAGTTGC 812
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## RESULT 7

US-08-456-265A-37

Sequence 37, Application US/08456265A

Patent No. 5767369

GENERAL INFORMATION:

APPLICANT: Alexander, Danny C.

APPLICANT: Ryals, John A.

APPLICANT: Goodman, Robert M.

APPLICANT: Stinson, Jeffrey R.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 520 White Plains Road, P.O. Box 2005

US-08-456-265A-37

CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,265A  
FILING DATE: 31-MAY-95  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/181,271  
FILING DATE: 13-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA

## Alignment Scores:

Pred. No.: 4.84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-456-265A-37 (1-1079)

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Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 93 CAAACCTCGGTTGGCTCCAAACCTCTGTTGCATCGCTTCGTTACTGTTGGTACCGAC 152
Qy 23 AspGlnTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 153 GATGATACCTCGGTTGGATGCGATCGATCGTCTTGTAGA-----GGTAGTGGAAC 206
Qy 43 SerGlyGlyGlyAlaAlaAsnValAlaSerValValThrGlySerPheAsnGlyIle 62
Db 207 CCGACCGGAGG-----TCGGTCGGTAGCATTTGTACACAAAGTTTCTTTAAACAATATT 260
Qy 63 LysAsnGlnAlaGlySerGlyCysGlnGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
Db 261 ATCAACCAAGCTGGAATGTTGGCGGGGAAAGATTCTACACCCGCTGACTCTTTCGTT 320
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 321 AACCCCGCTAATCTTTCCCACTTTGCCAATCTCTGTACC-----AGACGT 368
Qy 103 GluIleAlaAlaPhePheAlaHisGlnThrHisGlnThrGlyHisPheCysTyrIleSer 122
Db 369 GAAATTGCTACCATGTTGCTCAATTCACCTACGAGACCGGACATTTCTGCTACATAGAA 428
Qy 123 GluIleSer----LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
Db 429 GAGATTACCGGACCAACGATGTAATCTACTGCCAGAGCAGCACACACAATACCCATGTGCA 488
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly 161
Db 489 CCGGAAGAGGCTACTTCTCGGTCGGTGGTCCGATCACTATCATGAACTACACTACGGA 548
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAsp 181
Db 549 CGGTGTGTCAAAGTCTCGGTCCTGACCTTCTACGCCAGCCCGAACCTTGTGGGTAGCAAC 608
Qy 182 AlaValAlaAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
Db 609 CCAACTGTAGCTTTTCAGTCTCGGTTGTTGGTGGTGGATGATAGCTAATGATGCGGTTCTG 668
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
Db 669 AACCAAGGTTTGGAGCCCACTTAGACTATTATGGA---ATGGATGTAACCGGTGGT 725
Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 726 AATTCGGTGCAGTCAACGCAAGGATTTGGATCTACTATAGAGACTATTGTGGACAGCTTGGT 785
Qy 242 ValAspProGlyProAsnLeuThrCys 250
Db 786 GTGACCCCTGCTCTCACTTACTTGTTC 812
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## RESULT 8

US-08-455-416-37  
; Sequence 37, Application US/08455416  
; Patent No. 577200  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.

APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,416  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:

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Db      726 AATTCCGGTCAGTCACGCAAGATGGATATGATAGACTATTGTGGACAGCTTGGT 788
Qy      242 ValaaspProGlyProAsnLeuThrCys 250
Db      786 GTGACACCTGGTCTCAACCTTAGTTGTC 812

RESULT 9
US-08-455-244-37
; Sequence 37, Application US/08455244
; Patent No. 5789214
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Utnes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,244
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504

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FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-455-244-37

Alignment Scores:  
Pred. No.: 4,84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-455-244-37 (1-1079)

Qy 3 GlnAsnGlyGlyCysGlnProAsnValCysCysSerLysPheGlyThrThr 22  
Db 93 CAAAACTCGGTTGGCTCCAAACCTCTGTCAGTCAGTTCGGTTACTGGTACCGAC 152

Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTCGGTTGGATGCGATCGATCGATCTTGTAGA-----GGTAGTGGAAAC 206

Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGlyLeu 62  
Db 207 CCGACCGGAGG-----TCGGTCGGTAGCTGTGACACACAGGTTCTTTAACAATATT 260

Qy 63 LysGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
Db 261 ATCAACCAAGCTGGTAATGGTTGGCGGGGAAAGATTCTACCCGGTACTTTTGGTT 320

Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACGCGCTAATACTTCTCCCACTTTCCTGCTTGTACC-----AGAGCT 368

Qy 103 GluLeuAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTGCTACCATGTTTGTCTCAATTCCTACTCAGACCGGACATTTCTGCTACATAGAA 428

Qy 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAla 141  
Db 429 GAGATTAAACGGCAACACGTAATCTACTGCGACGACGACCAACACACAAATACCATGTGCA 488

Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrGly 161  
Db 489 CCGGAAAGAGCTACTTCGGTCTGGTCCGATCCAACTATCATGGAACACTACCACTCGGA 548

Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181  
Db 549 GCGTGTGTCAAAAGTCTCGGCTTTCACCTTCTACGCCAGCCCGAACTTGTGGGTAGCAAC 608

Qy 182 AlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHisArgValMet 201  
Db 609 CCAACTGTAGCTTTCAGTTCGGTTCGGTTTGTGGTATGATAGCTTAAGCCCGTTCTG 668

Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGlyCysAspGlyAsn 221  
Db 669 AACCAAGGTTTGGAGCCACCATTTAGAGCTATTAAATGGA---ATGGAATGTAAACGGTGGT 725

Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrLysGlnTyrCysArgGlnLeuGly 241  
Db 726 AATTCCGGTCAGTCAACGCAAGGATTGGATCTATATAGAGACTATTGTGGACAGCTTGGT 785

Qy 242 ValAspProGlyProAsnLeuThrCys 250  
Db 786 GTGACCCCTGCTCTTAACCTTAGTTGC 812

RESULT 10  
US-08-454-876-37  
Sequence 37, Application US/08454876  
Patent No. 5804693  
GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/454,876  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA: US 07/937,197  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/Pl/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-454-876-37

Alignment Scores:
Pred. No.: 4,848-81 Length: 1079
Score: 830.00 Matches: 148
Percent Similarity: 73.0% Conservative: 34
Best Local Similarity: 59.4% Mismatches: 57
Query Match: 58.9% Indels: 10
DB: 1 Gaps: 5

US-10-692-367-70 (1-250) x US-08-454-876-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 93 CAAAACTGGGTGGCTCCAAACCTCTGTTGCAGTCAGTTCGGTTACTGTTGTTACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 153 CATGCATCTGCGGTGGTGGATGCGGATCGGTCTCTGTAGA-----GGTAGTGGAAACC 206
Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyIle 62
Db 207 CCGACCGGAGGG-----TCGGTCGGTAGCATTTGTGACACAAAGGTTTCTTTAAACAATATT 260

Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheIeu 82
Db 261 ATCAACCAAGCTGGTAATATGTTGGCGGGGAAAAGATTCTACACCGTGACTCTTTCTGTT 320
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 321 AACCGCGCTAATATCTTTCCCAACTTTGCCAATTTCTGTTACC-----AGACGT 368
Qy 103 GluIleAlaAlaPhePheAlaHisGluThrHisGluThrGlyHisPheCysTyrIleSer 122
Db 369 GAATTTGCTACCATGTTTGTCTCAITTCACACGAGACCGGACATTTCTGCTACATAGAA 428
Qy 123 GluIleSer-----LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
Db 429 GAGATTAAACGGAGCAACACAGTAACCTACTGCCAGAGCAGCAACACACATATCCCATGTGCA 488
Qy 142 AlaGlyGlnLysTyrTyrGlyValGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGly 161
Db 489 CCGGAAAGAGCTACTTCGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 548
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
Db 549 GCGTGTGCTCAAGTCTCGGTCTTGTGACCTTCTACGCCAGCCCGAAGTGTGGGTAGCAAC 608
Qy 182 AlaValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgValMet 201
Db 609 CCAACTGTAGCTTTTCAGTCTGGGTTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 668
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
Db 669 AACCAAGGTTTGGAGCCACCATTTAGAGCTATTATATGA---ATGGAATGTAACGGTGGT 725
Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 726 AATTCGGGTGCGAGTCAAGCAAGGATTTGGATCTATAGAGACTATTGTGGACAGCTTGGT 785
Qy 242 ValAspProGlyProAsnLeuThrCys 250
Db 786 GTGGACCTCGTCTCAACTAGTCTTAGTTGC 812

RESULT 11
US-08-457-364-37
; Sequence 37, Application US/08457364
; Patent No. 5847258
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr. Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,364  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/948,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-457-364-37

Alignment Scores:  
Pred. No.: 4.84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34

Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 2 Gaps: 5

US-10-692-367-70 (1-250) x US-08-457-364-37 (1-1079)

Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAAACTCGCGTTCGGCTCCAAACCTCTGTTGCAGTCAGTTCGGTACTGTTGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlyGlySer 42  
Db 153 GATGCATACCTCGCGTGTGGATGCCGATCGAGTCTCTTTAGTA-----GGTAGTGGAAAC 206  
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyIle 62  
Db 207 CCGACCGGAGG-----TCGGTCGTGAGCATTGTGACACAAAGTTTCTTTAAACAATAT 260  
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
Db 261 ATCAACCAAGCTGGTAATGTTGCGCGGGAAGATTCTACACCGGTGACTCTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACGCCGCTAATACTTTCCCAACTTTGCCAATTTCTGTATCC-----AGACGT 368  
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATGCTACCATGTTGCTCATTTCACTACGAGACCGGACATTTCTGCTCATAGAA 428  
Qy 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141  
Db 429 GAGATTAAACGAGCAACACAGTAACTACTGCGCAGACGAGCAACACACAATACCCATGTGCA 488  
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly 161  
Db 489 CCGGGAAGAGGCTACTTCGGTGGTCCGATCCAACTATCATGGAACATCACTACCACTACGGA 548  
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAsp 181  
Db 549 GCGTGTGTCAAGTCTCGGTCTTGACCTTCTACGCCAGCCCGCACTTGTGGGTAGCAAC 608  
Qy 182 AlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnValHisArgValMet 201  
Db 609 CCAACTGTAGCTTTTCAGGTCGGGTTTGTGGTGGATGAATAGCGTAAGCCCGTTCGTG 668  
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221  
Db 669 AACCAAGGGTTTGGAGCCCACTTAGAGCTATTAAATGGA---ATGGAATGTAAACGGTGGT 725  
Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241  
Db 726 AATTCGGTGCAGTCAACGACCAAGATTGGATGATATATAGACTATTTGTCGACACTTGGT 785  
Qy 242 ValAspProGlyProAsnLeuThrCys 250  
Db 786 GTGGACCTGCTCTCAACTTAGTTGTC 812

RESULT 12  
US-08-456-262-37  
Sequence 37, Application US/08456262  
Patent No. 5851766  
GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.

APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,262  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1079 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-456-262-37  
Alignment Scores:  
Pred. No.: 4.84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 2 Gaps: 5  
US-10-692-367-70 (1-250) x US-08-456-262-37 (1-1079)  
Qy 3 GlnAenCysGlyCysGlnProAenValCysCysSerLysPheGlyTyrcysGlyThrThr 22  
Db 93 CAAAACCTGCGGTTCGCTCCAAACCTCTGTTGCGAGTCAGTTCGGTTACTGTGGTACCCGAC 152  
Qy 23 AspGluTyrcysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTGCGGTGTTGGATGCCGATCAGGTCTCTGTAGA-----GGTAGTGAACC 206  
Qy 43 SerGlyGlyGlyAlaAenValAenValAenValAenValAenValAenValAenValAenVal 62  
Db 207 CCGACCGGAGGG-----TCGGTCGGTAGCATTCGACACAAAGGTTCTTTAAACAATATT 260  
Qy 63 LysAenGlnAlaGlySerGlyCysGluGlyLysAenPheTyrcysGlyThrArgSerAlaPheLeu 82  
Db 261 ATCAACCAAGCTGTGTATGTTGCGCGGGGAAAGATTCTACACCGTGACTCTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrcysGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACGCGCTAATACTTTCCCACTTTCGCAATCTCTGTACC-----AGAGGT 368  
Qy 103 GluileAlaAlaPhePheAlaHisAlaThrHisGlnThrGlyHisPheCysTyrcysSer 122  
Db 369 GAAATTGCTACCATGTTGCTCATTTCTACTCAGAGACCGGACATTTCTGCTACATAGAA 428  
Qy 123 GluileSer---LysSerAenAlaTyrcysAspProThrLysArgGlnTrpProCysAla 141  
Db 429 GAGATTACGGAGCAACACGTAATCTGTCAGAGCAGCAGCAACACATACCATGTCGA 488  
Qy 142 AlaGlyGlnLysTyrcysGlyArgGlyProLeuGlnIleSerTrpAenTyrcysGly 161  
Db 489 CCGGAAAAAGGCTACTTCGGTCGTGGTCCGATCAACTATCATGGAACCTACAACTACGGA 548  
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181  
Db 549 GCGTGTGCTCAAGCTCTCGGTCTTGACCTTACGCCAGCCCGAACCTTGTGGTGAACAC 608  
Qy 182 AlaValAlaAlaPheLysAlaAlaLeuTrpPheTrpMetAenAenValHisArgValMet 201  
Db 609 CCAACTGTAGCTTTTCAGTCGGGTTTGGTTTGGATGGAATAGCTTAAGCCCGGTTCTG 668  
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAenGlyAlaLeuGluCysAspGlyAen 221  
Db 669 AACCAAGGGTTTGGAGCCACCATTAGACTATTATGGA---ATGGAATGTAACCGTGT 725  
Qy 222 AenProAlaGlnMetAenAlaArgIleGlyTyrcysGlnTyrcysGlnTyrcysGlnLeuGly 241  
Db 726 AATTCCGGTGCAGTCAACGCAAGGATTGGATATATAGAGACTATTGTGGACAGCTGTGT 785  
Qy 242 ValAspProGlyProAenLeuThrCys 250  
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Db 786 GTGACCTGCTCTTAACCTTAGTTGC 812  
RESULT 13.  
US-08-456-240-37  
; Sequence 37, Application US/08456240  
; Patent No. 5856154  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.  
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/456,240  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/181,271  
; FILING DATE: 13-JAN-94  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT 1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/768,122  
; FILING DATE: 27-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431  
; FILING DATE: 7-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672  
; FILING DATE: 20-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018  
; FILING DATE: 24-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957  
; FILING DATE: 12-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-456-240-37  
Alignment Scores:  
Pred. No.: 4.84e-81 Length: 1079  
Score: 830.00 Matches: 148  
Percent Similarity: 73.09% Conservative: 34  
Best Local Similarity: 59.44% Mismatches: 57  
Query Match: 58.95% Indels: 10  
DB: 2 Gaps: 5  
US-10-692-367-70 (1-250) x US-08-456-240-37 (1-1079)  
Qy 3 GluAsnCySGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
Db 93 CAAAACTGCGGTTCGCTCAAACTCTGTTCAGTCAGTTCGCTTACTGGGTACCGAC 152  
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
Db 153 GATGCATACCTGCGGTGTGGATGCCGATCAGGTCTTTGTAGA-----GGTAGTGAACC 206  
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyIle 62  
Db 207 CCGACCGGAGG-----TCGGTCGGTAGCATTTGACACAAAGGTTTCTTTACATATT 260  
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
Db 261 ATCAACCAAGCTGGTAATGTTGCGCGGGAAGATTCTACCCCGTACTCTTCGTT 320  
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102  
Db 321 AACGCCGCTAATCTTTCCCACTTTGCCAATTCCTGTACC-----AGAGGT 368  
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
Db 369 GAAATTGCTACCATGTTTGTCTCATTTCACTCACGAGACCGACATTTCTGCTACATAGAA 428  
Qy 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTTPProCysAla 141  
Db 429 GAGATTAAACGAGAGCAACAGTAATCTGTCAGAGCAGCAACACACATATCCCATGTGCA 488  
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTTPAsnTyrAsnTyrGly 161  
Db 489 CCGGAAAAGGCTACTTTCGTTCCGATCCCACTATCATCATGTAAGTCACTCACTCGGA 548  
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181

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Db 549 CGGTGTGCTCAAGTCTCGGTCTGACCTTACGCCAGCCGCACTTGTGGTAGCAAC 608
Qy 182 AlaValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
Db 609 CCAACTGTAGCTTTCAGGTGCGGTTTGTGTTTGGATGAATAGGTAAGCGCGGTTCTG 668
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
Db 669 AACCAAGGGTTTGGAGCCACCATTAGAGCTATTATGGA---ATGGAATGTAAACGGTGT 725
Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 726 AATCCGGTGCAGTCAACGACGAGGATTGGATGACTATAGACTATTGTGGACAGCTTGGT 785
Qy 242 ValAspProGlyProAsnLeuThrCys 250
Db 786 GTGGACCTGCTTAACTTAGTTGC 812

RESULT 14
US-08-455-736-37
; Sequence 37, Application US/08455736
; Patent No. 5880328
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESS: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,736
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-1994
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
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; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-455-736-37

Alignment Scores:
Pred. No.: 4.84e-81 Length: 1079
Score: 830.00 Matches: 148
Percent Similarity: 73.09% Conservative: 34
Best Local Similarity: 59.44% Mismatches: 57
Query Match: 58.95% Indels: 10
DB: 2 Gaps: 5

US-10-692-367-70 (1-250) x US-08-455-736-37 (1-1079)
Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 93 CAAAACCTGCGGTTCGCTCCAAACCTCTGTTGCAGTCAGTTCGGTTACTGTGTACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 153 GATGCATACCTCGGTGTTGGATGCCGATCCAGTCTCTGTAGA-----GGTAGTGAACC 206
Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValThrGlySerPhePheAsnGlyIle 62
Db 207 CCGACCGGAGGG-----TCGGTCGTAGCATTTGACACACAGGTTCTTTTAAACATATT 260
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
Db 261 ATCAACCAAGCTGGTAAATGGTTGCGCGGGGAAAGATTCTACACCCGCTCTTTCGTT 320
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Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlySerGlnValGlnGlyLysArg 102
Db 321 AACGCCGCTAACTACTTCCCAACTTTCGCAATTCGTTACC-----AGACGT 368
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
Db 369 GAAATTGCTACCATGTTTGGCTCATTTCTACTCACGAGACCGGACATTTCTGCTACATAGAA 428
Qy 123 GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141
Db 429 GAGATTACGGAGCAACACGTAACCTACTGCCAGACGACGACACACATACCATGTCGA 488
Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly 161
Db 489 CCGGAAAAGGCTACTTCGGTGGTCCGATCCAACTATCATGGAACCTCAACTACGGA 548
Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp 181
Db 549 CGGTGGTCAAGTCTCGGTCTTGACCTTCTACGCCAGCCGAACTTGTGGTAGCAAC 608
Qy 182 AlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet 201
Db 609 CCAACTGTAGCTTTCAGTCGGTGTGGTTTGGATGGAATAGCGTAAGCCGCTTCG 668
Qy 202 ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn 221
Db 669 AACCAAGGGTTGGAGCCACCATTAGAGCTATTAAATGA---ATGGAATGTAACGGTGT 725
Qy 222 AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241
Db 726 AATTCGGTGCAGTCAACGCAAGGATTGGTACTATAGAGACTATTGTGGACAGCTTGT 785
Qy 242 ValAspProGlyProAsnLeuThrCys 250
Db 786 GTGACCCCTGCTCTTAACCTTAGTTGC 812

RESULT 15
US-08-971-217-37
; Sequence 37, Application US/08971217
; Patent No. 5942662
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Harms, Christian
; APPLICANT: Friedrich, Leslie
; APPLICANT: Beck, James
; APPLICANT: Uknes, Scott
; APPLICANT: Ward, Eric
; TITLE OF INVENTION: INDUCIBLE HERBICIDE RESISTANCE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5942662artis Corporation
; STREET: 3054 Cornwallis Road, P.O. Box 12257
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,217
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,364
; FILING DATE: 31-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/181,271
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,301
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; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV5/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-971-217-37

Alignment Scores:
Pred. No.: 4.84e-81 Length: 1079
Score: 830.00 Matches: 148
Percent Similarity: 73.09% Conservative: 34
Best Local Similarity: 59.44% Mismatches: 57
Query Match: 58.95% Indels: 10
DB: 2 Gaps: 5

US-10-692-367-70 (1-250) x US-08-971-217-37 (1-1079)
Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThr 22
Db 93 CAAAACCTGCGGTGGCTGCCAACCTCTGTTGCAGTCAGTTCGTTACTGTGTACCGAC 152
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 153 GATGCATACCTGCGGTGTTGGATGCCGATCAGTCTCTTTGTAGA-----GGTAGTGAACC 206
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43	Qy	SerGlyGlyGlyGlyAlaAsnValaIaSerValValThrGlySerPhePheAsnGlyIle	62
207	Db	CCGACCGGAGG-----TCGGTCGGTAGCATGTGCACACAAGGTTCTCTTTAACCAATATT	260
63	Qy	LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu	82
261	Db	ATCAACCAAGCTGGTAATGGTTGCGCGGGAAAAGATTCTACACCGGTGACCTCTTTCGTT	320
83	Qy	SerLavalValysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg	102
321	Db	AACGCGCGTAATACTTTCCCAACATTGCGCAATCTGTTTACC-----AGACGT	368
103	Qy	GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer	122
369	Db	GAATTTGCTACCATGTTTGTCTCATTTCTACTACGAGACCGACATTTCTGCTACATAGNA	428
123	Qy	GluIleSer---LysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla	141
429	Db	GAGATTAAACGGAGCAACACGTAACCTACTTCCAGAGCAGCAACACACAATACCCATGTGCA	488
142	Qy	AlaGlyGlnLysTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGly	161
489	Db	CCGGGAAAAGCGTACTTCGGTCGTGGTCGATCCAACTATCATATGAACACTACAACTACCGA	548
162	Qy	ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAsp	181
549	Db	CGGTGTGTCAAAGTCTCGGTCTTGACCTTCTACGCCAGCCGCAACTTGTGGGTAGCAAC	608
182	Qy	AlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMet	201
609	Db	CCAACTGTAGCTTTTCAGTCGGGTTTGTGGTTTTCGATGAATAGCGTAAGGCCGGTTCCTG	668
202	Qy	ProGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsn	221
669	Db	AACCAAGGGTTTGGAGCCACCATTAGAGCTATTAAATGGA---ATSGAATGTAAACCGTGGT	725
222	Qy	AsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly	241
726	Db	AATTCGGGTGCAGTCAACGCAAGGATTGGATACTATAGACTATTGTTCGACAGCTTGGT	785
242	Qy	ValAspProGlyProAsnLeuThrCys	250
786	Db	GTGACCCCTGGTCTTAACCTTAGTTGC	812

Search completed: May 23, 2005, 20:45:52  
Job time : 131.74 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2005, 17:04:03 ; Search time 2237.67 Seconds  
(without alignments)  
4252.663 Million cell updates/sec

Title: US-10-692-367-70

Perfect score: 1408

Sequence: 1 SMQNCQPNNVCCSKFQCG.....GYKQYCRQLGVDPGNLTC 250

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2 1/USPTO fastcap -SUPPIX=rat -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-DB=EST -OPMT=fastcap -SUPPIX=rat -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10692367 @CGN 1.1 3556 @runat 20052005 172255 20018 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gse1.\*  
9: gb\_gse2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1271.5	90.3	1179	3	AY103546 Zea mays
2	1237	87.9	855	4	BG837663
3	1166	82.8	737	6	CD435649
4	1161.5	82.5	958	4	BG837479
5	1160	82.4	767	7	C0524416
6	1099.5	78.1	837	7	CN133023
7	1062.5	75.5	710	6	CD443492
8	1016	72.2	647	6	CA197556
9	994	70.6	628	4	BM736454 952051A06

10	982	69.7	625	5	BM895383	BM895383	952073H05
11	980	69.6	978	9	CG328450	CG328450	OG3CW08TV
12	978	69.5	786	6	CA270202	CA270202	SCGSLB205
13	975	69.2	741	6	CD994869	CD994869	QBB18D07.
14	973	69.1	578	6	CD994156	CD994156	QBB13F07.
15	971	69.0	753	6	CD994885	CD994885	QBB18E05.
16	970	68.9	820	6	CD995497	CD995497	QBB25F07.
17	967	68.7	575	6	CD994132	CD994132	QBB13E04.
18	967	68.7	688	6	CA281399	CA281399	SCAGSD104
19	965	68.5	578	6	CD994454	CD994454	QBB15F08.
20	962	68.3	801	7	CN151443	CN151443	WOUNDI.75
21	960	68.2	812	7	CN132942	CN132942	OX1.9.D11
22	956.5	67.9	716	7	C0520138	C0520138	3530.1.13
23	954	67.8	856	6	CB981065	CB981065	CAB70003
24	954	67.8	870	6	CB982079	CB982079	CAB70005
25	954	67.8	895	6	CB981562	CB981562	CAB70004
26	953	67.7	887	6	CB981996	CB981996	CAB70005
27	953	67.7	893	6	CB980773	CB980773	CAB70003
28	953	67.7	904	6	CB981568	CB981568	CAB70004
29	953	67.7	920	6	CB981043	CB981043	CAB70003
30	952	67.6	861	6	CB980332	CB980332	CAB70002
31	952	67.6	889	6	CB982059	CB982059	CAB70005
32	951	67.5	889	6	CB980998	CB980998	CAB70003
33	950	67.5	880	7	CF200723	CF200723	RR890915N
34	948	67.3	850	6	CB980173	CB980173	CAB70002
35	948	67.3	874	7	CF200575	CF200575	RR89015N0
36	946	67.2	851	6	CB980181	CB980181	CAB70002
37	944	67.0	754	6	CD995176	CD995176	QBB20H11.
38	941	66.8	977	9	CG091347	CG091347	FUFQC18TB
39	940	66.8	845	6	CB981100	CB981100	CAB70003
40	940	66.8	855	6	CB980750	CB980750	CAB70003
41	939.5	66.7	618	2	BE918591	BE918591	OVL.8.G11
42	939	66.7	680	6	CA100718	CA100718	SCCCL700
43	935	66.4	550	6	CF001565	CF001565	QBS4f06.x
44	935	66.4	559	6	CD999920	CD999920	QBG10A02.
45	935	66.4	562	6	CF000010	CF000010	QBG11a02.

#### ALIGNMENTS

RESULT 1	AY103546	1179 bp	mRNA	linear	HTC	16-OCT-2002
LOCUS	AY103546	Zea mays	PC0155066	mRNA sequence.		
DEFINITION	AY103546					
ACCESSION	AY103546.1	GI:21206624				
VERSION	AY103546.1					
KEYWORDS	HTC.					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 1179)					
AUTHORS	Coe, E.H.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.					
FEATURES	Location/Qualifiers					
source	1..1179					
	/organism="Zea mays"					

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/mol_type="mRNA"
/db_xref="MaizeDB:638921"
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/cloned_lib="Maize Mapping Project/DuPont Cornsensus
Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN
Alignment Scores:
Pred. No.: 4,12e-120 Length: 1179
Score: 1271.50 Matches: 222
Percent Similarity: 92.16% Conservative: 13
Best Local Similarity: 87.06% Mismatches: 13
Query Match: 50.31% Indels: 7
DB: 3 Gaps: 1
US-10-692-367-70 (1-250) x AY103546 (1-1179)

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DB 149 CAGAACTCGCGCTGCGACCAAACTTCTGCTGCAGCAAGTTTCGGCTACTGCGGCACGACC 208
QY 23 AspGlnTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
DB 209 GACGCTACTCGCGGACGGGTGCGGCTGCGGCGGCTGCGGCGGCGGCGGCGGCGG 268
QY 43 SerGlyGly-----GlyGlyAlaAsnValAlaSerValValThr 55
DB 269 GCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 328
QY 56 GlySerPheAsnGlyLysValAsnGlnAlaGlySerGlyCysGlnGlyLysAsnPhe 75
DB 329 GACGCGTTCTTCAACGGCATCAAGAACAGCGCGGCGGCGGCGGCGGCGGCGGCGG 388
QY 76 TyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGly 95
DB 389 TACACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 448
QY 96 SerGlnValGlnGlyLysArgGlnLeuAlaPheAlaHisAlaThrHisGlyThr 115
DB 449 ACGGAGGTGGAGGCGGAGCGGAGATCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 508
QY 116 GlyHisPheCysTyrLysSerGlnLysSerLysSerAsnAlaTyrCysAspProThrLys 135
DB 509 GGACATTTCTCTATCATCAGCGGAGATCAACAGAGCAACGCGCTACTGCGGCGGCAAC 568
QY 136 ArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnLys 155
DB 569 AGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 628
QY 156 TrpAsnTyrAsnTyrGlyProAlaGlyArgAspLysGlyPheAspGlyLeuGlyAspPro 175
DB 629 TGGAACTACAACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 688
QY 176 GlyArgValAlaArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTrpMetAsn 195
DB 689 AACAGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 748
QY 196 AsnValHisArgValMetProGlnGlyPheGlyAlaThrLysArgAlaLysGlyVal 215
DB 749 AACGTGCACCGGTGTATGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 808
QY 216 LeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgLysGlyTyrLysGln 235
DB 809 CTCGAGTGCAACGGGAACAACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 868
QY 236 TyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250

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Db 869 TACTGCCAGCAGCTCCGCGTGCAGCCAGCGGCCCAACCTCACTTGC 913
RESULT 2
LOCUS BG837663/c
DEFINITION Zm10_01e10 A Zm10_AAPC_ECORC_Fusarium_graminearum_corn_silk Zea
ACCESION BG837663
VERSION BG837663.1 GI:14203986
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 855)
Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Maize Silk Six Hours After Silk
Channel Inoculation with Fusarium graminearum
Unpublished (2001)
Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harris@agr.gc.ca.
Location/Qualifiers
1. 855
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="CO388"
/db_xref="taxon:4577"
/clone="Zm10_01e10"
/tissue type="Silk"
/dev stage="4-5 days post-silk emergence"
/clone_lib="Zm10_AAPC_ECORC_Fusarium_graminearum_corn_silk"
/notes="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
Site 2: XhoI; Field-grown corn was silk channel-inoculated
in the morning (-10 am) with 1 ml of a macroconidial
suspension (500,000 spores/ml) of Fusarium graminearum and
silk channels were collected and immediately frozen in
liquid nitrogen 6 hours later. RNA was extracted from
silk tissue between 1 cm below and above the inoculation
point in the silk channel, RNA from five silk channels was
pooled."
ORIGIN
Alignment Scores:
Pred. No.: 9,49e-117 Length: 855
Score: 1237.00 Matches: 228
Percent Similarity: 97.50% Conservative: 6
Best Local Similarity: 95.00% Mismatches: 6
Query Match: 87.86% Indels: 2
DB: 4 Gaps: 0
US-10-692-367-70 (1-250) x BG837663 (1-855)
QY 11 ValCysCysSerLysPheGlyTyrCysGlyThrThrAspGlnTyrCysGlyCys 30
DB 854 GTATGCTGCAGCAAGTTTGGCTACTGCGGCACGACCGAGTACTGCGGCGGCGGTC 795
QY 31 GlnSerGlyProCysArgSerGlyGlyGlySerSerGlyGlyGlyAlaAsnVal 50
DB 794 CAGTCGGGCGCGTC-CGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGTCG 736
QY 51 AlasSerValValThrGlySerPheAsnGlyLysGlnAlaGlySerGlyCys 70
DB 735 GCTAGCGTCGTCACCGCGCTCTCTTCTTCAACGGCATCAAGAGCGGCGGCGGTCG 676

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Qy 71 GluGlyLysAsnPheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGly 90
Db 675 GAGGGCAAGAACTTCTACACCGGAGCGGTCTCTGAGCGCGTCAAGCGGTACCCAG- 617
Qy 91 PheAlaHisGlyGlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHis 110
Db 616 TTCGCCCATGCGGGTTCAGGTGAGGCAAGCGGAGATCGCGCTCTTTCGCGCAC 557
Qy 111 AlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSerLysSerAsnAlaTyr 130
Db 556 GCCACGCACGAGACCGGGCAATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCCTAC 497
Qy 131 CysAspProThrLysArgGlnTyrProCysAlaAlaGlyGlnLysTyrTyrGlyArgGly 150
Db 496 TGCACACCGACCAAGAGCGAGTGGCGGTGCGCGCGGCGGAGATCTACGCGCGCGGC 437
Qy 151 ProLeuGlnIleSerTyrAsnTyrAsnTyrGlyProAlaGlyArgAspIleGlyPheAsp 170
Db 436 CCGCTGCAGATCTCTGTGGAACTACAACTACGCGCGCGGAGGGCCATCGGCTTCGAC 377
Qy 171 GlyLeuGlyAspProGlyArgValAlaAlaArgAspAlaValAlaPheLysAlaAlaLeu 190
Db 376 GGGCTCGGGGACCCCGCGCAGCGTGGCGGACCGGTGGTGGCGTTCAAGCGCGCGCTC 317
Qy 191 TrpPheTrpMetAsnValHisArgValMetProGlnGlyPheGlyAlaThrIleArg 210
Db 316 TGGTCTTGATGAACAGCGTGCAGGGTGGTGGCGCAGGGGTTTCGGCGCCACCCAGG 257
Qy 211 AlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsnAlaArgIle 230
Db 256 GCCATCAACGGCGCCCTCAGTGGCGGGGAACAAACCCCGCCAGATGAACGGCGCGTC 197
Qy 231 GlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGlyProAsnLeuThrCys 250
Db 196 GGCTACTACAGCAGTACTGCGCGCAGCTCGCGCTCGACCCCGCGGCCCAACCTCACCTGC 137

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RESULT 3
CD435649
LOCUS EL01N0364B04.b EndospERM_3 Zea mays cDNA, mRNA linear EST 03-JUN-2003
DEFINITION CD435649
ACCESSION CD435649
VERSION CD435649.1 GI:31351292
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

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REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
Larkins, B., Beecraft, P. and Messing, J.
Characterization of the maize endospERM transcriptome and its
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Wakeman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakeman.rutgers.edu
Seq primer: T3.
Location/Qualifiers
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## ORIGIN

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Alignment Scores:
Pred. No.: 1.59e-109 Length: 737
Score: 1166.00 Matches: 211
Percent Similarity: 95.96% Conservative: 3
Best Local Similarity: 94.62% Mismatches: 4
Query Match: 82.81% Indels: 5
DB: 6 Gaps: 1

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US-10-692-367-70 (1-250) x CD435649 (1-737)

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Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 83 CAGAACTCGCGCTGCCAGCAACAGCTCTGCTGCAAGATTCGGCTACTCTGGGACAGACC 142
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 143 GACGAGTACTGCGCGCAGCGGTGCCAGTTCGGGCCGCTCGCGCTCGGGCGGC----- 193
Qy 43 SerGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGlyIle 62
Db 194 ---GGCGCGGTGGTGGCAACAGTGGCTAGCGTCTCACCGCTCTCTTCTTCAACGGCATC 250
Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysPheTyrThrArgSerAlaPheLeu 82
Db 251 AAGAACGAGCGCGGAGCGGTGGCGGCAAGAACTTCTACACCCGAGGCGCTTCTCTG 310
Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 311 AGCGCGTCAAGGGTACCCAGGGTTCGCCCATCGCGGTTCGAGGTGCAGGGCAAGCGC 370
Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
Db 371 GAGATCGCGCTTCTTTCGGCGCAGCCACGACGAGACCGGGCATTTCTGCTACATCAGC 430
Qy 123 GluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAla 142
Db 431 GAGATCAACAAAGAGCAACGGCTTCTGCGACCCGCAAGAGGAGTGGCGCTCGCGCGC 490
Qy 143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGlyPro 162
Db 491 GGGCAGAGTACTACGCGCGCGCGCGCGCTGCGAGATCTCGTGAACATCACTACGGGCC 550
Qy 163 AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAspAla 182
Db 551 GCGGGAGGGCCATCGCGCTTCAGCGGTTCGGGACCCCGCGAGGTGGCGCGGAGCGCC 610
Qy 183 ValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHis-ArgValMetPr 202
Db 611 GTGGTGGCGTTCAGAGGCGCGCTCTGGTTCCTGGATGAACAGCGTGCACGGGGTGGTGC 670
Qy 202 oGlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyValAlaLeuGluCysAspGlyAsnAs 222
Db 671 CGAGGGTTCGGCGCCACCCAGCGGCATCAACGGCGCCCTTCGAGTGGCGGGGACAA 730
Qy 222 nProAla 224
Db 731 CCGCGCC 737

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RESULT 4
BG837479
LOCUS Zm10_10h09_A Zm10 AAFC ECORC_Fusarium_graminearum_corn_silk Zea
DEFINITION BG837479
ACCESSION BG837479
VERSION BG837479.1 GI:14203802
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

```



mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
Pred. No.: 6.96e-109 Length: 767  
Score: 1160.00 Matches: 206  
Percent Similarity: 98.5% Conservative: 4  
Best Local Similarity: 96.71% Mismatches: 3  
Query Match: 82.39% Indels: 0  
DB: 7 Gaps: 0

US-10-692-367-70 (1-250) x C0524416 (1-767)

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Db 127 CAGAACTCGCGCTGCCAGCCAAACGATGCTGCAGCAGATTGGCTACTCGGCACAGCC 186

Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 187 GACGAGTACTCGCGCGACGGGTGCGAGTCGCGCGCGCTGCGCGCGCGCGCGCGCAGC 246

Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPheAsnGlyTle 62
Db 247 AGTGGCGCGGTGGTGGCAACGTGGCTAGCGTCTGTCACCGGCTCCTCTTCAACGGCATC 306

Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82
Db 307 AAGAGCCAGCGCGGAGCGGTGGAGGGGCAAGAACTTCTACCCCGAGCGCGTCTCTG 366

Qy 83 SerAlaValIysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArg 102
Db 367 AGCGCGGTCAAGCGGTACCCAGGCTTCGCCCATCGCGGTTCGAGGTGACGGGCAAGCGC 426

Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122
Db 427 GAGATCGCGCGCTCTTTCGCGCAGCGCCACGACGAGACCGGGCATTTCTGCTACATCAGC 486

Qy 123 GluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAla 142
Db 487 GAGATCAACAGAGCAACGCTTACTGCGACCGCGACCAAGAGCGAGTGGCGCGCGCGC 546

Qy 143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGlyPro 162
Db 547 GGGCAGAGTACTACGGCGCGCGCGCGCTGCGAGATCTCTGTGGAACCTACACTACGGGCC 606

Qy 163 AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAla 182
Db 607 GCGGGGAGGGCCATCGCGGTTCGACGGGTTCGCGGGACCCCGCGAGCGGTGGCGGGACGCC 666

Qy 183 ValValAlaPheLysAlaAlaLeuTyrPheTyrMetAsnValHisArgValMetPro 202
Db 667 GTGTGGCGGCTTCAAGCGCGCGCTCTGGTTCTGGATGAACAGCGTGACGGGGTGTGCGCG 726
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Qy 203 GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAla 215
Db 727 CAGGGGTTCCGGCGCCACCACCGCGCCATCAACGGCGCC 765
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## RESULT 6

LOCUS CN133023 837 bp mRNA linear EST 01-APR-2004  
DEFINITION OX1\_9\_D11.g1\_A002 Oxidatively-stressed leaves and roots Sorghum  
bicolor cDNA clone OX1\_9\_D11\_A002 5', mRNA sequence.

## ACCESSION

CN133023

## VERSION

CN133023.1

## KEYWORDS

EST

## SOURCE

Sorghum bicolor (sorghum)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.

## REFERENCE

1 (bases 1 to 837)

## AUTHORS

Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,  
Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.

## TITLE

An EST database from Sorghum: oxidatively stressed leaves and roots

## JOURNAL

Unpublished (2003)

## COMMENT

Other ESTs: OX1\_9\_D11.b1.A002

Contact: Cordonnier-Pratt, M.M.

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo Institute of Medical

Science; plant material and RNA prepared at Texas A &amp; M University;

sequencing done in the Laboratory for Genomics and Bioinformatics,

University of Georgia. Sequence ends have been trimmed to exclude

vector and regions below Phred quality 16. Three-prime sequences

are presented as their reverse complement and have been trimmed to

exclude polyA.

Seq primer: Sug5 (CTTCGTCTTAAAGCTCGC).

## FEATURES

Location/Qualifiers

1..837

/organism="Sorghum bicolor"

/mol\_type="mRNA"

/cultivar="BTx623"

/db\_xref="taxon:4558"

/Clones="OX1\_9\_D11\_A002"

/lab\_host="DH10B-T1 phage-resistant E. coli"

/clone\_lib="Oxidatively-stressed leaves and roots"

/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site 1:

XhoI; Site 2: XhoI; The library was prepared from polyA+

RNA from oxidatively stressed, hydroponically grown

sorghum seedlings. At 8 days of age, growth medium was

supplemented with hydrogen peroxide to 0.003% and leaves

were misted with 10 uM methyl viologen. Leaves and roots

were harvested at 3, 12 and 27 hr after treatment and all

tissue pooled. Double-stranded cDNA was cloned

unidirectionally into different DraIII sites of the

pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,

3-prime DraIII site is CACCATGTG). XhoI excises the cDNA

inert."

## ORIGIN

Alignment Scores:

Pred. No.: 1.33e-102 Length: 837

Score: 1099.50 Matches: 198

Percent Similarity: 87.45% Conservative: 11

Best Local Similarity: 82.85% Mismatches: 25

Query Match: 78.09% Indels: 5

DB: 7 Gaps: 2

US-10-692-367-70 (1-250) x CN133023 (1-837)



Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
 Db 134 CAGAACTACGGCTGCGCAGCAGGTTACTGCTGCAGCAAGTTTCGGTTACTGCGGCAGCAGC 193  
 Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42  
 Db 194 GACGAGTACTCGCGCAGCGGTGCGAGTTCGGGCCGCTCGCGCGCGCAGCAGT 253  
 Qy 43 SerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGlyTle 62  
 Db 254 -----GAGGTGGGAGAGTGGCTGGCTGTTCACCGACGCAATTTTCAACAGCATC 304  
 Qy 63 LysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeu 82  
 Db 305 AAGAACCGCGCGGAGCGGTGCGAGGCAAGAACTTCTACCGCGAGCGGTTCCTG 364  
 Qy 83 SerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyArg 102  
 Db 365 AGCGCGCGCGACGCGGTACAAAGGCTTC-----GGTGGCAGGTGCGTGCAGGGCAAGCGC 418  
 Qy 103 GluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSer 122  
 Db 419 GAGATCGCGCTTCTTCGCCACATCAGCAGCAGCGGACATTTCTGTACATCAGC 478  
 Qy 123 GluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAla 142  
 Db 479 GAGATCAACAAGAACCAAGCGCTACTGCGACTCGAGCAACAGCAGTGGCGCGTGC 538  
 Qy 143 GlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGlyPro 162  
 Db 539 GGTGAGAAAGTACTACGGCGCGCGCGCTGCAAAATCTCTGTGGAATCAACATCAGGCGCT 598  
 Qy 163 AlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaAspAla 182  
 Db 599 CGCGGGAGGACATCGGCTTTCAGCGGCTTCGGAACCGCGACAGGTGGCGCAAGACGCC 658  
 Qy 183 ValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetPro 202  
 Db 659 GTGGTCGGCTTCAAGACGCGCTCTGTGTTCTGGACCAACACGTCGACCGGGTGTATGTCG 718  
 Qy 203 GlnGlyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsn 222  
 Db 719 CAGGGTTCGGCGCCACCATCAGGCGCATCAACGCGCGCTCGAGTGTCAACCGCAAGAAAT 778  
 Qy 223 ProAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGly 241  
 Db 779 ACTGCCAGATGACCGCGGCTGGCTACTACAGGCACTACTGCCAGCAGCTCGGC 835

RESULT 7  
 CD443492 710 bp mRNA linear EST 03-JUN-2003  
 LOCUS EL01N0427B11.b Endosporm\_4 Zea mays cDNA, mRNA sequence.  
 DEFINITION CD443492  
 ACCESSION CD443492  
 VERSION CD443492.1 GI:31359135  
 KEYWORDS EST.  
 ORGANISM Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 710)  
 Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,  
 Larkins, B., Beckett, P. and Messing, J.  
 Characterization of the maize endosporm transcriptome and its  
 comparison to the rice genome  
 Genome Res. 14 (10), 1932-1937 (2004)  
 Contact: Lai, Jinsheng  
 Dr. Joachim Messing's lab  
 Wakeman Institute, Rutgers University  
 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA  
 Tel: 732-445-3801  
 Fax: 732-445-5735  
 Email: jlai@wakeman.rutgers.edu

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

# FEATURES

## source

Seq primer: T3.  
 Location/Qualifiers  
 1..710  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="W22"  
 /db\_xref="taxon:4577"  
 /tissue\_type="Endosporm of 7-23DAP"  
 /clone\_lib="Endosporm 4"  
 /note="Vector: pbluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI"

# ORIGIN

Alignment Scores:  
 Pred. No.: 6,87e-99 Length: 710  
 Score: 1062.50 Matches: 189  
 Percent Similarity: 97.95% Conservative: 2  
 Best Local Similarity: 96.92% Mismatches: 3  
 Query Match: 75.46% Indels: 1  
 DB: 6 Gaps: 1  
 US-10-692-367-70 (1-250) x CD443492 (1-710)  
 Qy 3 GlnAsnCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22  
 Db 126 CAGAACTACGGCTGCGCAGCAGGTTACTGCTGCAGCAAGTTTCGGTTACTGCGGCAGCAGC 185  
 Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSer---GlyGlyGlyGly 41  
 Db 186 GACGAGTACTGTCGCGAGCGGTGCGAGTCCAGTCCGCGCCGCTCGCGCGCGCGCGCGC 245  
 Qy 42 SerSerGlyGlyGlyGlyAlaAsnValAlaSerValValThrGlySerPhePheAsnGly 61  
 Db 246 GGCAGTGGTGGCGGTGGTGGCAACGTCGTAGCGTGTGTCACCGCTCTCTTCTTCAACGGC 305  
 Qy 62 IleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPhe 81  
 Db 306 ATCAAGAACCAAGCGCGGAGCGGTGCGAGGCAAGAACTTCTACACCGCGAGCGCGTTC 365  
 Qy 82 LeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLys 101  
 Db 366 CTGAGCGCGGTCAAGCGGTACCCAGGCTTCCGCCATGCGCGGTGCGAGTGCAGGGCAAG 425  
 Qy 102 ArgGluIleAlaAlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIle 121  
 Db 426 CGCGAGATCGCGCTTCTTCGCGCACGCCACGACGAGACCGGGCATTTCTGCTACATC 485  
 Qy 122 SerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCysAla 141  
 Db 486 AGCGAGATCAACAGACCAACGCTTACTGCGACCCGACCAAGAGGCAAGTGGCGCGCC 545  
 Qy 142 AlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGly 161  
 Db 546 CGCGGGCAGAAAGTACTACGGCGCGCGCGCTGCGAGTCTGCTGGAACACTACACTACGGG 605  
 Qy 162 ProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAsp 181  
 Db 606 CCGCGGGGAGGGGCATCGGCTTCAGCGGCTCGGGACCCCGGACAGGTGGCGCGCGGAC 665  
 Qy 182 AlaValAlaAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsn 196  
 Db 666 GCGGTGGTGGCTTCAAGCGCGCGCTCTGTTCTTGGATGAACAGC 710

# RESULT 8

LOCUS CAL197556 647 bp mRNA linear EST 25-SEP-2003  
 DEFINITION SCBFAD1067A11.g AD1 Saccharum officinarum cDNA clone SCBFAD1067A11  
 5', mRNA sequence.  
 ACCESSION CAL197556  
 VERSION CAL197556.1 GI:35227930  
 KEYWORDS EST.  
 SOURCE Saccharum officinarum  
 ORGANISM Saccharum officinarum



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Pred. No.: 6.59e-92 Length: 628
Score: 994.00 Matches: 179
Percent Similarity: 94.15% Conservative: 14
Best Local Similarity: 87.32% Mismatches: 12
Query Match: 70.60% Indels: 1
DB: 4 Gaps: 0

US-10-692-367-70 (1-250) x BM736454 (1-628)

Qy 46 GlyGlyAlaAenValAlaSerValThrGlySerPhePheAenGlyIleIysAenGln 65
Db 3 GGGCGGGGGAAGTGGTAAAGTGGC-AGCGACGGTGTCTTCAACGGCATCAAGAACCGAG 61
Qy 66 AlaGlySerGlyCysGluGlyLysAenPheTyrThrArgSerAlaPheLeuSerAlaVal 85
Db 62 GCGCGGAGGGTGGCGAGGCAAGAACTTCTACACCGGAGCGGTCTCTAGGCGCGTCTC 121
Qy 86 LysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArgGluIleAla 105
Db 122 AACAAAGTACCGGGGCTTCGCCATGGCGGAGCGAGGTGGAGGGCAAGCGCGAGATGCC 181
Qy 106 AlaPhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSer 125
Db 182 GCGTCTTTCGGCGCAGCTCACCGACGAGACCGGACATTTCTGCTACATCAGCGAGATCAAC 241
Qy 126 LysSerAenAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAlaGlyGlnLys 145
Db 242 AAGAGCAACGCTACTGCGAGCAAGCAAGGAGGAGTGGCGCGCGGGCGGAGAG 301
Qy 146 TyrTyrGlyArgGlyProLeuGlnIleSerTrpAenTyrAenTyrGlyProAlaGlyArg 165
Db 302 TACTACGGCGCGCGCGCTCGAGATCTCGTGAACACTACAACTACGGCGCGCGGGAGG 361
Qy 166 AspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAArgAspAlaValAla 185
Db 362 GACATCGCGCTCAACGGGCTCGCCACCCCAACAGGGGTGGCGAGGACCGCGTATCGCG 421
Qy 186 PheLysAlaAlaLeuTyrPheTrpMetAenAenValHisArgValMetProGlnGlyPhe 205
Db 422 TTCAAGCGCGCGCTCTGCTTCTGGATGAACAACTGACCGCTGTGATGCCGCGGGCTTC 481
Qy 206 GlyAlaThrIleArgAlaAlaAenGlyAlaLeuGlyCysAspGlyAenAenProAlaGln 225
Db 482 GCGCGCACCATCAGGGCCATCAACGGCGCGCTCGAGTCAACAGCGGAAACAAACCGCGCCAG 541
Qy 226 MetAenAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGly 245
Db 542 ATGAACGCGCGCTGCGCTACTTACAAGCAGTACTGCCAGCAGCTCCGCGTCGACCCAGGG 601
Qy 246 ProAenLeuThrCys 250
Db 602 CCCAACCTCACTTGC 616

RESULT 10
LOCUS BM895383
DEFINITION 952073H05.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
ACCESSION BM895383
VERSION BM895383.1 GI:19350851
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 625)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
JOURNAL
COMMENT Contact: Walbot V
Department of Biological Sciences
```

Stanford University  
855 California Ave., Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 952073 row: H column: 05.

FEATURES  
Location/Qualifiers  
1..625  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="BMS (Black Mexican Sweet)"  
/db\_xref="taxon:4577"  
/tissue\_type="suspension culture"  
/dev\_stage="mixed logarithmic and stationary growth phases"  
/lab\_host="DH10B"  
/clone\_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"  
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

## ORIGIN

Alignment Scores:  
Pred. No.: 1.13e-90 Length: 625  
Score: 982.00 Matches: 178  
Percent Similarity: 91.04% Conservative: 15  
Best Local Similarity: 83.96% Mismatches: 13  
Query Match: 69.74% Indels: 7  
DB: 5 Gaps: 1

US-10-692-367-70 (1-250) x BM895383 (1-625)

Qy 35 CysArgSerGlyGlyGlySerSerGlyGlyGlyAlaAenValAlaSerValVal 54  
Db 7 TGTGCG-----GGAGGCGAGTGGCGGTGCGAACGTGGCTTAACGG-GTC 47  
Qy 55 ThrGlySerPheAenGlyIleLysAenGlnAlaGlySerGlyCysGluGlyLysAen 74  
Db 48 AGCAGCGGTCTTCAACGGCATCAGAACAGCCGGAGCGGGTGGAGGGCAAGAAC 107  
Qy 75 PheTyrThrArgSerAlaPheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGly 94  
Db 108 TTCTACACCGGAGCGGTCTCTGAGCGCGCTCAACAAGTACCGGGCTTCGCCCATGGC 167  
Qy 95 GlySerGlnValGlnGlyLysArgGluIleAlaAlaPhePheAlaHisAlaThrHisGlu 114  
Db 168 GGGACGGAGGTGGAGGCAAGCGGAGATCGCCGCTTCTTCGGCGCACGTCAACCGAG 227  
Qy 115 ThrGlyHisPheCysTyrIleSerGluIleSerLysSerAenAlaTyrCysAspProThr 134  
Db 228 ACCGACATTTCTGCTACATCAGCGAGATCAACAGAGCAACGCTACTCGCGAGCGCAGC 287  
Qy 135 LysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyrGlyArgGlyProLeuGlnIle 154  
Db 288 AACAGGCGAGTGGCGTGGCGGGGCGGAGAGTACTACGGGCGCGCGCTCGCAGATC 347  
Qy 155 SerTrpAenTyrAenTyrGlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAsp 174  
Db 348 TCGTGAACATCACTACGGCGCGCGGGAGGAGACATCGGCTTCAACGGGCTCGCGCAC 407  
Qy 175 ProGlyArgValAlaAArgAspAlaValAlaPheLysAlaAlaLeuTyrPheTrpMet 194  
Db 408 CCCAACAGGGTGGCGAGGACGGCGTATCGCGTTCAAGAGCGGCGCTCTGGTTCTGATG 467  
Qy 195 AenAenValHisArgValMetProGlnGlyPheGlyAlaThrIleArgAlaAlaAenGly 214

```

Db      468 AACACGTGACCGTCTGATCCGAGGCTTCGGCGCCACATCAGGCGCCATCAACGGC 527
Qy      215 AlalaLeuGluCyAspGlyAsnAsnProAlaGlnMetAsnAlaArgIleGlyTyrTyrTyr 234
Db      528 GCCCTCGAGTCAACGGGGAACACCCCGCCAGATGAAGCGCGCTACTACAAG 587
Qy      235 GlnTyrCysArgGlnLeuGlyValAspProGlyPro 246
Db      588 CAGTACTGCCAGCAGCTCCGCGTCGACCCAGGGGCC 623

RESULT 11
CG328450/1
LOCUS   CG328450/1
DEFINITION  CG328450/1 978 bp DNA linear GSS 26-AUG-2003
          genomic survey sequence.
ACCESSION  CG328450
VERSION    CG328450.1 GI:34245716
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
REFERENCE  1 (bases 1 to 978)
AUTHORS    Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
          Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
          Citek,R.W., Numburg,A., Robbins,D. and Lakey,N.
TITLE      Consortium for Maize Genomics
JOURNAL    Unpublished (2002)
COMMENT    Other GSSs: OG328450
          Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: 1P
          Class: sheared ends.
FEATURES   Location/Qualifiers
            1..978
               /organism="Zea mays"
               /mol_type="genomic DNA"
               /strain="B73"
               /db_xref="taxon:4577"
               /clone="ZMMBMA0778B15"
               /clone_lib="ZM 0.7 1.5 KB"
               /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
               methylation filtered genomic DNA library"
ORIGIN
Alignment Scores:
Pred. No.: 3.33e-90 Length: 978
Score: 980.00 Matches: 186
Percent Similarity: 79.92% Conservative: 13
Best Local Similarity: 74.70% Mismatches: 14
Query Match: 69.60% Indels: 37
DB: 9 Gaps: 1

US-10-692-367-70 (1-250) x CG328450 (1-978)

Qy      38 GlyGlyGlySerSerGlyGlyGlyAlaAlaValAlaSerValValThrGlySer 57
Db      952 GCGCGCGGAGCGCGGAGCGAGTGGCGGTGCGAAGCGTGGCTAATGT-GTCAACCGACGC 894
Qy      58 PhePheAsnGlyIleLeuAsnGlnAlaGlySerGlyCysGluGlyLeuAsnPheTyrThr 77
Db      893 TTCTTCAACCGCATCAAGAACCGAGCGCGGTGCGGAGCGGCAAGAACTTCTACACC 834
Qy      78 Arg-SerAlaPheLeuSerAlaValLeuAlaTyr-ProGlyPheAlaHisGlyGlySerG1 97
Db      833 CGAGAGCGGCTTCTGAGCGCGGTCAACGCGTACCCGGGCTTCGCCCATCGCGGACGGA 774
```

```

Qy      97 nValGlnGlySerArgGluIleAlaPhePheAlaHisAlaThrHisGluThrGly-- 116
Db      773 GGTGGAGGGCAAGCGCGAGATCGCGCTTTCTTCGCGCACGTCAACGACGAGACCGGACG 714
Qy      116 -----
Db      713 TAAGTTATTAAACACCTTAACCTAACACACGGAACCTAGCATGCAGGACCTTTGATCTGACC 654
Qy      117 -----His-PheCysTyrIleSerG 123
Db      653 GACCGATCATCGTCTCATGCTGACCATGCAATTTTTCGATCAGATTTCTGCTTACATCAGCG 594
Qy      123 luileSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTyrProCysAlaAlaAG 143
Db      593 AGATCAACAAGAGACACGCTTACTGCGACGCGAGCAACAGCGAGTGGCGTGGCGCGCGG 534
Qy      143 lyGlnLysTyrTyrGlyArgGlyProLeuGlnIleSerTyrAsnTyrAsnTyrGlyProA 163
Db      533 GGCAGAGTACTACGGGCGCGCGCTGCGATCTCTGTGGAACCTACAACTACGCGGCGCG 474
Qy      163 laGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAspAlaV 183
Db      473 CCGGAGGAGCATCGGCTTCAACCGGCTCGCGACCCCAACAGCGGTGGCGGACGACGCG 414
Qy      183 alValAlaPheLeuAlaAlaLeuTyrPheTyrMetAsnAsnValHisArgValMetProG 203
Db      413 TGAATCGGCTTCAAGACGCGCGCTCTGGTCTGTGAGTGAACAGCTGACCGTGTGATCGCG 354
Qy      203 lnglyPheGlyAlaThrIleArgAlaIleAsnGlyAlaLeuGluCysAspGlyAsnAsnP 223
Db      353 AGGGCTTCGGCGCCACCATCAGGGCCATCAACGGCGCCCTCGAGTGAACGGGAACAACC 294
Qy      223 roAlaGlnMetAsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValA 243
Db      293 CCGCCAGATGAACGCGCGGTGCGTACTACAGCAGTACTGCGCAGCAGTCTCGCGCGTGC 234
Qy      243 spProGlyProAsnLeuThrCys 250
Db      233 ACCCAGGGGCCAACCTCACTTGC 211

RESULT 12
LOCUS   CA270202
DEFINITION  SCQSLB2051F10.g LB2 Saccharum officinarum cDNA clone SCQSLB2051F10
          5', mRNA sequence.
ACCESSION  CA270202
VERSION    CA270202.1 GI:35976513
KEYWORDS   EST.
SOURCE     Saccharum officinarum
ORGANISM   Saccharum officinarum
REFERENCE  1 (bases 1 to 786)
AUTHORS    Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE      The libraries that made SUCSER
JOURNAL    Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT    Contact: Arruda P
          Centro de Biologia Molecular e Engenharia Genetica
          Universidade Estadual de Campinas
          Caixa Postal 6010, 13083-970, Campinas SP, Brazil
          Tel: 55 19 3788 1137
          Fax: 55 19 3788 1089
          Email: parruda@unicamp.br
          Clone distribution: clone distribution information can be found
          through the Brazilian Clone Collection Center (BCCC) at
          http://www.bccccenter.fcav.unesp.br
          Plate: 051 row: F column: 10
          Seq primer: T7 Promoter Primer.
          Location/Qualifiers
            1..786
               /organism="Saccharum officinarum"
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/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCOSLB2051F10"
/lab_host="DH10B"
/clone_lib="Lb2"
/note="Organ: Lateral buds from plants adult plants
growing in greenhouse; Vector: pSort1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [lateral buds from plants adult plants growing in
greenhouse]. cDNA was prepared from polyA+ mRNA using
Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucet.lad.ic.unicamp.br/public"

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 3,97e-90 Length: 786
Score: 978.00 Matches: 182
Percent Similarity: 86.34% Conservatives: 14
Best Local Similarity: 80.18% Mismatches: 23
Query Match: 69.46% Indels: 8
DB: 6 Gaps: 2

US-10-692-367-70 (1-250) x CA270202 (1-786)

Qy 3 GlnAenCysGlyCysGlnProAsnValCysCysSerLysPheGlyTyrCysGlyThrThr 22
Db 117 CAAAACTCGCGTGCACCAAACTACTGTCGACCAAGTTTCGGGTACTGCGGCACGACC 176
Qy 23 AspGluTyrCysGlyAspGlyCysGlnSerGlyProCysArgSerGlyGlyGlySer 42
Db 177 GACGACTACTGTGGGACGGGTGCGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 236
Qy 43 SerGlyGly-----GlyGlyAlaAsnValAlaSerValValThrGlySerPheAsn 60
Db 237 GCGGTGGCAGCAGTGGTGGTGGGAACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 296
Qy 61 GlyIleLysAsnGlnAlaGlySerGlyCysGluGlyLysAsnPheTyrThrArgSerAla 80
Db 297 GGCATCAAAACCCAGCGCGGACCGGTCGAGGCGGACCAAGTCTTCTACCCCGGAGTGG 356
Qy 81 PheLeuSerAlaValLysAlaTyrProGlyPheAlaHisGlyGlySerGlnValGlnGly 100
Db 357 TTCCTGACGCGCGGCGGACTCTGACAAAGGTTTC-----GGTGGCGGTCGTTGGAGGC 410
Qy 101 LysArgGluIleAlaAlaPheAlaHisAlaThrHisGluThrGlyHisPheCysTyr 120
Db 411 AAGCGGAGATCGCGGCTTCTTCGCGCACGTCTACGACGACGACGACGACGACGACGAC 470
Qy 121 IleSerGluIleSerLysSerAsnAlaTyrCysAspProThrLysArgGlnTrpProCys 140
Db 471 ATCAGCGAAATCAACAAGAACAGCCCTACTGCGACTCTGAGCAACAGCAGTGGCGGTC 530
Qy 141 AlaAlaGlyLysLysTyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyr 160
Db 531 CCGCGGACAGAGTACTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 590
Qy 161 GlyProAlaGlyArgAspIleGlyPheAspGlyLeuGlyAspProGlyArgValAlaArg 180
Db 591 GGGCTGCGCGGAGGAGACATCGGCTTCAACGGGCTCGGGAACCCCGACAGGTTGGCGCAG 650
Qy 181 AspAlaValValAlaPheLysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgVal 200
Db 651 GACGCGGTGATCGCGTTCACAGACGCGGCTCTGGTCTTGTGATGAACAACTTGCACCGGTG 710
Qy 201 -MetProGlnGlyPheGlyAlaThr-ileArgAlaIle-AsnGlyAla-LeuGluCysAs 219
Db 711 AATGTCNCGGGTTCGACCCACCCATTCAGGCTATTAAACGGAACCCCTCGAGTGCAA 770
Qy 219 pGlyAsnAsnPro 223

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Db 771 AGGAAACCAACCC 783

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## RESULT 13

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CD994869
LOCUS QBB18407.xg QBB Zea mays cDNA clone QBB18407, mRNA sequence.
DEFINITION CD994869
ACCESSION CD994869
VERSION CD994869.1 GI:32855108
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

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```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 741)

```

## REFERENCE

```

AUTHORS Genoplatte.
TITLE Genoplatte, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com
and http://genoplatte-info.infobiogen.fr).

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## FEATURES

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location/Qualifiers
source
1..741
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QBB18407"
/tissue_type="embryo"
/clone_lib="QBB"

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## ORIGIN

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Alignment Scores:
Pred. No.: 7,47e-90 Length: 741
Score: 975.00 Matches: 173
Percent Similarity: 97.81% Conservatives: 6
Best Local Similarity: 94.54% Mismatches: 4
Query Match: 69.25% Indels: 0
DB: 6 Gaps: 0

US-10-692-367-70 (1-250) x CD994869 (1-741)

Qy 68 SerGlyCysGluGlyLysAsnPheTyrThrArgSerAlaPheLeuSerAlaValLysAla 87
Db 1 AGCGGGTTCGAGGGCAAGAACTTCTACACCGGAGCGCGTTCCTGAGCGCGTCAAGCG 60
Qy 88 TyrProGlyPheAlaHisGlySerGlnValGlnGlyLysArgGluIleAlaAlaPhe 107
Db 61 TACCCAGGCTTCGCCCAACGCGGGTTCGAGGTGCGAGGCAAGCGCGAGATCGCGCTTC 120
Qy 108 PheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSerLysSer 127
Db 121 TTCGCGCACCCACGACGACGAGACCGGGCATTTCTGTACTACGACGAGATCAACAGAGC 180
Qy 128 AsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyr 147
Db 181 AACGCTTACTGCGACCCGACGAGGAGGACGTGGCGGTGCGCTGCGGGGAGAGTACTAC 240
Qy 148 GlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIle 167
Db 241 GGGCGCGCGCGCTGCGAGATCTCGTGGAACTACAACTACGCGCGCGGAGGCGCATC 300
Qy 168 GlyPheAspGlyLeuGlyAspProGlyArgValAlaAlaArgAspAlaValAlaPheLys 187
Db 301 GGCTTCACCGGCTTCGGGGACCCCGGAGGAGGTGGCGGAGGACCGCGTGTGGCTTCAG 360
Qy 188 AlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPheGlyAla 207

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Db      361 GGGGCGCTCTGGTTCGTGATGACAGCGTGCACGGGGTGGTCCCGCAGGGGTTCGGCGCC 420
Qy      208 ThrileArgAlaileAsnGlyValaleuGluCysAspGlyAsnAsnProAlaGlnMetAsn 227
Db      421 ACCACAGGGCCATCAACGGCGCCCTCGAGTGGCGGGGAACAACCCCGCCAGATGAAC 480
Qy      228 AlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGlyProAsn 247
Db      481 GCGCGCTGGCTACTACAGGCGAGTACTGCGCGCAGCTCGGGTGCAGCCCGGGGCCAAC 540
Qy      248 LeuThrCys 250
Db      541 CTCACCTGC 549

RESULT 14
LOCUS   CD994156 578 bp mRNA linear EST 16-JUL-2003
DEFINITION QBB13f07.xg QBB Zea mays cDNA clone QBB13f07, mRNA sequence.
ACCESSION CD994156
VERSION CD994156.1 GI:32854475
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 578)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..578
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QBB13f07"
/tissue_type="embryo"
/clone_lib="QBB"

ORIGIN
Alignment Scores:
Pred. No.: 8,55e-90 Length: 578
Score: 973.00 Matches: 172
Percent Similarity: 97.28% Conservative: 7
Best Local Similarity: 93.48% Mismatches: 5
Query Match: 69.11% Indels: 0
DB: 6 Gaps: 0

US-10-692-367-70 (1-250) x CD994156 (1-578)

Qy      67 GlySerGlyCysGluGlyValAsnPheTyrThrArgSerAlaPheLeuSerAlaVallys 86
Db      1 GGGAGCGGGTCGAGGGGACAGAACTTCTACACCGGAGCGGTTCCTGAGCGCGTCAAG 60
Qy      87 AlaTyrProGlyPheAlaHisGlySerGlnValGlnGlyValArgGluIleAlaAla 106
Db      61 GGGTACCCAGAGCTTCGCCACGGCGGGTGCAGGTGAGGGGACGCGGAGATCGCCGCC 120
Qy      107 PhePheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSerlys 126
Db      121 TTCTTCGCGCAGCCACGACGAGACCGGCGATTTCTGTTCTTCAGCGAGATCAACAAG 180
Qy      127 SerAsnAlaTyrCysAspProThrIlyArgGlnTrpProCysAlaAlaGlyGlnIlyTyr 146

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Db      181 AGCAACGCCCTACTCGGACCCGACAGAGGCGATGGCGCTGCGCGCGGGCGAGAGTAC 240
Qy      147 TyrGlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAsp 166
Db      241 TAGCGGCGCGCGCTCGAGATCTCGTGGAACTACAACCTACGGGCGCGCGGAGGGGCC 300
Qy      167 IledglyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValAlaPhe 186
Db      301 ATCGGCTTCGACGGGCTCGGGGACCCGCGAGGGTGGCGGGACGCGCGTGGTGGCGTTC 360
Qy      187 LysAlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPheGly 206
Db      361 AAGCGGCGCTCTGTTCTGATGACAGCGTGCACGGGGTGGTGGCCGACGGGGTTCGGC 420
Qy      207 AlaThrIleArgAlaIleAsnGlyValaleuGluCysAspGlyAsnAsnProAlaGlnMet 226
Db      421 GCCACCAACGAGGGCCATCAACGGCGCCCTCGAGTGGCGGGGAACAACCCCGCCAGATG 480
Qy      227 AsnAlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGlyPro 246
Db      481 AACGCGCGCTCGGCTACTACAGGCGAGTACTGCGCGCAGCTCGGGCTCGAGCCCGGGGCC 540
Qy      247 AsnLeuThrCys 250
Db      541 AACCTCACCTGC 552

RESULT 15
LOCUS   CD994885 753 bp mRNA linear EST 16-JUL-2003
DEFINITION QBB18e05.xg QBB Zea mays cDNA clone QBB18e05, mRNA sequence.
ACCESSION CD994885
VERSION CD994885.1 GI:32855204
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 753)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
Location/Qualifiers
1..753
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QBB18e05"
/tissue_type="embryo"
/clone_lib="QBB"

ORIGIN
Alignment Scores:
Pred. No.: 1.97e-89 Length: 753
Score: 971.00 Matches: 172
Percent Similarity: 97.27% Conservative: 6
Best Local Similarity: 93.99% Mismatches: 5
Query Match: 68.96% Indels: 0
DB: 6 Gaps: 0

US-10-692-367-70 (1-250) x CD994885 (1-753)

Qy      68 SerGlyCysGluGlyValAsnPheTyrThrArgSerAlaPheLeuSerAlaVallysAla 87

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Db 1 AGCGGGTCGAGGGCAAGAACTTCTACACCGGAGCGGTTCTCAGCGCGGTCGAAGGCG 60
Qy 88 TyrProGlyPheAlaHisGlyGlySerGlnValGlnGlyLysArgGluIleAlaAlaPhe 107
Db 61 TACCCAGGCTTCGCCACGCGGGTCGAGGTCAGGGCAAGCGGAGATCGCGCCCTTC 120
Qy 108 PheAlaHisAlaThrHisGluThrGlyHisPheCysTyrIleSerGluIleSerLysSer 127
Db 121 TTGCGCAGCCACGACGACGAGACCGGGCATTTCTGCTACTTCAGCGAGATCAACAAGAGC 180
Qy 128 AsnAlaTyrCysAspProThrLysArgGlnTrpProCysAlaAlaGlyGlnLysTyrTyr 147
Db 181 AACGCCTACTGCGACCCGAGCAAGAGGAGTGGCGGTGCGCGGGCGAGAACTACTAC 240
Qy 148 GlyArgGlyProLeuGlnIleSerTrpAsnTyrAsnTyrGlyProAlaGlyArgAspIle 167
Db 241 GGGCGGCGCCGCTCGAGATCTCGTGGAACTACAACTACGGGCGCGGGGAGGGCCATC 300
Qy 168 GlyPheAspGlyLeuGlyAspProGlyArgValAlaArgAspAlaValAlaPheLys 187
Db 301 GGCCTTCGACGGGCTCGGGGACCCCGGACAGGTGGCGCGGACGCGCGTGTGGCGTTCAAG 360
Qy 188 AlaAlaLeuTrpPheTrpMetAsnAsnValHisArgValMetProGlnGlyPheGlyAla 207
Db 361 GCGGCGCTCTGGTTCTGGATGAACACAGCGTGCACGGGGTGGTCCCGCAGGGGTTCGGCGCC 420
Qy 208 ThrIleArgAlaIleAsnGlyValAlaLeuGluCysAspGlyAsnAsnProAlaGlnMetAsn 227
Db 421 ACCACGAGGCCATCAGCGGCCCTCGAGTGGCGGGGAAACCCCGCCAGATGAAC 480
Qy 228 AlaArgIleGlyTyrTyrLysGlnTyrCysArgGlnLeuGlyValAspProGlyProAsn 247
Db 481 GCGGCGTTCGGTACTACAGGCAGTACTGCGCCAGCTCGGGCTCGACCCCGGGCCCAAC 540
Qy 248 LeuThrCys 250
Db 541 CTCACCTGC 549
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